

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 15, 2004, 13:55:24 ; Search time 97 Seconds
(without alignments)
1842.208 Million cell updates/sec

Title: US-10-079-111-1
Perfect score: 1657
Sequence: 1 MARCFSLVLLTTSIWTRLL.....NPESKSPSKTTVRCLEAEV 322

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Issued Patents NA -QPMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=Bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES			
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Result No.	Score	Query Match Length DB ID	Description
1	1657	100.0 2029 4	US-09-232-160-13 m.w Sequence 13, Appl
2	1657	100.0 2372 4	US-09-907-794A-200 Sequence 200, App
3	1657	100.0 2372 4	US-09-905-125A-200 Sequence 200, App
4	1657	100.0 2372 4	US-09-902-775A-200 Sequence 200, App
5	1657	100.0 2404 4	US-09-833-381-849 Sequence 849, App
6	1657	100.0 2404 4	US-09-833-381-853 Sequence 853, App
7	1651	99.6 2313 2	US-08-892-880-1 Sequence 1, Appli
8	1103	66.6 1896 4	US-09-724-864-28 Sequence 28, Appl
9	354	21.4 492 2	US-08-892-880-12 Sequence 12, Appl
10	349	21.1 466 2	US-08-892-880-13 Sequence 13, Appl
11	286.5	17.3 498 2	US-08-892-880-15 Sequence 15, Appl
12	234.5	14.2 1537 6	Patent No. 5504194-1

13	224	13.5	3207	1	US-07-946-497-1	Sequence 1, Appli
14	224	13.5	3207	1	US-08-483-322-1	Sequence 1, Appli
15	224	13.5	3207	2	US-08-478-882-1	Sequence 1, Appli
16	213	12.9	1794	3	US-09-213-719-1	Sequence 1, Appli
17	210	12.7	1297	4	US-09-023-655-876	Sequence 876, App
18	199.5	12.0	4675	4	US-09-566-921-97	Sequence 97, Appl
19	145	8.8	1414	1	US-08-024-868-1	Sequence 1, Appli
20	145	8.8	1414	2	US-08-242-097-1	Sequence 1, Appli
21	145	8.8	1414	3	US-09-206-695-1	Sequence 1, Appli
22	145	8.8	1414	4	US-09-799-118-1	Sequence 1, Appli
23	133.5	8.1	1734	4	US-09-484-970B-63	Sequence 63, Appl
24	128.5	7.8	3259	5	PCT-US95-03747-1	Sequence 1, Appli
25	127.5	7.7	1985	4	US-09-907-794A-212	Sequence 212, App
26	127.5	7.7	1985	4	US-09-905-125A-212	Sequence 212, App
27	127.5	7.7	1985	4	US-09-902-775A-212	Sequence 212, App
28	121	7.3	1587	4	US-09-010-147B-19	Sequence 19, Appl
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30	114.5	6.9	5191	5	PCT-US93-07306-1	Sequence 1, Appli
31	113	6.8	8224	6	5180808-1	Patent No. 5180808
32	112	6.8	1190	1	US-08-310-370-1	Sequence 1, Appli
33	111	6.7	1720	4	US-09-148-545-53	Sequence 53, Appl
34	107	6.5	1400	2	US-08-001-078A-2	Sequence 2, Appli
35	107	6.5	1400	2	US-08-463-218-2	Sequence 2, Appli
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37	107	6.5	1520	1	US-08-225-477B-1	Sequence 1, Appli
38	107	6.5	1520	5	PCT-US95-04353-1	Sequence 1, Appli
39	107	6.5	2589	1	US-08-325-267A-3	Sequence 3, Appli
40	107	6.5	2685	3	US-08-362-525-21	Sequence 21, Appl
41	107	6.5	4614	1	US-08-325-267A-1	Sequence 1, Appli
42	106.5	6.4	1482	4	US-09-016-434-230	Sequence 230, App
43	106.5	6.4	2455	3	US-09-103-429A-1	Sequence 1, Appli
44	106.5	6.4	2821	3	US-09-103-429A-2	Sequence 2, Appli
45	103	6.2	1519	1	US-08-225-477B-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-232-160-13
; Sequence 13, Application US/09232160
; Patent No. 6368794
; GENERAL INFORMATION:
; APPLICANT: Steve Daniel
; APPLICANT: James Gilmore
; APPLICANT: Susan G. Stuart
; APPLICANT: Laura Stuve
; TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: PA-0003 US
; CURRENT APPLICATION NUMBER: US/09/232,160
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 2029
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 3044710
US-09-232-160-13

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Pred. No.:	4.6e-177	Matches:	322
Score:	1657.00	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	100.00%	Gaps:	0
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QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

Db 243 GTCCAAGGCTCTTTGCGTGCAGAAAGCTTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 302

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Db 303 ATCACCTTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTTCACAGAAGCTAAGGAGGCC 362

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Db 363 TGTAGGCTGCTGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 422

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

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QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

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QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

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Db 783 TGTGTACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 842

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240

Db 843 GAAATAAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 902

QY 241 LeuValLeuAlaLeuLeuphePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260

Db 903 CTAGTGCTTGCTCTCTCTTCTTTGGTGTGCTGAGCTGGTCTTGGATTTTGCTATGTCAA 962

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RESULT 2

US-09-907-794A-200
; Sequence 200, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi

Alignment Scores:

Pred. No.: 5,92e-177 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0

US-09-907-794A-200

TYPE: DNA

LENGTH: 2372

SEQ ID NO 200

NUMBER OF SEQ ID NOS: 423

PRIOR FILING DATE: 2000-01-05

PRIOR FILING DATE: 1999-12-20

PRIOR FILING DATE: 1999-12-20

PRIOR FILING DATE: 1999-12-20

PRIOR FILING DATE: 1999-12-20

PRIOR FILING DATE: 1999-12-20

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PRIOR FILING DATE: 1999-12-20

PRIOR FILING DATE: 1999-12-20

PRIOR FILING DATE: 1999-12-20

FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/907,794A

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2001-07-17

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR FILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: PCT/US99/28214

PRIOR FILING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR FILING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: PCT/US99/30911

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US99/30999

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US00/00219

PRIOR FILING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William, I.

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Mather, Jennie P.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Hillan, Kenneth, J.

APPLICANT: Gurney, Austin L.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Goddard, A.

APPLICANT: Gerritsen, Mary E.

APPLICANT: Gerber, Hanspeter

APPLICANT: Gao, Wei-Qiang

APPLICANT: Fong, Sherman

APPLICANT: Filvaroff, Ellen

APPLICANT: Ferrara, Napoleone

APPLICANT: Eaton, Dan L.

APPLICANT: Desnoyers, Luc

APPLICANT: Botstein, David

Best Local Similarity: 100.00%		Mismatches: 0
Query Match: 100.00%		Indels: 0
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QY	61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80	
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QY	81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100	
Db	400 AGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGGATTCGTGGTCTATCTTAGGATT 459	
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QY	121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140	
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QY	161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180	
Db	640 GAATTTATTGTGACGTACAGTACCTACTCGTGGTGGCATCCCTTACTTACAATACCTGCC 699	
QY	181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200	
Db	700 CCTACTACTACTCCTCCTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759	
QY	201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220	
Db	760 TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819	
QY	221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240	
Db	820 GAAATATAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCACGGCTCTG 879	
QY	241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260	
Db	880 CTAGTGCTTGCTCTCCTCTTCTTTGGTGTGCTGAGTGGTCTTGGATTTTGTATGTCAA 939	
QY	261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280	
Db	940 AGGTATGTGAAGCCTTCCCTTTTACAAACCAAGATCAGCAGAGGAAATGATCGAAACC 999	
QY	281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300	
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RESULT 3
US-09-905-125A-200
; Sequence 200, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
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; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-905-125A-200

Alignment Scores:
  5.92e-177      Length:      2372
  1657.00        Matches:     322
  100.00%        Conservative: 0
  100.00%        Mismatches:  0
  100.00%        Indels:      0
  4              Gaps:        0

US-10-079-111-1 (1-322) x US-09-905-125A-200 (1-2372)

QY      1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db      |||||||
160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219
QY      21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      |||||||
220 GTCCAAGGCTCTTTTGGGTGCGAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279
QY      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      |||||||
280 ATCACCTTGTGAGCAAAAGCGGAACCCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC 339
QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      |||||||
340 TGTAGGCTGTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
QY      81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100
Db      |||||||
400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGTGGAGATGGATTCTGGTCACTCTTAGGATT 459
QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      |||||||
460 AGCCCAACACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTGATTTGGAGGTTCCAGTG 519
QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      |||||||
520 AGCCGACAGTTTGCAGCCTATTGTTTACAACTCATCTGATACTTGGACTAACTCGTGCATT 579
QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      |||||||
580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACACAACA 639
QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      |||||||
640 GAATTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699
QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      |||||||
700 CCTACTACTCTCTCTCTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db      |||||||
760 TGTGTACAGAGAAGTTTTTATGGAAGTGAAGCTGTGCTGAGGTGTCCACGAACTGAACCATTTGTT 819
QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      |||||||
820 GAAAAATAAGCAGCATTCAAGATGAAGCTGTGGTGTGCTGAGGTGTCCCCACGGCTCTG 879
QY      241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      |||||||
880 CTAGTGCTTGCTCTCTCTCTTTTGGTGTGCTGAGCTGGTCTTGGATTTTGCTATGTCAAA 939
QY      261 ArgTyrValLysAlaPhePropheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      |||||||
940 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGATCAGCAGAGGAAATGATCGAAACC 999
QY      281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db      |||||||
1000 AAAGTAGTAAAGGAGGAGGAGGCCCAATGATAGCAACCTTAATGAGGAATCAAGAAAACT 1059
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QY      301 AsPLysAsnProGluSerLysSerProSerLysThrValArgCysLeuGluAla 320
Db      |||||||
1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCTGGAAGCT 1119
QY      321 GluVal 322
Db      |||||||
1120 GAAGTT 1125

RESULT 4
US-09-902-775A-200
; Sequence 200, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-775A-200

Alignment Scores:
Pred. No.:      5.92e-177      Length:      2372
Score:          1657.00      Matches:      322
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:              4              Gaps:          0

US-10-079-111-1 (1-322) x US-09-902-775A-200 (1-2372)

QY      1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db      160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219

QY      21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      220 GTCCAGGCTCTTTGCGTGCAGAGAGCTTTCCATCCAGGTGCATGCAGAAATTATGGGG 279

QY      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      280 ATCACCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 339

QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      340 TGTAGGCTGCTGGGACTAAGTTTGGCGGAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

QY      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db      400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCGTGTCATCTCTAGGATT 459

QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      460 AGCCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTGGAAAGGTTCCAGTG 519

QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGGACTAACTCGTGCATT 579

QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCACACAAACAACA 639

QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACATACCTGCC 699

QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTTCCACGGAGAAAAAATTGATT 759

QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      760 TGTGTCACAGAAGTTTTTATGGAACACTAGCACCATGTCTACAGAAACTGAACCAATTGTT 819

QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      820 GAAAAATAAGCAGCATTTCAAGATGAAGCTGTGGGTTTGGAGGTGTCCCCACGGCTCTG 879

QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      880 CTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGTATGTCAAA 939

261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      940 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC 999

281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db      1000 AAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCCTAATGAGGAATCAAGAAACT 1059

301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db      1060 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAAACCTACCGTGCATGCCCTGGAAGCT 1119

QY      321 GluVal 322
Db      1120 GAAGTT 1125

RESULT 5
US-09-833-381-849
; Sequence 849, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 849
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-849

Alignment Scores:
Pred. No.:      6.05e-177      Length:      2404
Score:          1657.00      Matches:      322
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:              4              Gaps:          0

US-10-079-111-1 (1-322) x US-09-833-381-849 (1-2404)

QY      1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db      190 ATGCCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 249

QY      21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      250 GTCCAAGGCTCTTTCGTGCAGAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGG 309

QY      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      310 ATCACCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 369

QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      370 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 429

QY      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db      430 AGCTTTGAAACTTGACGCTATGGCTGGGTGGAGATGGATTTCGTGGTCACTCTTAGGATT 489

101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      490 AGCCCCAACCCCAAGTGTGGGAAAAAATGGGGTGGGTGCTCTGATTTGGAAAGGTTCCAGTG 549

121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
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09/833382

Dianna

Restoration

Db 550 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTATTGGACTAACTCGTGCAATT 609
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 610 CCAGAAATTATCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 669
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 670 GAATTATTGTGAGTACAGTACCTACTCGGTGGCATCCCCCTACTCTACAATACCTGCC 729
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 730 CCTACTACTACTCCTCCTCGTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 789
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 790 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATTGCTACAGAAAACTGAACCAATTGTT 849
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 850 GAAATAAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 909
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 910 CTAGTGCTTGCTCTCCTCTCTTTTGGTGTGCAGCTGGTCTTGATTTTGCTATGTCAA 969
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db 970 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAAGAAATGATGAAACC 1029
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1030 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCTAATGAGGAATCAAAGAAACT 1089
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1090 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTCCGATGCTGGAAGCT 1149
QY 321 GluVal 322
Db 1150 GAAGTT 1155

RESULT 6
US-09-833-381-853
; Sequence 853, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 853
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-853

Alignment Scores:
Pred. No.: 6.05e-177 Length: 2404
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-079-111-1 (1-322) x US-09-833-381-853 (1-2404)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20

Db 190 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 249
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 250 GTCCAAAGGCTCTTTGGTGCAGAAAGAGCTTTCCATCCAGGTGTCTGCAGAAATTATGGGG 309
QY 41 IleThrLeuValSerLysLysAlaAsnGlnLysAspGlnValGluThrAlaLysGluAla 60
Db 310 ATCACCTTGTGAGCAAAAGCGCAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 369
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 370 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGCCAAGTTGAAACAGCCTTGAAAGCT 429
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 430 AGCTTTGAAACTTGCAGCTATGGCTGGTGGATGGATTCGTTGGTTCATCTCTAGGATT 489
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 490 AGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTTGGAAGGTTCCAGTG 549
QY 121 SerArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 550 AGCCGACAGTTTGCAGCTATTGTTACAACCTCATCTGATCTTGGACTAATCTCGTGCAAT 609
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 610 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 669
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 670 GAATTATTGTGAGTACAGTACCTACTCGGTGGCATCCCCCTTACTCTACATACTGCTGCC 729
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 730 CCTACTACTACTCCTCCTCGTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 789
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 790 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATTGCTACAGAAACTGAACCAATTGTT 849
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 850 GAAATAAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 909
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 910 CTAGTGCTTGCTCTCCTCTTTTGGTGTGCAGTGGTCTTGATTTTGCTATGTCAA 969
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db 970 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAAGAAATGATCGAAACC 1029
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1030 AAAGTAGTAAAGGAGGAGGAGGCCAATGATAGCAACCTAATGAGGAATCAAAGAAACT 1089
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1090 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTCCGATGCTGGAAGCT 1149
QY 321 GluVal 322
Db 1150 GAAGTT 1155

RESULT 7
US-08-892-880-1
; Sequence 1, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN

102(e)
issued Aug 24,99
fd 7/15/97

Ni et al.

APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK J.
TITLE OF INVENTION: CD44-LIKE PROTEIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,880
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021,762
FILING DATE: 15-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0490001
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2313 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 91..1056
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 154..1056
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 91..153
US-08-892-880-1

Alignment Scores:
Pred. No.: 2,71e-176 Length: 2313
Score: 1651.00 Matches: 321
Percent Similarity: 99.69% Conservative: 0
Best Local Similarity: 99.69% Mismatches: 1
Query Match: 99.64% Indels: 0
DB: 2 Gaps: 0

US-10-079-111-1 (1-322) x US-08-892-880-1 (1-2313)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 91 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCAAGGCTCCTG 150
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 151 GTCCAGGCTCTTTGCGTGCAGAGAGCTTCCATCCAGGTGTCTATGCAGAAATTATGGGG 210
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 211 ATCACCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 270
QY 61 CysArgLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 271 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAGACT 330

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 331 AGCTTTGCAACTTGCAGCTATGGCTGGTGGGATGGATTGCTGTGCTATCTTAGGATT 390
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 391 AGCCCAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTGGAAGGTTCCAGTG 450
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 451 AGCCGACAGTTTGCAGCCTATTGTTACAACATCATCTGATACCTTGGACTAACTCGTGCA 510
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 511 CCAGAAATTATCACCAAGATCCCATATTTCAACACTTCAAACTGCAACACAAACAACA 570
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 571 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACATACCTGCC 630
QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 631 CCTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCACGAGAAAAAATTGATT 690
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 691 TGTGTACAGAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 750
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 751 GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGTGTGGAGGTGTCCCCACGGCTCTG 810
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 811 CTAGTGCTTGCTCTCTCTCTTTTGGTGTGCTGCAGCTGGTCTTGGATTGCTATGTCAAA 870
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 871 AGGTATGTGAAGGCCTTCCCTTTTACAACAAGAATCAGCAGAGGAATGATCGAAACC 930
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 931 AAAGTAGTAAAGGAGGAGAGGCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT 990
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 991 GATAAAAACCCAGAGAGTCCAGAGTCCAGAGTCCAGCAAAACTACCGTGGATGCCTGGAAGCT 1050
QY 321 GluVal 322
Db 1051 GAAGTT 1056
RESULT 8
US-09-724-864-28
; Sequence 28, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1896
; TYPE: DNA
; ORGANISM: Mouse

US-09-724-864-28

Alignment Scores:
Pred. No.: 1.62e-114 Length: 1896
Score: 1103.00 Matches: 221
Percent Similarity: 79.18% Conservative: 30
Best Local Similarity: 69.72% Mismatches: 62
Query Match: 66.57% Indels: 4
DB: 4 Gaps: 3

US-10-079-111-1 (1-322) x US-09-724-864-28 (1-1896)

QY	6	SerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeuValGlnGlySerLeu	25
Db	77	AGCTGGTGTACTCCTCGCTCTATTGGACCCTAGGACCCAGTCCAAGGTGCCGAC	136
QY	26	ArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGlyIleThrLeuValSer	45
Db	137	CTCGTGCAAGACCTTTCATTCT--ACATGCAGAAATCATGGCGCTTGCCCTTGTGGGC	193
QY	46	LysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAlaCysArgLeuLeuGly	65
Db	194	AGAAACAAAACCCACAGATGAATTCACAGAAGCCACGAGGCCTGTAAGATGCTGGGA	253
QY	66	LeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAlaSerPheGluThrCys	85
Db	254	CTGACTCTGGCCAGCAGGGACCAGGTAGAGTCAGCGCAGAAATCTGGCTTTGAGACTTGC	313
QY	86	SerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIleSerProAsnProLys	105
Db	314	AGCTATGGAATGGGTGGAGAACAGTTCTCTGTCTATCCCTCGGATTTTCTCAAACCCAGG	373
QY	106	CysGlyLysAsnGlyValGlyValLeuIleTrpLysValProValSerArgGlnPheAla	125
Db	374	TGTGGGAAGATGGCAAGGTGTCTGTGATTTGGAATGTCCTCCAGCCAAAAGTTCAAA	433
QY	126	AlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIleProGluIleIleThr	145
Db	434	GCCTATTGCCACAACCTCATCCGACACCTGGGTAACTCCTGCATTCCAGAAATCGTTACC	493
QY	146	ThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThrGluPheIleValSer	165
Db	494	ACATTTTACCCCGTGTGGACACTCAA-----ACACCCGCAACAGAGTTTCTGTGACG	547
QY	166	AspSerThrTyrSerValAlaSerProTyrSerThrIleProAlaProThrThrThrPro	185
Db	548	AGCAGCGCTACTTGGCTTTCATCCCTGACTCCACAACACCTGTTTCTGCCACCACC---	604
QY	186	ProAlaProAlaSerThrSerIleProArgArgLysLysLeuIleCysValThrGluVal	205
Db	605	CGGGCTCCACCTTTGACCTCCATGGCAGGAAGACAAAAGATTGTATCACGGAAGTT	664
QY	206	PheMetGluThrSerThrMetSerThrGluThrGluProPheValGluAsnLysAlaAla	225
Db	665	TATACAGAAACCTATCACCATGGCTACAGAAACAGAGCATTTGTTCAGTGGAGCAGCA	724
QY	226	PheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeuLeuValLeuAlaLeu	245
Db	725	TTCAAGAACGAAGCAGCTGGGTGTGGAGGTGTCCCCACCGCCCTGCTGGTCTCTC	784
QY	246	LeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLysArgTyrValLysAla	265
Db	785	CTCTTCTTGTGTGCCGCTGTGCTGGCTGTTTGCTACGTGAAAAGGTATGTGAAGGCC	844
QY	266	PheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThrLysValValLysGlu	285
Db	845	TTCCCTTTCACAAACCAAGATCAACAGAAGGAAATGATCGAAACCAAGTTGTAAAGGAA	904
QY	286	GluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThrAspLysAsnProGlu	305
Db	905	GAGAAAGCTGATGACGTCAACGCTAATGAAGAATCAAGAAACCATTAATAAACCCAGAG	964
QY	306	GluSerLysSerProSerLysThrThrValArgCysLeuGluAlaGluVal	322

Db 965 GAGGCCAAGAGTCCACCCAAACTACGGTGGATGCTTAGAAGCTGAAGTT 1015
||||:|||||
RESULT 9
US-08-892-880-12
; Sequence 12, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 492 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-892-880-12

Alignment Scores:
Pred. No.: 7.76e-31 Length: 492
Score: 354.00 Matches: 83
Percent Similarity: 77.39% Conservative: 6
Best Local Similarity: 72.17% Mismatches: 12
Query Match: 21.36% Indels: 16
DB: 2 Gaps: 2

US-10-079-111-1 (1-322) x US-08-892-880-12 (1-492)

QY	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu	20
Db	99	ATGCCAGGTGCTTCAGCCTGGTGTGCTTNTCACATTCACACGAGGCTCCTG	158
QY	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	159	GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTATGCAGAAATTATGGG	218
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	219	ATCACCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTCACAGAAGCTAAGGAGCC	278
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	279	TGTAGGTTGTNGGACTAAGTTTGGCCGCAAGGCCAGTTG---AACAGCTTGAAAGT-	334

QY 81 SerPheGluThrCysSerTyrGlyTyrValGly----- 91
Db 335 AGCTTTGAAAT-TGCAGTTGGCTTGGTTGGGATGTTGNGNCATTTAGTTAGCCCAA 393
QY 92 -----AspGlyPheValValIleSerArgIleSerPro 102
Db 394 CCCANTTTGGAAANTGGTGGNNCNAATTTGNAGTCCCTTAGCCCN 438

RESULT 10
US-08-892-880-13
; Sequence 13, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-892-880-13

Alignment Scores:
Pred. No.: 2,61e-30 Length: 466
Score: 349.00 Matches: 89
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 82.41% Mismatches: 10
Query Match: 21.06% Indels: 8
DB: 2 Gaps: 2

US-10-079-111-1 (1-322) x US-08-892-880-13 (1-466)

QY 219 PheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThr 238
Db 15 TTTGTTGAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGAGGTGTCACG 74
QY 239 AlaLeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyr 258
Db 75 GCTCTGCTAGTGTCTCTCTCTCTTTGGTGTCTGAGCTGGTCTTGGATTGCTAT 134
QY 259 ValLysArgTyrVal-LysAlaPheProPheThrAsnLysAsnGlnLys-GluMetI 278

Db 135 GTCAAAAGGTATGTAAAGGCCTTCCCTTTTACAAAACAAGATCNGCAGAGGGAAATGA 194
QY 278 leGluThrLysValVal-LysGluGluLysAlaAsnAspSerAsnPro-AsnGluGluSe 297
Db 195 TCGAAACCAAAGTAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 254
QY 297 rLys---LysThrAspLysAsnPro---GluGluSerLysSerProSerLysThr-ThrV 315
Db 255 CAAAGGAAACTGNTTAAAAACCCAGTAGNAGTTCAGAGAGTNCACAAAGCAAACTTACCG 314
QY 315 al-ArgCysLeu 318
Db 315 TGTCGATGCCTG 326

RESULT 11
US-08-892-880-15
; Sequence 15, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-892-880-15

Alignment Scores:
Pred. No.: 3,35e-23 Length: 498
Score: 286.50 Matches: 62
Percent Similarity: 90.00% Conservative: 1
Best Local Similarity: 88.57% Mismatches: 4
Query Match: 17.29% Indels: 3
DB: 2 Gaps: 1

US-10-079-111-1 (1-322) x US-08-892-880-15 (1-498)

QY 254 LeuGlyPheCysTyrValLysArgTyrValLysAlaPheProPheThrAsnLysAsnGln 273
Db 14 CTGGATTGCTATGTCAAAAGGTATGTNAAGGCCTTCCCTTTTACAAAACAAGATCAG 73

REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16915/145
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3207 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: p-Meta-1
NAME/KEY: CDS
LOCATION: 113..1624
US-07-946-497-1

Alignment Scores:
Pred. No.: 7.8e-15 Length: 3207
Score: 224.00 Matches: 87
Percent Similarity: 37.68% Conservative: 43
Best Local Similarity: 25.22% Mismatches: 171
Query Match: 13.52% Indels: 44
DB: 1 Gaps: 12

US-10-079-111-1 (1-322) x US-07-946-497-1 (1-3207)

Qy 3 ArgCysPheSerLeuValLeuLeuLeuThr-----SerIleTrpThr 16
Db 86 AGATCCTTTGGTTTCATCCTGCACATCATGGACAAGTTTGGTGGCACACAGCTTGGGGA 145
Qy 17 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 36
Db 146 CTACTTTGCCTCTTACAGTTTGAGCTGGCACAGCAGCAGATCGATTGAATATAACCTGC 205
Qy 37 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 56
Db 206 CGTTACGCAAGTGTATTCCATGTGGAGAAAAATGGCCGCTACAGTATCTCCAGGACTGAA 265
Qy 57 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 76
Db 266 GCAGCTGACCTCTGCGAGGCTTTCAACACCACCTTGCCACCATGCTCAGATGGAGTTA 325
Qy 77 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 96
Db 326 GCCCTGAGAAAGGGGTTTGAAACATGCGAGTATGGTTTCATA--GAAGGACACGTGGTA 382
Qy 97 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 116
Db 383 ATCCCGAGGATCCACCCCAACGCTATCTGTGCAGGCCAACACACAGGAGTGTATATCCTC 442
Qy 117 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 136
Db 443 CTCGCATCCACACCTCCCACTATGACACATATGCTTCAATGCCTCAGCTCCTCTTGAA 502
Qy 137 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 156
Db 503 GAAGACTGT-----ACATCAGTCACAGACACCTACCCCAATTCCTTCGATGGA 547
Qy 157 ThrGlnThrThrGluPheIleValSerAspSerThr---TyrSerValAlaSerProTyr 175
Db 548 CCAGTTACCATAACTATTGTCAACCGTGTGGCACCCGCTACAGCAAGAGGGCGAGTAT 607
Qy 176 SerThr-----IleProAlaProThr----- 182
Db 608 AGAACACACCAAGAGACATCGATGCCTCAAAACATTATAGATGAGGATGTACGAGTGGA 667
Qy 183 -----ThrThrProAla---ProAlaSerThrSerIleProArgArg 196
Db 668 TCCACCATTGAGAGAGCACCACCCAGAGGCTACATTTTGCACACCGACCTTCCCACCTTCA 727

Qy 197 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThr---Glu 215
Db 728 CAGCCTACTGGAGACCGGATGACGCTTCTTTATTGGGAGCACCTTGGCCACCATGCA 787
Qy 216 ThrGluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGly 235
Db 788 ACTACTCCATGGGTTTCTGCCACACAAAACAGAACGAGAACGACCCAGTGGAACCCG 847
Qy 236 Val-----ProThrAlaLeuValLeuAlaLeuLeuPhePheGlyAlaAlaAla 252
Db 848 ATCCATTCAAAACCCAGAACTACTTTCAGACAAACCACGAGTACTGATATAGACAGA 907
Qy 253 GlyLeuGlyPheCysTyrValLysArgTyrValLys-----AlaPheProPheThrAsn 270
Db 908 AACAGCACCATGTCTCATGGAGAAAACCTGGACCCAGAACCAACAGCCTCTTCAATAAC 967
Qy 271 LysAsnGlnGlnLysGluMetIleGluThrLysValLysGluLysAlaAsnAsp 290
Db 968 CATGAGTATCAGGATGAAGAG---GAGACCCCATGCTACAAGCACAACTGGGCAGAT 1024
Qy 291 SerAsnProAsnGluGluSerLysLysThrAspLys-----AsnProGlu 305
Db 1025 CCTAATAGCACAAACAGAAAGCAGCTACCCAGAAAGGAGAGTGGTTTGAGAAATGAATGG 1084
Qy 306 GluSerLysSerPro 310
Db 1085 CAGGGAAGAACCCA 1099
RESULT 14
US-08-483-322-1
; Sequence 1, Application US/08483322
; Patent No. 5760178
; GENERAL INFORMATION:
; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut
; APPLICANT: GUENTHERT, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim
; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,322
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/946,497
; FILING DATE: 09-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

;
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: p-Meta-1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 113..1624
US-08-483-322-1

Alignment Scores:
Pred. No.: 7.8e-15 Length: 3207
Score: 224.00 Matches: 87
Percent Similarity: 37.68% Conservative: 43
Best Local Similarity: 25.22% Mismatches: 171
Query Match: 13.52% Indels: 44
DB: 1 Gaps: 12

US-10-079-111-1 (1-322) x US-08-483-322-1 (1-3207)

QY 3 ArgCysPheSerLeuValLeuLeuLeuThr-----SerIleTrpThr 16
Db 86 AGATCCTTTGGTTTCATCTGCACATCATGGACAAGTTGGTGGCACACAGCTTGGGA 145
QY 17 ThrArgLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 36
Db 146 CTACTTTGCCCTTACAGTTGAGCCTGGCACAGCAGCAGATCGATTGAATATAACCTGC 205
QY 37 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 56
Db 206 CGTTACGCAGGTGATTCCATGTGGAGAAATATGSCCGCTACAGTATCTCCAGGACTGAA 265
QY 57 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 76
Db 266 GCAGCTGACCTCTCGAGGCTTTCAACACCACCTTGCCCAACCATGGCTCAGATGGATTA 325
QY 77 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 96
Db 326 GCCCTGAGAAAGGGTTTGAACATGCAGGTATGGTTTCATA--GAAGACACGTGGTA 382
QY 97 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 116
Db 383 ATCCCGAGGATCCACCCCAACGGCTATCTGTGAGCCCAACAACACAGAGTGTATATCCTC 442
QY 117 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 136
Db 443 CTGCGATCAACACCTCCCACTATGACATATTTGTTCAATGCCTCAGCTCCTCTTGAA 502
QY 137 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 156
Db 503 GAAGACTGT-----ACATCAGTCACAGACCTACCCAATTCTTCGATGGA 547
QY 157 ThrGlnThrThrGluPheIleValSerAspSerThr--TyrSerValAlaSerProTyr 175
Db 548 CCAGTTACCATAACTATTGTCAACCGTGATGGCACCCGCTACAGCAAGAGGGCGAGTAT 607
QY 176 SerThr-----IleProAlaProThr----- 182
Db 608 AGAACACACCAAGAAGACATCGATCGCTCAACATTATAGATGAGGATGTGAGCTGGA 667
QY 183 -----ThrThrProProAla--ProAlaSerThrSerIleProArgArg 196
Db 668 TCCACCATTTGAGAAGAGCACCCCAAGAGGCTACATTTTGCACACCGACCTTCCCACTTCA 727
QY 197 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThr---Glu 215
Db 728 CAGCCTACTGGAGACCGGGATGACGCCCTTCTTTATTGGGAGCACCTTGCCCACTTGA 787
QY 216 ThrGluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGly 235
Db 788 ACTACTCCATGGGTTTCTGCCACACAAAAACAGAACCCAGGACCGGACCGTGGAAACCG 847
QY 236 Val-----ProThrAlaLeuLeuValLeuAlaLeuLeuPhePheGlyAlaAlaAla 252
Db 348 ATCCATTCAAACCCAGAGTACTACTTCAGACAAACCACCAAGGATGACTGATATAGACAGA 907

QY 253 GlyLeuGlyPheCysTyrValLysArgTyrValLys-----AlaPheProPheThrAsn 270
Db 908 AACAGCACCAAGTCTCATGGAGAAAAGTGGACCCAGGAACACAGCCTCTTCAATAAC 967
QY 271 LysAsnGlnGlnLysGluMetIleGluThrLysValLysGluLysAlaAsnAsp 290
Db 968 CATGAGTATCAGGATGAGAG--GAGACCCCATGTACTACAAGCACACCTGGGAGAT 1024
QY 291 SerAsnProAsnGluGluSerLysLysThrAspLys-----AsnProGlu 305
Db 1025 CCTAATAGCACAAACAGAGAAGCAGCTACCCAGAAGGAGAAGTGGTTTGAGAAATG 1084
QY 306 GluSerLysSerPro 310
Db 1085 CAGGGGAAGAACCCA 1099

RESULT 15

US-08-478-882-1
; Sequence 1, Application US/08478882
; Patent No. 5885575
; GENERAL INFORMATION:
; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut
; APPLICANT: GUENTHER, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim
; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,882
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,497
; FILING DATE: 19921109
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: p-Meta-1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 113..1624
US-08-478-882-1

Alignment Scores:
Pred. No.: 7.8e-15 Length: 3207
Score: 224.00 Matches: 87

Blank

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 15, 2004, 11:26:54 ; Search time 4676 Seconds
(without alignments)
2984.700 Million cell updates/sec

Title: US-10-079-111-1
Perfect score: 1657
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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1657	100.0	1755	6	BD123566	BD123566 Secretory
4	1657	100.0	1755	9	AK075443	AK075443 Homo sapi
5	1657	100.0	2029	6	AR204700	AR204700 Sequence
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9	1657	100.0	2372	6	AX454446	AX454446 Sequence
10	1657	100.0	2372	6	AX490924	AX490924 Sequence
11	1657	100.0	2372	6	AX697609	AX697609 Sequence
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14	1657	100.0	2372	6	BD172711	BD172711 Secreted
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22	1103	66.6	2027	10	BC038653	BC038653 Mus muscu
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31	389	23.5	239307	2	AC129402	AC129402 Rattus no
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ALIGNMENTS

AF127670 AF127670 1285 bp mRNA linear PRI 13-OCT-2000
LOCUS Homo sapiens hyaluronic acid receptor (HAR) mRNA, complete cds.
DEFINITION AF127670
ACCESSION AF127670
VERSION AF127670.2 GI:10800121
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1285)
AUTHORS Winkelmann,J.C., Basu,S., Ozdemir,E. and Blough,R.I.
TITLE HAR: a novel homolog of CD44 and putative hyaluronic acid receptor encoded by a gene on human chromosome 11p15
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1009)
AUTHORS Winkelmann,J.C., Basu,S., Ozdemir,E. and Blough,R.I.
TITLE Direct Submission
JOURNAL Submitted (11-FEB-1999) Hematology-Oncology, University of Cincinnati, 231 Bethesda Avenue, Cincinnati, Ohio 45267-0508, USA
REFERENCE 3 (bases 1 to 1285)
AUTHORS Winkelmann,J.C., Basu,S., Ozdemir,E. and Blough,R.I.
TITLE Direct Submission
JOURNAL Submitted (12-OCT-1999) Hematology-Oncology, University of Cincinnati, 231 Bethesda Avenue, Cincinnati, Ohio 45267-0508, USA
REMARK Sequence update by submitter
COMMENT On Oct 13, 2000 this sequence version replaced gi:5732667.
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source

gene

CDS

ORIGIN

Alignment Scores:

Pred. No.: 1.62e-127 Length: 1285
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
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US-10-079-111-1 (1-322) x AF127670 (1-1285)

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RESULT 2
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LOCUS AX136227 1755 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 149 from Patent EP1067182.
ACCESSION AX136227
VERSION AX136227.1 GI:14272635
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
TITLE Secretory protein of membrane protein
JOURNAL Patent: EP 1067182-A 149 10-JAN-2001;
Helix Research Institute (JP)

FEATURES

source

CDS

Location/Qualifiers

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Alignment Scores:

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DB:

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Indels:
Gaps:

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ORIGIN

US-10-079-111-1 (1-322) x AX136227 (1-1755)

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RESULT 3

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LOCUS

BD123566

DEFINITION

SECRETORY PROTEIN OR MEMBRANE PROTEIN.

ACCESSION

BD123566

VERSION

BD123566.1 GI:23218511

KEYWORDS

JP 2002017376-A/75.

SOURCE

HOMO SAPIENS (human)

ORGANISM

HOMO SAPIENS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1755)
Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
Secretory protein or membrane protein
Patent: JP 2002017376-A 75 22-JAN-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017376-A/75
PD 22-JAN-2002
PF 07-JUL-2000 JP 200253173
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,TOMOYASU
PI SUGIYAMA,
PI KOJI HAYASHI
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC 10,
PC C12P21/02,C12Q1/68//C12P21/08,C12N15/00,C12N5/00 CC
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FT CDS (201)..(1166).
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Pred. No.:
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Percent Similarity:
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DB:

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100.00%
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Matches:
Conservative:
Mismatched:
Indels:
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322
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US-10-079-111-1 (1-322) x BD123566 (1-1755)

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280

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RESULT 4 AK075443 1755 bp mRNA linear PRI 03-SEP-2002

LOCUS Homo sapiens cDNA PSEC0135 fis, clone PLACE1004850, highly similar

DEFINITION to Homo sapiens lymphatic endothelium-specific hyaluronan receptor

LYVE-1 mRNA.

ACCESSION AK075443

VERSION AK075443.1 GI:22761535

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

REFERENCE

AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayashi,K., Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T., Nakamura,Y., Nagahari,K., Sugano,S. and Isogai,T.

TITLE HRI human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1755)

AUTHORS Isogai,T. and Yamamoto,J.

TITLE Direct Submission

JOURNAL Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass sequencing, clone selection and full insert sequencing; Helix Research Institute (supported by Japan Key Technology Center etc.); cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center.

FEATURES

source

1..1755

Location/Qualifiers

1..1755

/organism="Homo sapiens"

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/clone="PLACE1004850"

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ORIGIN

Alignment Scores:

Pred. No.: 2.42e-127 Length: 1755

Score: 1657.00 Matches: 322

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

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Db 261 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCTATGCAGAAATTATGGG 320

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60

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Db 561 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTCATT 620

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2029)
AUTHORS Lal,P., Tang,Y.T., Gorgone,G.A., Corley,N.C., Guegler,K.J., Baughn,M.R., Akerblom,I.E., Young,J.A., Yue,H., Patterson,C., Reddy,R., Hillman,J.L. and Bandman,O.
TITLE Human signal peptide-containing protein
JOURNAL Patent: JP 2002519030-A 64 02-JUL-2002;
INCYTE PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002519030-A/64
PD 02-JUL-2002
PF 25-JUN-1999 JP 2000557363
PR 26-JUN-1998 US 60/090762,31-JUL-1998 US 60/094983 PR 01-OCT-1998 US 60/102686,11-DEC-1998 US 60/112129 PI PREETI LAL,Y TOM TANG,GINA A GORGONE,NEIL C CORLEY,KARL J PI GUEGLER, PI MARIAH R BAUGHN,INGRID E AKERBLOW,JANICE AU YOUNG,HENRY YUE, PI CHANDRA PATTERSON,ROOPA REDDY,JENNIFER L HILLMAN,OLGA BANDMAN PC C12N15/09,A61K38/00,A61K39/395,A61K45/00,A61P9/00,A61P15/00, PC A61P25/00, PC A61P29/00,A61P35/00,A61P43/00,C07K14/47,C07K16/18,C12N1/15, PC C12N1/19, PC C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/68//C12P21/08, PC C12N15/00, PC A61K37/02,C12N5/00 CC Incyte Clone No: 3044710 FT Key Location/Qualifiers
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source Location/Qualifiers
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Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db AGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCCTGATTTGAAGGTTCCAGTG 542
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

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QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
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QY 321 GluVal 322
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AR410761
LOCUS AR410761 2372 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 200 from patent US 6635468.
ACCESSION AR410761
VERSION AR410761.1 GI:40162261
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Ashkenazi,A., Botstein,D., Desnovers,L., Eaton,D.L., Ferrara,N., Filvaroff,E., Fong,S., Gao,W.-Q., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Hillan,K.J., Kljavin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A., Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: US 6635468-A 200 21-OCT-2003;
FEATURES Location/Qualifiers
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Db	220	GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG	279
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Db	280	ATCACCCCTTGTAGCAAAAAGCGGAACCCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC	339
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ACCESSION	AX092274	AX092274				
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ORGANISM	Homo sapiens					
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AUTHORS		Secreted and transmembrane polypeptides and nucleic acids encoding the same				
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Db	220	GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG	279			
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Db	280	ATCACCCCTTGTGAGCAAAAAGCGGAACCCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC	339			
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QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120			
Db	460	AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGTGTCTCTGATTTGAAGTTTCCAGTG	519			
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Db	580	CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA	639			
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180			
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RESULT 9
AX454446
LOCUS AX454446
DEFINITION Sequence 31 from Patent WO0208284.
ACCESSION AX454446
VERSION AX454446.1 GI:21713847

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.

TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0208284-A 31 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)

FEATURES
source Location/Qualifiers
1. .2372
/organism="Homo sapiens"
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ORIGIN
Alignment Scores:
Pred. No.: 3.56e-127 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US10-079-111-1 (1-322) x AX454446 (1-2372)

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QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrrLysValProVal 120
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTCTCTGATTTGGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrrThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACATCATCTGATCTTGGACTAACTCGTGCAATT 579
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QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
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AX490924
LOCUS AX490924
DEFINITION Sequence 31 from Patent WO0200690.

AX490924 2372 bp DNA linear PAT 16-AUG-2002

ACCESSION AX490924
VERSION AX490924.1 GI:22323799
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.
TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0200690-A 31 03-JAN-2002;
Genentech, Inc. (US)
FEATURES
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1. .2372
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Alignment Scores:
Pred. No.: 3.56e-127 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
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QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
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LOCUS AX697609 2372 bp DNA linear PAT 02-APR-2003
DEFINITION Sequence 200 from Patent WO0104311.
ACCESSION AX697609
VERSION AX697609.1 GI:29498705
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ashkenazi,A.J., Botstein,D., Desnoyers,L., Eaton,D.L., Ferrara,N.,
Filvaroff,E., Fong,S., Gao,W.Q., Gerber,H., Gerritsen,M.E.,
Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Hillan,K.J.,
KlJavin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A.,
Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0104311-A 200 18-JAN-2001;
Genentech Inc. (US)
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/mol_type="unassigned DNA"
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Pred. No.: 3.56e-127 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Db	340	TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT	399
QY	81	SerPheGluThrCysSerTyrGlyTirpValGlyAspGlyPheValValIleSerArgIle	100
Db	400	AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCATCTTAGGATT	459
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTirpLysValProVal	120
Db	460	AGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGTGCTCTGATTTGGAAGGTTCAGTG	519
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTirpThrAsnSerCysIle	140
Db	520	AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCA	579
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA	639
QY	161	GlupheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTTATTGTCAGTGACAGTACCTACTCTCGGTGGCATCCCTTACTCTACAATACCTGCC	699
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	700	CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	759
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTACAGAAAGTTTTTATGGAACTAGCACCATGTCTACAGAACTGAACCATTTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAAATAAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG	879
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Db	880	CTAGTGTCTGCTCTCCTCTTCTTTGGTGTGCAGCTGGTCTTGGATTGTGCTATGTCAA	939
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAAATGATCGAAACC	999
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluSerLysLysThr	300
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QY	301	AspLysAenProGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
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RESULT 12
BD075532

LOCUS BD075532 2372 bp DNA linear PAT 27-AUG-2002
DEFINITION Secretory and transmembrane polypeptide and nucleic acid encoding the same.

ACCESSION BD075532
VERSION BD075532.1 GI:22621135
KEYWORDS JP 2001516580-A/165.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE

JOURNAL

COMMENT

1 (bases 1 to 2372)
Wood,W.I., Gurney,A.L., Goddard,A., Penica,D., Chen,J. and Yuan,J.
Secretory and transmembrane polypeptide and nucleic acid encoding the same
Patent: JP 2001516580-A 165 02-OCT-2001;
GENENTECH INC
OS Homo sapiens (human)
PN JP 2001516580-A/165
PD 02-OCT-2001
PF 16-SEP-1998 JP 2000511867
PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR
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21-OCT-1997 US 60/063486,24-OCT-1997 US 60/062816 PR
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03-NOV-1997 US 60/064248,07-NOV-1997 US 60/064809 PR
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21-NOV-1997 US 60/066364,24-NOV-1997 US 60/066772 PR
24-NOV-1997 US 60/066466,24-NOV-1997 US 60/066770 PR
24-NOV-1997 US 60/066511,24-NOV-1997 US 60/066453 PR
25-NOV-1997 US 60/066840
PI WILLIAM I WOOD,AUSTIN L GURNEY,AUDLEY GODDARD,DIANE PENICA, PI
JEAN CHEN,
PI JEAN YUAN
PC C12N15/09,C07K14/47,C07K14/705,C07K16/18,C07K16/28,C07K19/00,
PC C12N1/19,
PC C12N1/21,C12N5/10,C12P21/02,C12P21/08,C12Q1/02//(C12P21/08, PC
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encoding the same
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ORIGIN

Alignment Scores:

Pred. No.: 3.56e-127 Length: 2372
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Db 880 CTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGATTTTGCTATGTCAA 939

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RESULT 13
BD172392
LOCUS BD172392 2372 bp DNA linear PAT 18-FEB-2003
DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding the same.

ACCESSION BD172392
VERSION BD172392.1 GI:28413692
KEYWORDS JP 2002223786-A/165.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2372)

AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: JP 2002223786-A 165 13-AUG-2002;
COMMENT GENENTECH INC
OS Homo sapiens (human)
PN JP 2002223786-A/165

PD 13-AUG-2002 JP 2001385135
PF 18-DEC-2001 60/059115,17-SEP-1997 US 60/059184 PR
PR 17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR
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24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR
24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
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REFERENCE 1 (bases 1 to 2372)

AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.
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JOURNAL Patent: JP 2002238586-A 165 27-AUG-2002;
GENENTECH INC
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REFERENCE		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 2372)	
	Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.	
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Copyright (c) 1993 - 2004 Compugen Ltd.
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15	1657	100.0	2372	10	US-09-904-820-200	Sequence 200, App
16	1657	100.0	2372	10	US-09-904-786-200	Sequence 200, App
17	1657	100.0	2372	10	US-09-906-646-200	Sequence 200, App
18	1657	100.0	2372	10	US-09-906-700-200	Sequence 200, App
19	1657	100.0	2372	10	US-09-903-786-200	Sequence 200, App
20	1657	100.0	2372	10	US-09-902-903-200	Sequence 200, App
21	1657	100.0	2372	10	US-09-903-749A-200	Sequence 200, App
22	1657	100.0	2372	10	US-09-904-119-200	Sequence 200, App
23	1657	100.0	2372	10	US-09-904-956-200	Sequence 200, App
24	1657	100.0	2372	10	US-09-902-736-200	Sequence 200, App
25	1657	100.0	2372	10	US-09-907-794-200	Sequence 200, App
26	1657	100.0	2372	10	US-09-903-943-200	Sequence 200, App
27	1657	100.0	2372	10	US-09-904-462-200	Sequence 200, App
28	1657	100.0	2372	10	US-09-907-925-200	Sequence 200, App
29	1657	100.0	2372	10	US-09-902-692-200	Sequence 200, App
30	1657	100.0	2372	10	US-09-903-520-200	Sequence 200, App
31	1657	100.0	2372	10	US-09-905-056-200	Sequence 200, App
32	1657	100.0	2372	10	US-09-909-064-200	Sequence 200, App
33	1657	100.0	2372	10	US-09-904-553-200	Sequence 200, App
34	1657	100.0	2372	10	US-09-905-381-200	Sequence 200, App
35	1657	100.0	2372	10	US-09-905-088-200	Sequence 200, App
36	1657	100.0	2372	10	US-09-907-575-200	Sequence 200, App
37	1657	100.0	2372	10	US-09-905-075-200	Sequence 200, App
38	1657	100.0	2372	10	US-09-902-759-200	Sequence 200, App
39	1657	100.0	2372	10	US-09-902-634-200	Sequence 200, App
40	1657	100.0	2372	10	US-09-902-713-200	Sequence 200, App
41	1657	100.0	2372	10	US-09-907-979-200	Sequence 200, App
42	1657	100.0	2372	10	US-09-902-615-200	Sequence 200, App
43	1657	100.0	2372	10	US-09-903-925-200	Sequence 200, App
44	1657	100.0	2372	10	US-09-906-760A-200	Sequence 200, App
45	1657	100.0	2372	10	US-09-903-823-200	Sequence 200, App

ALIGNMENTS

RESULT 1
US-10-079-111-2
; Sequence 2, Application US/10079111
; Publication No. US20030124543A1
; GENERAL INFORMATION:
; APPLICANT: Stuart, Susan G.
; APPLICANT: Streeter, David G.
; TITLE OF INVENTION: BREAST CANCER MARKER
; FILE REFERENCE: PC-0053 CIP
; CURRENT APPLICATION NUMBER: US/10/079,111
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 09/232,160
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 2029
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124543A1 3044710CB1
US-10-079-111-2

Alignment Scores:				
Pred. No.:	1.74e-188	Length:	2029	
Score:	1657.00	Matches:	322	
Percent Similarity:	100.00%	Conservative:	0	
Best local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	15	Gaps:	0	
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QY	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTyrThrArgLeuLeu	20	
Db	183	ATGCCAGGTGCTTCAGCCTGGTGTCTCTCACTTCCATCTGGACCAGGCTCCTG	242	
QY	21	ValGlnGlySerLeuArgAlaGluGluSerIleGlnValSerCysArgIleMetGly	40	
Db	243	GTCCAAGGCTCTTTGCGTGCAGAAAGACTTCCATCCAGGTGTCATGCAGAATTATGGGG	302	
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60	
Db	303	ATCACCCCTGTGAGCAAAAAGGCGAACACGACGCTGAATTTACAGAAGCTAAGGAGCC	362	
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80	
Db	363	TGTAGGCTGCTGGGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGACCTTGAAAAGCT	422	
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100	
Db	423	AGCTTTGAACATTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGTCATCTCTAGGATT	482	
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120	
Db	483	AGCCCCAAACCCCAAGTGTGGAAAAAATGGGTGGGTGTCTCTGATTGGAAGGTTCCAGTG	542	
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140	
Db	543	AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGTATACITGGACTAACTCGTGCATT	602	
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160	
Db	603	CCAGAAATTATCACCCACCAAGATCCCATATTCAACACTCAAACTGCAACACAACA	662	
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180	
Db	663	GAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	722	
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200	
Db	723	CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	782	
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220	
Db	783	TGTGTACAGAAGTTTTTATGGAAGAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	842	
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240	
Db	843	GAATAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGAGGTGTCCCCACGGCTCTG	902	
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260	
Db	903	CTAGTGTCTGCTCTCTCTCTTTTGGTGTGCAGCTGGTCTTGGAATTTTGCTATGTCAAA	962	
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280	
Db	963	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC	1022	
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300	
Db	1023	AAAGTAGTAAAGGAGGAGGAGGCCAATGATAGCAACCCTAATGAGGAATCAAGAGAAACT	1082	
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320	

Db	1083	GATAAAACCCAGAGAGTCCAAGAGTCCAAAGCTCCAAAGCAAACTACCGTGCATGCGTGAAGCT	1142	
QY	321	GluVal 322		
Db	1143	GAAGTT 1148		
RESULT 2				
US-09-909-320-200				
; Sequence 200, Application US/09909320				
; Patent No. US20020132240A1				
; GENERAL INFORMATION:				
; APPLICANT: Genentech, Inc.				
; APPLICANT: Ashkenazi, Avi				
; APPLICANT: Botstein, David				
; APPLICANT: Desnoyers, Luc				
; APPLICANT: Eaton, Dan L.				
; APPLICANT: Ferrara, Napoleone				
; APPLICANT: Filvaroff, Ellen				
; APPLICANT: Fong, Sherman				
; APPLICANT: Gao, Wei-Qiang				
; APPLICANT: Gerber, Hanspeter				
; APPLICANT: Gerritsen, Mary E.				
; APPLICANT: Goddard, A.				
; APPLICANT: Godowski, Paul J.				
; APPLICANT: Grimaldi, Christopher J.				
; APPLICANT: Gurney, Austin L.				
; APPLICANT: Hillan, Kenneth, J.				
; APPLICANT: Kljavin, Ivar J.				
; APPLICANT: Mather, Jennie P.				
; APPLICANT: Pan, James				
; APPLICANT: Paoni, Nicholas F.				
; APPLICANT: Roy, Margaret Ann				
; APPLICANT: Stewart, Timothy A.				
; APPLICANT: Tumas, Daniel				
; APPLICANT: Williams, P. Mickey				
; APPLICANT: Wood, William, I.				
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic				
; TITLE OF INVENTION: Acids Encoding the Same				
; FILE REFERENCE: 10466-14				
; CURRENT APPLICATION NUMBER: US/09/909,320				
; CURRENT FILING DATE: 2002-01-04				
; PRIOR APPLICATION NUMBER: PCT/US00/04414				
; PRIOR FILING DATE: 2000-02-22				
; PRIOR APPLICATION NUMBER: US 60/143,048				
; PRIOR FILING DATE: 1999-07-07				
; PRIOR APPLICATION NUMBER: US 60/145,698				
; PRIOR FILING DATE: 1999-07-26				
; PRIOR APPLICATION NUMBER: US 60/146,222				
; PRIOR FILING DATE: 1999-07-28				
; PRIOR APPLICATION NUMBER: PCT/US99/20594				
; PRIOR FILING DATE: 1999-09-08				
; PRIOR APPLICATION NUMBER: PCT/US99/20944				
; PRIOR FILING DATE: 1999-09-13				
; PRIOR APPLICATION NUMBER: PCT/US99/21090				
; PRIOR FILING DATE: 1999-09-15				
; PRIOR APPLICATION NUMBER: PCT/US99/21547				
; PRIOR FILING DATE: 1999-09-15				
; PRIOR APPLICATION NUMBER: PCT/US99/23089				
; PRIOR FILING DATE: 1999-10-05				
; PRIOR APPLICATION NUMBER: PCT/US99/28214				
; PRIOR FILING DATE: 1999-11-29				
; PRIOR APPLICATION NUMBER: PCT/US99/28313				
; PRIOR FILING DATE: 1999-11-30				
; PRIOR APPLICATION NUMBER: PCT/US99/28564				
; PRIOR FILING DATE: 1999-12-02				
; PRIOR APPLICATION NUMBER: PCT/US99/28565				
; PRIOR FILING DATE: 1999-12-02				
; PRIOR APPLICATION NUMBER: PCT/US99/30095				
; PRIOR FILING DATE: 1999-12-16				
; PRIOR APPLICATION NUMBER: PCT/US99/30911				
; PRIOR FILING DATE: 1999-12-20				
; PRIOR APPLICATION NUMBER: PCT/US99/30999				
; PRIOR FILING DATE: 1999-12-20				


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; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-909-320-200

Alignment Scores:
Pred. No.:      2.23e-188      Length:      2372
Score:          1657.00      Matches:      322
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              9          Gaps:      0

US-10-079-111-1 (1-322) x US-09-909-320-200 (1-2372)

QY      1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db      160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTCCATCTGGACCACGAGGTCCTG 219

QY      21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      220 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCATCCAGGTGTCTATGCAGAATTATGGG 279

QY      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      280 ATCACCTTGTGAGCAAAAAGCGAACCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 339

QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAAACAGCCTTGAAAGCT 399

QY      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db      400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGTCATCTCTAGGATT 459

QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      460 AGCCCAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCCTGATTGTGAAGGTTCCAGTG 519

QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATT 579

QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580 CCAGAAATTATCACCCCAAAGATCCCATATTCAACACTCAAACCTGCAACACACAAACA 639

QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640 GAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACTGCC 699

QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      760 TGTGTCACAGAAGTTTTTATGGAAGACTAGCACCATGTCTACAGAAACTGAACCAATTGTT 819

QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      820 GAAAATAAGCAGCATTTCAAGATGAAGCTGTGGGTTTGGAGGTGTCCCCACGGCTCTG 879

QY      241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      880 CTAGTGTCTGCTCTCCTCTTCTTTGGTGTGTCAGCTGGTCTTGGATTTTGTCTATGTCAAA 939

QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
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Db      940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAATGATCGAAACC 999

QY      281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db      1000 AAAGTAGTAAAGGAGGAGGAGGCCAATGATAGCAACCTAATGAGGAATCAAAGAAAACT 1059

QY      301 AspLysAsnProGluGluSerLysSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db      1060 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCTGGAAGCT 1119

QY      321 GluVal 322
Db      1120 GAAGTT 1125

RESULT 3
US-09-909-088B-200
; Sequence 200, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,088B
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
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; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-909-088B-200

Alignment Scores:
Pred. No.:      2.23e-188      Length:      2372
Score:          1657.00      Matches:      322
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              9          Gaps:      0

US-10-079-111-1 (1-322) x US-09-909-088B-200 (1-2372)

QY      1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db      160 ATGCCAGGTCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219

QY      21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      220 GTCCAAGGCTCTTTGCGTGCAGAGAGCTTCCATCCAGGTGTATGCAGAATTATGGGG 279

QY      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      280 ATCACCTTGTGAGCAAAAGGCGAACCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 339

QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      340 TGTAGGCTGCTGGGACTAAGTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

QY      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db      400 AGCTTTGAAACTTGACGCTATGGCTGGGTTGGAGATGGATTCCGTGCATCTCTAGGATT 459

QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCCTGATTGGAAGGTTCCAGTG 519

QY      121 SerArgGlnPheAlaIatyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATT 579

QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580 CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639

QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699

QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      700 CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      760 TGTGTACAGAGAGTTTTTATGGAAACTTAGCACCATGTCTACAGAAACTGAACCAATTGTT 819

QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240

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QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrVallys 260
      |||||||
Db      880 CTAGTGTCTGCTCTCCTCTTCTTTGGTGTGCAGCTGGTCTTGGATTCTGCTATGTCAA 939

QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
      |||||||
Db      940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAAGGAATGATCGAAACC 999

QY      281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
      |||||||
Db      1000 AAAGTAGTAAAGGAGGAGAGAGGCCCAATGATAGCAACCTTAATGAGGAATCAAAGAAACT 1059

QY      301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
      |||||||
Db      1060 GATAAAACCAGAGAGTCCAAGAGTCCAAGAGTCCAAGCAAACCTACCGTGCATGCCCTGGAAGCT 1119

QY      321 GluVal 322
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Db      1120 GAAGTT 1125

RESULT 4
US-09-905-291A-200
; Sequence 200, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15

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; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-905-291A-200

Alignment Scores:

Pred. No.:	2.23e-188	Length:	2372
Score:	1657.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-079-111-1 (1-322) x US-09-905-291A-200 (1-2372)

QY	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu	20
Db	160	ATGGCCAGGTGCTTTCAGCTGGTGTGCTTCTCACATTCATCTGGACCCAGGAGGCTCTG	219
QY	21	ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	220	GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGCATGCAGAAATTATGGGG	279
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	280	ATCACCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTCACAGAAGCTAAGGAGGCC	339
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT	399
QY	81	SerpPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	400	AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATCGTGGTCATCTCTAGGATT	459
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValIleuIleTrpLysValProVal	120
Db	460	AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCCTGATTTGGAAGGTTCCAGTG	519
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	520	AGCGACAGTTTGACGCCTATTGTTACAACTCATCTGATACTTGACTAACTCGTGCATT	579
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA	639
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	699
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200

Db	700	CCTACTACTCCTCCTCCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	759
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTCACAGAGTTTTTATGGAAACTAGCACCATTGCTACAGAAACTGACCATTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCACGGCTCTG	879
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGTCTGCTCCTCTTCTTTTGGTGTGCTGAGCTGGTCTTTGGATTTTGTATGTCAA	939
QY	261	ArgTyrValLysAlaPhePropheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC	999
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1000	AAAGTAGTAAAGGAGAGAGGCCAATGATAGCAACCTTAATGAGGAATCAAAAGAAACT	1059
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCCTGGAAGCT	1119
QY	321	GluVal	322
Db	1120	GAAGTT	1125

RESULT 5
US-09-902-853-200
; Sequence 200, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28


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; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-902-853-200

Alignment Scores:
Pred. No.:      2.23e-188      Length:      2372
Score:          1657.00        Matches:     322
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:     0
Query Match:      100.00%      Indels:       0
DB:              9            Gaps:        0

US-10-079-111-1 (1-322) x US-09-902-853-200 (1-2372)

QY      1  MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db      160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCAAGGCTCCTG 219
QY      21  ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279
QY      41  IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      280 ATCACCCCTGTGAGCAAAAGCGCAACCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 339
QY      61  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      340 TGTAGGCTGCTGGGACTAAGTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
QY      81  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db      400 AGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGGATTCTGGTGCATCTCTAGGATT 459
QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeulleTrpLysValProVal 120
Db      460 AGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCCTGATTTTGGAAGGTTCCAGTG 519
QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520 AGCCGACAGTTTGCAGCCTATTGTTACAACACTCATCTGACTTGGACTAACTCGTGCATT 579
QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

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Db      580 CCAGAAATTATCACCAACCAAGATCCCATATTTCAACACTCAAACCTGCAACACAAACA 639
QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640 GAATTTATTGTCAGTGACAGTACCTACTCGTGGCATCCCTTTACTCTACAATACCTGCC 699
QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      700 CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db      760 TGTGTCACAGAAAGTTTATTGAAACTAGCACCATTGCTACAGAAACTGAACCATTTGTT 819
QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      820 GAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      880 CTAGTGCTTGCTCTCTCTCTTTTGGTGTGCTGCAGCTGGTCTTGGATTTTGTATGTCAA 939
QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGAAATGATCGAAACC 999
QY      281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db      1000 AAAGTAGTAAAGGAGGAGAGGCAATGATAGCAACCTTAATGAGGAATCAAAGAAACT 1059
QY      301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db      1060 GATAAAAACCCAGAAAGAGTCCAAAGAGTCCAAGCAGTCCAAGCAAACCTACCGTGCATGCCTGGAAGCT 1119
QY      321 GluVal 322
Db      1120 GAAGTT 1125

RESULT 6
; US-09-907-824-200
; Sequence 200, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; CURRENT FILING DATE: 2001-07-17

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; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-907-824-200

Alignment Scores:
Pred. No.:      2,23e-188      Length:      2372
Score:          1657.00      Matches:      322
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              9           Gaps:        0

US-10-079-111-1 (1-322) x US-09-907-824-200 (1-2372)

QY      1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
      |||
Db      160 ATGGCCAGGTGCTTCAGCGTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219

QY      21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
      |||
Db      220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279

QY      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
      |||
Db      280 ATCACCTTGTGAGCAAAAGGGCAACCAGCAGCTGAATTCACAGAAGCTAAGAGGCC 339

QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
      |||
Db      340 TGTAGGCTGCTGGGACTAAGTTGGCCGGCAAGGACCAGTGAAGTGAACAGCCCTTGAAAGCT 399

QY      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
      |||
Db      400 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTGCTGGTCACTCTAGGATT 459
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QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
      |||
Db      460 AGCCCAAAACCCCAAGTGTGGGAAAATGGGGTGGGTGCTCTGATTTGGAGGTTCCAGTG 519

QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
      |||
Db      520 AGCCGACAGTTTGCAGCCTATTGTTACAACATCATCTGATACTTGGACTAATCGTGCAAT 579

QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
      |||
Db      580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639

QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
      |||
Db      640 GAAATTTATTGTCAGTGACAGTACCTACTCGTGGCATCCCCTTACTTACAATACCTGCC 699

QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
      |||
Db      700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
      |||
Db      760 TGTGTCACAGAGTTTTATGGAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
      |||
Db      820 GAAATATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGGCTCTG 879

QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
      |||
Db      880 CTAGTGTCTGCTCCTCTTCTTTTGGTGTGTCAGCTGGTCTTTGGATTTTGGCTATGTCAAA 939

QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
      |||
Db      940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAAGGAAATGATCGAAACC 999

QY      281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
      |||
Db      1000 AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCTTAATGAGGAATCAAGAAAACT 1059

QY      301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
      |||
Db      1060 GATAAAACCCCAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCTGGAAGCT 1119

QY      321 GluVal 322
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Db      1120 GAAGTT 1125

RESULT 7
US-09-907-841-200
; Sequence 200, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
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```
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
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; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-907-841-200

Alignment Scores:
Pred. No.:      2.23e-188      Length:      2372
Score:          1657.00      Matches:      322
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              9      Gaps:      0

US-10-079-111-1 (1-322) x US-09-907-841-200 (1-2372)

QY      1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db      160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219
QY      21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGCATGCAGAATTATGGGG 279
QY      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      280 ATCACCCCTGTGAGCAAAAAGCGCAACGACGAGCTGAATTTCACAGAAGCTAAGGAGGCC 339
QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      340 TGTAGGCTGTGGGACTTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAGACT 399
QY      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db      400 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCTGGTTCATCTCTAGGATT 459
QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      460 AGCCCAAACCCCAAGTGTGGGAAAAAATGGGTGGGTGCTCTGATTGTGAAGGTTCCAGTG 519
QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
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Db      520 AGCCGACAGTTTGCAGCCTATTGTTACAAACTCATCTGATACTTGGACTAACTCGTGCAAT 579
QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACACTGCAACACAAACA 639
QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640 GAATTTATTGTTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC 699
QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db      760 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      820 GAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      880 CTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGATTTTGCTATGTCAA 939
QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAATGATCGAAACC 999
QY      281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db      1000 AAAGTAGTAAAGGAGGAGAGGCAATGATAGCAACCTTAATAGGAATCAAAGAAACT 1059
QY      301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db      1060 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAACTACCGTGCGATGCGTGAAGCT 1119
QY      321 GluVal 322
Db      1120 GAAGTT 1125

RESULT 8
US-09-904-011-200
; Sequence 200, Application US/09904011
; Publication No. US20030003530A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
```


; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,011
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-011-200

Alignment Scores:
Pred. No.: 2,23e-188 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-904-011-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCTGGTGTGTTCTCTCATCTCCATCTGGACCACGAGGCTCCTG 219

QY 21 valGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTTGGTGCAGAAAGAGCTTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTACAGAAGCTAAGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyYaspGlyPheValValIleSerArgile 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGATGGATTCGTGGTCACTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTCTGATTTGAAGGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACCTGGACTAACTCGTGCA 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAAACTCAAACCTGCAACACAAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699

QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTCTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db 760 TGTGTACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyLeuGlyPheCysTyrValLys 240
Db 820 GAAAAATAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTCTGCTCTCTCTTCTTTTGGTGTGTCAGCTGGTCTTTGGATTTTGTCTATGTC 939

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCTTCCCTTTTACAAACCAAGAATCAGCAGAGGAATGATCGAAAAAC 999

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGAGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAAA 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAACCCAGAGAGTCCAGAGTCCAAAGCAAAAACTACCGTGCATGCCCTGGAAGCT 1119

QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 9
US-09-906-742-200
; Sequence 200, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-906-742-200

Alignment Scores:				
Pred. No.:	2.23e-188	Length:	2372	
Score:	1657.00	Matches:	322	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	10	Gaps:	0	

US-10-079-111-1 (1-322) x US-09-906-742-200 (1-2372)

Qy 1 MetaAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
|
Db 160 ATGCCACGGTGCTTCAGCCTGGTGTGCTTCTCACITCCATCTGGACCACGAGGCTCCTG 219
|
Qy 21 ValGinGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
|

Db 220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCATCCAGGTGTCTAGCAGAAATATGGGG 279
|
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
|
Db 280 ATCACCCCTGTGAGCAAAAAGCGAACCAGCAGCTGAATTTTCACAGAAGTAAGGAGGCC 339
|
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
|
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGAAGGACCAAGTTGAAACAGCCCTTGAAAGCT 399
|
Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
|
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGTCATCTCTAGGATT 459
|
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
|
Db 460 AGCCCCAAACCCCAAGTGTGGGAAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG 519
|
Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
|
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACITTGACTAACTCGTGCATT 579
|
Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
|
Db 580 CCAGAAATTATCACCCAAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639
|
Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
|
Db 640 GAATTTATTGTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC 699
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Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
|
Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
|
Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
|
Db 760 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
|
Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
|
Db 820 GAAAAATAAAGCAGCATTCAGAAGATGAAGCTGCTGGGTTTGGAGGTGTCCCAACGGCTCTG 879
|
Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
|
Db 880 CTAGTGCTTGCTCTCCTCTTCTTGTGTGCTGCAGCTGGTCTTGATTTTGCTATGTCAA 939
|
Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
|
Db 940 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAAATGATCGAAACC 999
|
Qy 281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
|
Db 1000 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACT 1059
|
Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
|
Db 1060 GATAAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAAAGCT 1119
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Qy 321 GluVal 322
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Db 1120 GAAGTT 1125
|

RESULT 10

US-09-906-838-200

; Sequence 200, Application US/09906838

; Publication No. US20030027143A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,838
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-906-838-200

Alignment Scores:
Pred. No.: 2.23e-188 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-10-079-111-1 (1-322) x US-09-906-838-200 (1-2372)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCATTCCATCTGGACCAACGAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGGGTGCAGAAAGAGCTTTCCATCCAGGTGTATGCAGATTATGGGG 279
QY 41 IleThrLeuValSerLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTTGTGAGCAAAAAGGCGAACAGCAGCTGAATTTTCACAGAAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGTGGGACTAAGTTTGGCCGGCAAGACCAAGTTGAAACAGCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGTGGTGGAGATGGATTCTGGTTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTTGGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGACGCTATTGTTACAACCTCATCTGATACCTTGGACTAACCTGTCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAAAAGATCCCATATTTCAACACTCAAACTGCAACACAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAAAGTTTATTGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 820 GAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCCAGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTCTTGTCTCTCTTCTTTTGGTGTCTGCAGCTGGTCTTTGGATTTTGTATGTCAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAAACAAGAATCAGCAGAGGAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAGGAGGAGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACT 1059
QY 301 AspLysAsnProGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAAACCTACCGTCCGATGCCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125


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RESULT 11
US-09-907-613-200
; Sequence 200, Application US/09907613
; Publication No. US20030027145A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,613
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
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; ORGANISM: Homo sapiens
US-09-907-613-200
Alignment Scores:      2.23e-188      Length:      2372
Pred. No.:            1657.00        Matches:     322
Score:                100.00%        Conservative: 0
Percent Similarity:   100.00%        Mismatches:  0
Best Local Similarity: 100.00%        Indels:      0
Query Match:         100.00%        Gaps:        0
DB:                  10

US-10-079-111-1 (1-322) x US-09-907-613-200 (1-2372)

QY      1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
      |||||||
Db      160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGCACGAGGCTCCTG 219

QY      21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
      |||||||
Db      220 GTCCAGGCTCTTTGCGTGCAGAGAGCTTTCCATCCAGGTGTGATGAGGCTTATGGGG 279

QY      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
      |||||||
Db      280 ATCACCTTGTGAGCAAAAGCGAACCAGCAGCTGAATTTTCAGAAAGCTAAGGAGGCC 339

QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
      |||||||
Db      340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

QY      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
      |||||||
Db      400 AGCTTTGAAACTTGCAGCTATGCTGGTGGTGGAGATGGATTCTGTTGCTCTCTAGGATT 459

QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
      |||||||
Db      460 AGCCCAAAACCCCAAGTGTGGGAAAAAATGGGGTGGTGTCTCTGATTGGAAAGGTTCCAGTG 519

QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
      |||||||
Db      520 AGCCGACAGTTTGCAGCCTATTGTTACAACACTCATCTGATACTTGACTAACTCGTGCAATT 579

QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
      |||||||
Db      580 CCAGAAATTATCACCAACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACAACA 639

QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
      |||||||
Db      640 GAATTTATTGTCAGTGACAGTACCTACTCGTGGCATCCCTTACTCTACATACTACCTGCC 699

QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
      |||||||
Db      700 CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY      201 CysValThrGluValPheMetGluThrThrSerThrMetSerThrGluThrGluProPheVal 220
      |||||||
Db      760 TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
      |||||||
Db      820 GAAATAAAGCAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCAACGGCTCTG 879

QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
      |||||||
Db      880 CTAGTGCTTGCTCTCTCTCTCTTTTGGTGTGCTGCAGCTGGTCTTGGATTTTGTATGTCAAA 939

QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
      |||||||
Db      940 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAAAGGAAATGATCGAAACC 999

QY      281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
      |||||||
Db      1000 AAAGTAGTAAGGAGGAGAGGCCCAATGATAGCAACCCCTTAATGAGGAATCAAAGAAACT 1059
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QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
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Db 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCCTGGAAGCT 1119

QY 321 GluVal 322
|||||
Db 1120 GAAGTT 1125

RESULT 12
US-09-907-942-200
; Sequence 200, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,942
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-942-200

Alignment Scores:
Pred. No.: 2.23e-188 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10

US-10-079-111-1 (1-322) x US-09-907-942-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
|||||
Db 160 ATGGCCAGGTGCTTCAGCTGGTGTGTCTTCTCACTCCATCTGGACCACGAGGCTCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
|||||
Db 220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
|||||
Db 280 ATCACCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
|||||
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
|||||
Db 400 AGCTTTGAAACTTGCACTATGGCTGGTGGTGGAGATGGATTCTGGTGCATCTTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
|||||
Db 460 AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTGATTGGAAGGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
|||||
Db 520 AGCCGACAGTTTGCAGCTATTGTTACAACCTCATCTGATACTTGGACTAATCTCGTGCA 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
|||||
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
|||||
Db 640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699

QY 181 ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
|||||
Db 700 CCTACTACTCTCCTCGCTCCAGCTTCCACTTCCACTTATTCACGGAGAAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
|||||
Db 760 TGTGTCACAGAAGTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
|||||
Db 820 GAAAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
|||||
Db 880 CTAGTGTCTTCTCCTCTCTTTTGGTGTCTGCAGCTGGTCTTTGGATTTTTGTATGTCAAA 939

Qy		261	ArgTyrValLysAlapheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Dd		940	AGGTATGTGAAGGCCTTCCTTTACAAACAAGAATCAGCAGAAGGAATGATCGAACC	999
Qy		281	LysValVallYsGluGluLysAlaAsnAspSerAsnProAsnGluSerLysLysThr	300
Dd		1000	AAAGTAGTAAGGAGGAGGCCCAATGATAGCACCCCTAATGAGGAATCAAAGAAAACT	1059
Qy		301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Dd		1060	GATAAAAACCCAGAACAGTGCCAAGAGTCCAAGCAAAAACACTACCGTGGCATGCGAAGCT	1119
Qy		321	GluVal	322
Dd		1120	GAAGTT	1125

RESULT 13

US-09-904-859-200 ; Sequence 200, Application US/09904859
; Publication No. US20030036060A1

; GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I

```

; PRIOR APPLICATION NUMBER: PCT/US99/283113
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/285564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/285565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-859-200

```

Alignment Scores:

Alignment Scores:			
Pred. No.:	2.23e-188	Length:	2372
Score:	1657.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-079-111-1 (1-322) x US-09-904-859-200 (1-2372)

QY	1	Met	Ala	Arg	Cys	Phe	Ser	Leu	Val	Leu	Leu	Leu	Thr	Ser	Ile	Trp	Thr	Thr	Arg	Leu	Leu	20
DB	160	ATG	CC	AGG	TGCTT	CAG	CTGG	TGT	TGCTT	TCT	TCT	CAC	TTCC	ATCT	GGAC	CA	CGAG	GC	TCT	CTG	219	
QY	21	Val	Gln	Gly	Ser	Leu	Arg	Ala	Glu	Glu	Leu	Ser	Ile	Gln	Val	Ser	Cys	Arg	Ile	Met	Gly	40
DB	220	GTCC	AAG	GCCTCTT	TTC	GC	TGC	GAG	AAG	AGCTT	TTC	CAT	CC	AGG	TGTC	ATG	CAGA	ATAT	TAT	GGG	279	
QY	41	Ile	Thr	Leu	Val	Ser	Lys	Lys	Ala	A	Asn	Gln	Gln	Leu	Leu	Asn	Phe	Thr	Glu	Ala	Lys	60
DB	280	ATC	ACCC	TTGT	GAG	CA	AAAA	AGCG	GA	ACC	CAG	CAG	CTGA	ATT	TTC	ACA	GAG	CTAA	GGAG	GC	339	
QY	61	Cys	Arg	Leu	Leu	Gly	Leu	Ser	Leu	Ala	Gly	Lys	Asp	Gln	Val	Glu	Thr	Ala	Leu	Lys	Ala	80
DB	340	TGT	AGG	CTGCT	GGG	ACTA	AGT	TTG	GCG	CG	CA	AGG	ACCA	AGTT	TG	AA	CA	CAG	CC	TG	399	
QY	81	Ser	Phe	Glu	Thr	Cys	Ser	Tyr	Gly	Trp	Val	Gly	Asp	Gly	Phe	Val	Val	Ile	Ser	Arg	Ile	100
DB	400	AGC	TTT	GAA	ACTT	GC	AG	CTAT	GG	CTGG	TGG	GAT	TGG	ATG	GAT	TTC	GTG	GT	CAT	CT	459	
QY	101	Ser	Pro	Asn	Pro	Lys	Cys	Gly	Lys	Asn	Gly	Val	Gly	Val	Leu	Ile	Trp	Lys	Val	Pro	Val	120
DB	460	AGC	CAA	ACCC	CAAG	TGT	GGG	AAAA	AT	GGG	TGG	TGT	CTCT	GAT	TTG	GA	AGG	TTCC	AGT	G	519	
QY	121	Ser	Arg	Gln	Phe	Ala	Ala	Tyr	Cys	Tyr	Asn	Ser	Ser	Asp	Thr	Trp	Thr	Asn	Ser	Cys	Ile	140
DB	520	AGC	CG	CAG	AGT	TTG	CAG	CTAT	TGT	TACA	ACT	CAT	CTG	ATA	CTT	GG	ACTA	ACT	CGT	GC	579	
QY	141	Pro	Glu	Ile	Ile	Thr	Thr	Lys	Asp	Pro	Ile	Phe	Asn	Thr	Gln	Thr	Ala	Thr	Gln	Thr	Thr	160
DB	580	CC	AGAAA	TTAT	CA	CC	CA	CA	AGAT	CC	CA	TAT	TTCA	ACAC	CTCA	AACT	CG	CAAC	ACA	CA	639	
QY	161	Glu	Phe	Ile	Val	Ser	Asp	Ser	Thr	Tyr	Ser	Val	Ala	Ser	Pro	Tyr	Ser	Thr	Ile	Pro	Ala	180
DB	640	GAA	TTT	ATT	TG	TC	AGT	GAC	AGT	ACCT	ACT	CGG	TGG	CAT	CCCC	TTAC	TCT	ACA	AT	TAC	699	
QY	181	Pro	Thr	Thr	Thr	Pro	Ala	Pro	Ala	Ser	Thr	Ser	Ile	Pro	Arg	Arg	Lys	Lys	Leu	Ile	200	
DB	700	CCT	ACT	ACT	ACT	CT	CT	CT	CC	AGCT	TCC	ACT	TCT	TAT	TCC	ACG	GAG	AAAA	AA	TT	759	
QY	201	Cys	Val	Thr	Glu	Val	Phe	Met	Glu	Thr	Ser	Thr	Met	Ser	Thr	Glu	Thr	Glu	Pro	Phe	Val	220

Db 760 TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
|||||

Db 820 GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCACGGCTCTG 879

QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
|||||

Db 880 CTAGTGCTTGCTCTCCTCTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA 939

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
|||||

Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC 999

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
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Db 1000 AAAGTAGTAAAGGAGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
|||||

Db 1060 GATAAAAACCCAGAGAGTCCAAAGAGTCCAAAGCAAAAACACTACCGTGGATGCCCTGGAAGCT 1119

QY 321 GluVal 322
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Db 1120 GAAGTT 1125

RESULT 14

US-09-909-204-200

; Sequence 200, Application US/09909204

; Publication No. US20030036061A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/909,204

; CURRENT FILING DATE: 2001-07-18

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29

; PRIOR APPLICATION NUMBER: PCT/US99/28313

; PRIOR FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: PCT/US99/28564

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/28565

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/30095

; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: PCT/US99/30911

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US99/30999

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US00/00219

; PRIOR FILING DATE: 2000-01-05

; NUMBER OF SEQ ID NOS: 423

; SEQ ID NO 200

; LENGTH: 2372

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-909-204-200

Alignment Scores:

Pred. No.: 2.23e-188 Length: 2372

Score: 1657.00 Matches: 322

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-909-204-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
|||||

Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTGTTCTCTCACTCCATCTGGACCACGAGGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
|||||

Db 220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
|||||

Db 280 ATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTTCACAGAAGCTAAGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
|||||

Db 340 TGTAGGCTGTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
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Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGATGGATTTCGTGTCATCTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
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Db 460 AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCCTGATTTGGAAGGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
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Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACCTTGGACTAACTCGTGCATT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
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Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
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Db 640 GAATTTATTGTTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCCTCTCTTCTTTGTGCTGCAGCTGGTCTTGGATTTGCTATGTCAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCTAATGAGGAATCAAGAAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCAGAGAGTCCAGAGTCCAGAGTCCAGCAAAACTACCGTGGCATGCCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 15

US-09-904-320-200
; Sequence 200, Application US/09904820
; Publication No. US20030036094A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,820
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-820-200

Alignment Scores:

Pred. No.: 2.23e-188 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-904-820-200 (1-2372)

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QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
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QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTTGTGAGCAAAAAGCGCAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGATTGAAACAGCCTTGAAGACT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGGTCACTCTTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTTCAGAGGTTCCAGTG 519

QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	520	AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACCTTGGACTAATCGTGCATT	579
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATATATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAACAACA	639
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTTATTGTCACTGACAGTACCTACTCGTGGCATCCCTTACTCTACAATACCTGCC	699
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	700	CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	759
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal	220
Db	760	TGTGTCACAGAGTTTATTGGAACCTAGCACCATGTCTACAGAACTGAACCATTTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAAATATAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG	879
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGCTTGCTCTCTCTCTCTTTTGGTGCTGAGCTGGTCTTGGATTTTGCTATGTCAA	939
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAATCAGCAGAGGAATGATCGAAACC	999
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1000	AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAAGAAACT	1059
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAACCCAGAGAGTCCAGAGTCCCAAGCAAAACTACCGTGCATGCTCGAAGCT	1119
QY	321	GluVal	322
Db	1120	GAAGTT	1125

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 15, 2004, 13:19:40 ; Search time 3066 Seconds
(without alignments)
3136.211 Million cell updates/sec

Title: US-10-079-111-1
Perfect score: 1657
Sequence: 1 MARCFSLVLLTISIWTRLL.....NPESKSPSKTTVRCLEAEV 322

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO spool/US10079111/runat_13092004_102135_13568/app query.fasta_1.519
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosu62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10079111@cgn_1_1_3437 @runat_13092004_102135_13568 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1657	100.0	1154	9	AL550279	AL550279 AL550279
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3	1480	89.3	1015	9	AL552299	AL552299 AL552299
4	1476.5	89.1	1201	9	AL546669	AL546669 AL546669
5	1439	86.8	1201	9	AL551020	AL551020 AL551020
6	1323.5	79.9	1014	9	AL553858	AL553858 AL553858
7	1316	79.4	913	13	BX459046	BX459046 BX459046
8	1283	77.4	1201	13	BX366718	BX366718 BX366718
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10	1275	76.9	972	9	AL549512	AL549512 AL549512
11	1264	76.3	911	9	AL543874	AL543874 AL543874
12	1262	76.2	1201	9	AL547774	AL547774 AL547774
13	1253	75.6	1172	9	AL552127	AL552127 AL552127
14	1243.5	75.0	1201	13	BX402505	BX402505 BX402505
15	1243	75.0	1201	9	AL544430	AL544430 AL544430
16	1235	74.5	1201	13	BX366589	BX366589 BX366589
17	1230	74.2	1116	9	AL552661	AL552661 AL552661
18	1225.5	74.0	1151	9	AL550829	AL550829 AL550829
19	1224	73.9	839	9	AL546217	AL546217 AL546217
20	1211	73.1	970	9	AL550615	AL550615 AL550615
21	1207.5	72.9	1201	9	AL546623	AL546623 AL546623
22	1168	70.5	1074	9	AL552777	AL552777 AL552777
23	1160	70.0	863	12	BI761420	BI761420 603044235
24	1142	68.9	864	9	AL545331	AL545331 AL545331
25	1103	66.6	2607	11	AK004726	AK004726 Mus muscu
26	1054.5	63.6	760	14	CB959809	CB959809 AGENCOURT
27	1019	61.5	746	14	CD238639	CD238639 FNPBCH08
28	1005.5	60.7	990	13	BX418211	BX418211 BX418211
29	970	58.5	743	9	AL598709	AL598709 DKF2p313B
30	936	56.5	1201	9	AL553712	AL553712 AL553712
31	935.5	56.5	801	12	BG483354	BG483354 602504223
32	926	55.9	794	12	BG566260	BG566260 602585128
33	922	55.6	1201	13	BX366791	BX366791 BX366791
34	905	54.6	1023	13	BY704927	BY704927 BY704927
35	901	54.4	596	9	AA046671	AA046671 zf12d09.r
36	874.5	52.8	802	14	CB994314	CB994314 AGENCOURT
37	844	50.9	1201	9	AL546565	AL546565 AL546565
38	822.5	49.6	757	14	CB229605	CB229605 AGENCOURT
39	807	48.7	877	12	BI763579	BI763579 603050140
40	795.5	48.0	964	13	BU504417	BU504417 AGENCOURT
41	766	46.2	960	9	AL553920	AL553920 AL553920
42	737	44.5	487	14	CA407758	CA407758 1003907 H
43	733.5	44.3	1298	14	CF110966	CF110966 Shultzomi
44	712.5	43.0	974	14	CB988195	CB988195 AGENCOURT
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ALIGNMENTS

RESULT 1	AL550279	AL550279	1154 bp	mRNA	linear	EST 31-MAY-2003
LOCUS	AL550279	AL550279	Homo sapiens	PLACENTA	COT 25-NORMALIZED	Homo sapiens cDNA
DEFINITION	clone CS0DI039YJ06	5-PRIME, mRNA sequence.				
ACCESSION	AL550279					
VERSION	AL550279.2	GI:31272096				
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1	(bases 1 to 1154)				

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12887098.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI039DE03QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI039DE03QP1.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 9.19e-143 Length: 1154
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-079-111-1 (1-322) x AL550279 (1-1154)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 122 ATGCCAGGTGCTTCAGCCCTGGTGTGCTTCTCACTTCCATCTGGACCAGGCTCCTG 181
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 182 GTCCAGGCTCTTTGCGTGCAGAGAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG 241
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 242 ATCACCTTGTGAGCAAAAAGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 301
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 302 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 361
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
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QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
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QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 482 AGCCGCAGATTTCAGCCCTATTGTTACAACACTCATCTGATACCTTGGAATAACTCGTGCATT 541
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
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QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

Db 602 GAATTTATTGTGTCAGTGACAGTACTACTCGGTGGCATCCCCCTACTCTACAATACCTGCC 661
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
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QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 722 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 781
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 782 GAAATAAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 841
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 842 CTAGTGTGCTCTCCTCTTCTTTGGTGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAA 901
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 902 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAGAAATGATCGAAACC 961
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
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QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1022 GATAAAAACCCAGAGAGTCCACAGAGTCCAAGCAAACACTACCGTGGATGCCTGGAAGCT 1081
QY 321 GluVal 322
Db 1082 GAAGTT 1087
RESULT 2
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LOCUS AL550621 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI058YN14 5-PRIME, mRNA sequence.
ACCESSION AL550621 GI:31272438
VERSION AL550621.2
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12887768.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI058DG07QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI058DG07QP1.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
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primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 3.64e-129 Length: 1201
Score: 1510.50 Matches: 296
Percent Similarity: 95.53% Conservatives: 3
Best Local Similarity: 94.57% Mismatches: 11
Query Match: 91.16% Indels: 3
DB: 9 Gaps: 1

US-10-079-111-1 (1-322) x AL550621 (1-1201)

QY	1	MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu	20
Db	158	ATGGCCAGGTGCTTCAGCGTGGTGTGCTTCTCACTCCATCTGGACCACGAGGCTCCTG	217
QY	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	218	GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG	277
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	278	ATCACCCCTTGTAGCAAAAAGGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC	337
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	338	TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGCAAGCTTGAACAGCCCTGAAAGCT	397
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	398	AGCTTTGAAACTTGAGCTATGGCTGGGTGGAGATGGATTCTGTGTCATCTCTAGGATT	457
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	458	AGCCCCAAACCCCAAGTGGGAAAAATGGGGTGGGTGCTGATTTGGAAAGTTCAGTG	517
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	518	AGCCGACAGTTTGCAGCCTATTGTTACAACCTCACTCTGATACTTGGACTTAACCTCGTCATT	577
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	578	CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA	637
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	638	AAATTTATTGTGACGTACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	697
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	698	CCTACTACTACTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	757
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	758	TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	817
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	818	GAAAAATAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTGGAGGTGTCCCCACGGCTCTG	877
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	878	CTAGTGCTTGCTCTCCTCTTCTTTGGTGTCTGAGTGGTCTTGGAATTTTGCTATGTCAA	937
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	938	AGGTATGTGAAGGCCCTTCCCTTTTACAAAARAATATCAGCMGAAGGAAATGWTGADACC	997
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300

Db	998	MAAGTAGTAAAGGAGAGAGCCCAATGATWASCACCCYATGAGGGATCAAGAAAACT	1057
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThr	313
Db	1058	GWTAAACCCCG-----AAGAGTCCAGAGTCMAGC	1087
RESULT 3			
AL552299			
LOCUS	AL552299	Homo sapiens	PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION	AL552299	Homo sapiens	PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
ACCESSION	AL552299		
VERSION	AL552299.2	GI:31274114	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished (2001)		
COMMENT	On Feb 15, 2001 this sequence version replaced gi:12891068.		

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI069DG01QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI069DG01QP1.

FEATURES
source

1..1015
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI069YN02"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 1.9e-126 Length: 1015
Score: 1480.00 Matches: 288
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 89.32% Indels: 0
DB: 9 Gaps: 0

US-10-079-111-1 (1-322) x AL552299 (1-1015)

QY	1	MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu	20
Db	144	ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTCCATCTGGACCACGAGGCTCCTG	203
QY	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	204	GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG	263
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	264	ATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTTCACAGAAAGCTAAGGAGGCC	323
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80

Db 324 TGTAGGCTGCTGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 383

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
|||||

Db 384 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCTGGTTCATCTCTAGGATT 443

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
|||||

Db 444 AGCCCAAACCCCAAGTGTGGGAAAAATGGGTGGTGTCTCGATTGGAAGGTTCCAGTG 503

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
|||||

Db 504 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACCTTGGACTAACTCGTGCAAT 563

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
|||||

Db 564 CCAGAAATATATCACCAACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACAACA 623

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
|||||

Db 624 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 683

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
|||||

Db 684 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 743

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
|||||

Db 744 TGTGTACAGAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 803

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
|||||

Db 804 GAAATAAAGCAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 863

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260

Db 864 CTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTGTGCTATGTCAA 923

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
|||||

Db 924 AGGTATGTGAAGGCCTTCCCTTTTACAACAAGAATCAGCAGAGGAAATGATCGAAACC 983

QY 281 LysValValLysGluGluLysAla 288
|||||

Db 984 AAAGTAGTAAAGGAGGAGAGGCC 1007

RESULT 4
AL546669
LOCUS
DEFINITION AL546669 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI029YJ09 5-PRIME, mRNA sequence. EST 31-MAY-2003

ACCESSION AL546669
VERSION AL546669.2 GI:31268502
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12880008.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI029CE05QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI029CE05QP1.

FEATURES
source
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI029YJ09"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dt)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores: 5.13e-126 Length: 1201
Pred. No.: 1476.50 Matches: 302
Score: 96.24% Conservative: 5
Percent Similarity: 94.67% Mismatches: 11
Best Local Similarity: 89.11% Indels: 5
Query Match: 9 Gaps: 1
DB: 1
US-10-079-111-1 (1-322) x AL546669 (1-1201)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
|||||

Db 126 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 185

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
|||||

Db 186 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 245

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuLeuAsnPheThrGluAlaLysGluAla 60
|||||

Db 246 ATCACCTTGTGAGCAAAAAGCGCAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 305

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
|||||

Db 306 TGTAGGCTGCTGGACTAAGTTTGGCCGGCAAGGACCAAGITGAAACAGCCTTGAAAGCT 365

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
|||||

Db 366 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCTGGTTCATCTCTAGGATT 425

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
|||||

Db 426 AGCCCAAACCCCAAGTGTGGGAAAAATGGGTGGTGTCTCGATTGGAAGGTTCCAGTG 485

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
|||||

Db 486 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATCTGGACTAACTCGTGCAAT 545

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
|||||

Db 546 CCAGAAATATATCACCAACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACAACA 605

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
|||||

Db 606 GAATTTATTGTCAGTGACAGTACTCTCGTGGCATCCCTTACTCTACAATACCTGCC 665

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
|||||

Db 666 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 725

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
|||||

Db 726 TGTGTACAGAGAAGTTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 785

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
|||||

Db 786 GAAATAAAGCAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 845

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
|||||
Db 846 CTAGTGCTTGCTCTCCTCTCTTTGGTGTGCAGCTGGTCTTGGATTTTGTATGTCAAA 905

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
|||||
Db 906 AGGTATGTGAAGGCCTTCCTTTTACAAACAAGAAATCAGCAGAAGGAAATGATCGAAACC 965

QY 281 LysValValLysGluGlyLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
|||||
Db 966 ACAGTAGTAAAGGAGGR-GAGGGCAATGATAGCAM-CCTAATGRGGATC--AAAGAAACT 1021

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGlu 319
|||||
Db 1022 GATAAAAA-CCAGAAGAGTCCAGA---GTCCAGCAAACTTMCGTGCGATGCTCGGAG 1074

RESULT 5
AL551020 1201 bp mRNA linear EST 31-MAY-2003
LOCUS AL551020 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI066YL13 5-PRIME, mRNA sequence.
ACCESSION AL551020
VERSION AL551020.2 GI:31272837
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12888564.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI066CF07QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI066CF07QP1.

FEATURES
source
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI066YL13"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 1.53e-122 Length: 1201
Score: 1439.00 Matches: 300
Percent Similarity: 94.98% Conservative: 3
Best Local Similarity: 94.04% Mismatches: 14
Query Match: 86.84% Indels: 7
DB: 9 Gaps: 2

US-10-079-111-1 (1-322) x AL551020 (1-1201)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
|||||
Db 98 ATGCCAGGTGCTTCAGCGTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 157

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
|||||
Db 158 GTCCAAGGCTCTTTGCCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 217

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
|||||
Db 218 ATCACCTTGTGAGCAAAAAGCGCAACCAGCAGCTGAATTTTCACAGAAGCTAAGGAGGCC 277

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
|||||
Db 278 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAGACT 337

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
|||||
Db 338 AGCTTTGAAACTTTCAGCTATGGCTGGTGGATTCGTGGTTCATCTCTAGGATT 397

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
|||||
Db 398 AGCCCAAAACCCCAAGTGTGGGAAAAAATGGGGTGGGTGCTGATTGGAAGGTTCCAGTG 457

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
|||||
Db 458 AGCCGACAGTTTGCAGCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCAAT 517

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
|||||
Db 518 CCAGAAATTATCACCAACCAAGATCCCATATTTCAACACTCAAACGCAACACAACAACA 577

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
|||||
Db 578 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACATACTGCCC 637

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
|||||
Db 638 CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 697

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
|||||
Db 698 TGTGTACAGAGAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 757

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
|||||
Db 758 GAAATAAAGCAGCATTCAAGAAATGAAGCTGCTGGTTTGGAGGTGTCCCCCAGCGTCTGT 817

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
|||||
Db 818 CTAGTGCTTGCTCTCCTCTTCTTTGGTGTCTGCAGCTGGTCTTGGATTTTGTATGTCAA 877

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
|||||
Db 878 AGGTATGTGAAGGC-TTCCCTTTTACAAACACAGAATCAGCAGAAGGAAATGATCGAAACC 936

QY 281 LysValValLysGluGlyLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
|||||
Db 937 AAGTA-GTAAAGGCGAGAGGGC-AATGATAGCAA-CCTAATGAGGA-TCAAAGAAAACT 992

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGlu 319
|||||
Db 993 GATAAAAACC---AGAAGAGTCAAGAGTCCAGCAAAACTACGKG---CGATGCTKGCAG 1043

RESULT 6
AL553858 1014 bp mRNA linear EST 31-MAY-2003
LOCUS AL553858 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI077YJ17 5-PRIME, mRNA sequence.
ACCESSION AL553858
VERSION AL553858.2 GI:31275672
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1014)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12894087.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI077CE09QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI077CE09QP1.

FEATURES
source
1. .1014
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI077YJ17"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 5.96e-112 Length: 1014
Score: 1323.50 Matches: 272
Percent Similarity: 98.55% Conservative: 0
Best Local Similarity: 98.55% Mismatches: 4
Query Match: 79.87% Indels: 4
DB: 9 Gaps: 0

US-10-079-111-1 (1-322) x AL553858 (1-1014)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 162 ATGCCAGGTGCTTCAGCCCTGGTGTGCTTCTCACTTCCATCTGCACACGAGGCTCCTG 221
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 222 GTCCAAAGGCTCTTTCGCTGCAGAAAGAGCTTCCATCCAGGTGTCATGCAGAAATTATGGG 281
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 282 ATCACCTTGTGAGCAAAAGCGAACCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 341
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 342 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 401
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
Db 402 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGGTTCATCTCTAGGATT 461
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 462 AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCTCTGATTGGAAGGTTCCAGTG 521
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerSerAspThrTrpThrAsnSerCysIle 140
Db 522 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACCTTGGACTTAACCTCGTGCATT 581
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 582 CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACACAACAACA 641

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 642 GAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTTCTACATACTGCC 701
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 702 CCTACTACTACTCTCTGCTCCAGCTTCCACTTCTATCCACGAGAAAAAATTGATT 761
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db 762 TGTGTCACAGAAAGTTTTTATGGAAGTACCATGTCTACAGAAACTGAACCATTTGTT 821
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 822 GAAATAAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGGAGGTGT-CCCACGGCTCTG 880
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 881 CTAGTGCTTGCTCTCTCTTCTTTGGTGTGCAGCTGGTCTTGGATTTTGTATGTCAA- 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGlu 276
Db 940 AGGTATGTGAAGGCTT--CCYTTTACAAACAR-AATCAGCAGAGAGGAA 984

RESULT 7
BX459046
LOCUS BX459046 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE011YN20
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BX459046
VERSION BX459046.1 GI:31021086
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 913)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DE011DG10QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DE011DG10QP1.

FEATURES
source
1. .913
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE011YN20"
/tissue type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN
Alignment Scores:
Pred. No.: 2.53e-111 Length: 913
Score: 1316.00 Matches: 260
Percent Similarity: 99.62% Conservative: 0
Best Local Similarity: 99.62% Mismatches: 1
Query Match: 79.42% Indels: 1

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 972)
TITLE Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12885569.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI044DG08QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI044DG08QP1.
FEATURES
source
1. .972
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI044YN16"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Alignment Scores:
Pred. No.: 1.74e-107 Length: 972
Score: 1275.00 Matches: 261
Percent Similarity: 96.36% Conservative: 4
Best Local Similarity: 94.91% Mismatches: 9
Query Match: 76.95% Indels: 4
DB: 9 Gaps: 1
US-10-079-111-1 (1-322) x AL549512 (1-972)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu 20
Db 143 ATGCCAGGTGCTTCAGCCTGGTGTCTCTCACTCCATCTGGACCAGGCTCCTG 202
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 203 GTCCAAGGCTCTTTGGCTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGG 262
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 263 ATCACCCCTTGTAGCCAAAGCGAACCAGCAGCTGAATTTACAGAAGCYAAGGAGGCC 322
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 323 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGACCAAGTTGAAACAGCCTTGAAAGCY 382
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 383 AGCTTTGAAACTTGCACTATGGCTGGGTTGGAGATGGATTCTGTGTCATCTCTAGGATT 442
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 443 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCCTGATTGGAAAGTTCCAGTG 502
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 503 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCA 562

QY 141 ProGluIleIleThrThrLysAspPheAsnThrGlnThrAlaThrGlnThrThr 160
Db 563 CCAGAAATTATCACCAACCAAGATCCCATATTCAAACTGCAACACAAACA 622
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 623 GAATTTATTGTGAGTACAGTACCTACTCGTGGCATCCCTTACTCTACAATACCTGCC 682
QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 683 CCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 742
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 743 TGTGTSACAGAAAGTTTTTATGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 802
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 803 GAAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCMCG-GCTCTK 861
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 862 CTAGTGTCTTKCTCTCTCTCTTTTGGTGCTG-GCTGGTCTTGGATTGCTATGT-AAA 919
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLys 275
Db 920 AGGTATGTRAGGSCT--TCCTTTTWCAMAAGAATAASAGAAGG 961
RESULT 11
AL543874
LOCUS
DEFINITION AL543874 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI005YG13 5-PRIME, mRNA sequence.
ACCESSION AL543874
VERSION AL543874.2 GI:31265719
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 911)
TITLE Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12876353.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI005AD07QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI005AD07QP1.
FEATURES
source
1. .911
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI005YG13"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Alignment Scores:

Pred. No.:	1.65e-106	Length:	911
Score:	1264.00	Matches:	251
Percent Similarity:	99.60%	Conservative:	0
Best Local Similarity:	99.60%	Mismatches:	1
Query Match:	76.28%	Indels:	1
DB:	9	Gaps:	0
US-10-079-111-1 (1-322) x AL543874 (1-911)			
Qy	1	MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu	20
Db	155	ATGGCCAGGTGCTTCAGCCTGGTGTCTCACTTCCATCTGGACCAGGCTCCTG	214
Qy	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	215	GTCCAAAGGCTCTTTCGTGCAGAGAGCTTCCATCCAGGTGTATGCAGAATTATGGGG	274
Qy	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	275	ATCACCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC	334
Qy	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	335	TGTAGGCTGTGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT	394
Qy	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	395	AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCACTCTAGGATT	454
Qy	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	455	AGCCCAAACCCCAAGTGTGGAAAAATGGGTGGGTGTCTGTATTTGGAAGGTTCCAGTG	514
Qy	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	515	AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACCTGGACTAACTCGTGCA	574
Qy	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	575	CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAACAACA	634
Qy	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	635	GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	694
Qy	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	695	CCTACTACTACTCCTCCTGTCTCCAGCTTCCACTTCTATTCCAGGAGAAAAAATTGATT	754
Qy	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	755	TGTGTACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	814
Qy	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	815	GAAAATAAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGGAGGTGT-CCCACGGCTCTG	873
Qy	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAla	252
Db	874	CTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCT	909
RESULT 12			
AL547774			
LOCUS	AL547774	1201 bp	mRNA linear EST 31-MAY-2003
DEFINITION	AL547774 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA		
	clone CS0DI033YD11 5-PRIME, mRNA sequence.		
ACCESSION	AL547774		
VERSION	AL547774.2	GI:31269603	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		

REFERENCE	1	(bases 1 to 1201)
AUTHORS	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.	
TITLE	Full-length cDNA libraries and normalization	
JOURNAL	Unpublished (2001)	
COMMENT	On Feb 15, 2001 this sequence version replaced gi:12882152. Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CS0DI033CB06QP1&cluster=5952.r. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DI033CB06QP1.	
FEATURES	Location/Qualifiers	
source	1. .1201 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DI033YD11" /tissue type="PLACENTA COT 25-NORMALIZED" /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED" /note="1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."	
ORIGIN		
Alignment Scores:	3.81e-106	Length: 1201
Pred. No.:	1262.00	Matches: 262
Score:	96.00%	Conservative: 2
Percent Similarity:	95.27%	Mismatches: 10
Best Local Similarity:	76.16%	Indels: 5
Query Match:	9	Gaps: 1
DB:	US-10-079-111-1 (1-322) x AL547774 (1-1201)	

Qy	1	MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu	20
Db	263	ATGGCCAGGTGCTTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG	322
Qy	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	323	GTCCAAAGGCTCTTTGCGTGCAGAAAGAGCTTTCATCCAGGTGTATGCAGAATTATGGGG	382
Qy	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	383	ATCACCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC	442
Qy	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	443	TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT	502
Qy	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	503	AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCACTCTAGGATT	562
Qy	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValIleIleTrpLysValProVal	120
Db	563	AGCCCAAACCCCAAGTGTGGAAAAAATGGGTGGGTGCTCTGATTTTGGAAAGGTTCCAGTG	622
Qy	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerSerAspThrTrpThrAsnSerCysIle	140
Db	623	AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCA	682
Qy	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	683	CCAGAAATTATCACCACCAAGATCCCATATTTCAAACACTCAAACTGCAACACAACAACA	742

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSIAI012ZA06QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSIAI012ZA06QP1.

FEATURES
source
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI045YA10"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 1.97e-104 Length: 1201
Score: 1243.50 Matches: 259
Percent Similarity: 97.74% Conservative: 0
Best Local Similarity: 97.74% Mismatches: 6
Query Match: 75.05% Indels: 5
DB: 13 Gaps: 0

US-10-079-111-1 (1-322) x BX402505 (1-1201)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
DB 212 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCATTCCATCTGGACCACGAGGCTCTCTG 271
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
DB 272 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG 331
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
DB 332 ATCACCTTGTGAGCAAAAGCGAACCCAGCAGCTGAATTCACAGAAGCTAAGGAGGCC 391
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
DB 392 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 451
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
DB 452 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGTCATCTCTAGGATT 511
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
DB 512 AGCCCAACCCCAAGTGTGGGAAAAATGGGTGGTGTCTGTGATTGGAAGGTTCCAGTG 571
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
DB 572 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACCTTGGACTAACTCGTGCATT 631
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
DB 632 CCAGAAATTATCACCCACCAAGATCCCATATTCAACACTCAAACTGCAACACAACA 691
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

Db 692 GAATTTATTGTCTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC 751
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
DB 752 CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATTGATT 811
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
DB 812 TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATTGCTACAGAAACTGAACCATTTGTT 871
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
DB 872 GAAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGT-CCCACGGCTCTG 930
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrVallys 260
DB 931 CTAGTGCTTGTCT-CTCTTCTTTGTTGCTGCTGCAGY-GGTCTTGGATTGGS-TATKTCAA 987
QY 261 ArgTyrVallysAla 265
DB 988 AG-TATGTGAAGGCT 1001

RESULT 15
AL544430
LOCUS
DEFINITION AL544430 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI018YG12 5-PRIME, mRNA sequence.
ACCESSION AL544430
VERSION AL544430.2 GI:31266274
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12876910.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI018BD06QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI018BD06QP1.

FEATURES
source
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI018YG12"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 2.2e-104 Length: 1201
Score: 1243.00 Matches: 256
Percent Similarity: 95.90% Conservative: 1
Best Local Similarity: 95.52% Mismatches: 9
Query Match: 75.02% Indels: 5
DB: 9 Gaps: 2

US-10-079-111-1 (1-322) x AL544430 (1-1201)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTyrPThrThrArgLeuLeu 20
Db ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCGATCTGGACCCAGGCTCCTG 298

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db GTCCAAGGCTCTTTGCCGTGCAGAAGAGCTTTCCATCCAGGTGTATGCAGAAATATGGGG 358

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db ATCACCCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 418

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 478

QY 81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100
Db AGCTTTGAAACTTGCGAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCATCTTAGGATT 538

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTyrLysValProVal 120
Db AGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTTGGAAGGTTCCAGTG 598

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTyrPThrThrAsnSerCysIle 140
Db AGCCGACAGTTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT 658

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAAAACAACA 718

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db GAATTTATTGTAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC 778

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTTCCACGGAGAAAAAATTGATT 838

QY 201 CysValThrGluValPheMetGluThrSerThrSerThrMetSerThrGluThrGluPropheVal 220
Db TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 898

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db GAAAATAAAGCAGCATTCAAGAAATGAAGCTGCTGGSTTTGGAGGTGT-CCCACGGCTCTG 957

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db CTAGTGCTTGCTCT-CTCTTCTTTGGTGTCKSAGYGGTCT---TGGATTTGCTATGTCAA- 1012

QY 261 ArgTyrValLysAlaPheProPhe 268
Db AGGTATGTRAGGCYT---CCCTTT 1033

Black

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 15, 2004, 11:24:09 ; Search time 493 Seconds
(without alignments)
2774.685 Million cell updates/sec

Title: US-10-079-111-1
Perfect score: 1657
Sequence: 1 MARCFSLVLLTSIWTTRLL.....NPESKSPSKTTVRCLEAEV 322

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10079111/runat_13092004_102133_13546/app_query.fasta_1.519
-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10079111@cgn_1_1_470@runat_13092004_102133_13546 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2002s:*
6: Geneseqn2003as:*
7: Geneseqn2003bs:*
8: Geneseqn2003cs:*
9: Geneseqn2004s:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1657	100.0	1755	5 AAF93818	Aaf93818 Human CDN
2	1657	100.0	2027	10 ADE71449	Ade71449 Human CDN
3	1657	100.0	2029	3 AAZ98172	Aaz98172 Human sig
4	1657	100.0	2029	10 ADE71445	Ade71445 Human CDN
5	1657	100.0	2372	2 AAX52250	Aax52250 Protein P
6	1657	100.0	2372	3 ADC78520	Adc78520 Human PRO
7	1657	100.0	2372	4 AAF72408	Aaf72408 Human PRO
8	1657	100.0	2372	4 AAF92060	Aaf92060 Human PRO

9	1657	100.0	2372	6 ABS74380	Abs74380 Human CDN
10	1657	100.0	2372	6 ABL88087	Abl88087 Human PRO
11	1657	100.0	2372	6 ABL95576	Abl95576 Human ang
12	1657	100.0	2372	7 ACA59060	Aca59060 Human PRO
13	1657	100.0	2372	7 ACA58457	Aca58457 cDNA enco
14	1657	100.0	2372	7 ACA60164	Aca60164 Human CDN
15	1657	100.0	2372	7 ACD07554	Ac07554 Novel hum
16	1657	100.0	2372	7 ACA91166	Aca91166 Novel hum
17	1657	100.0	2372	7 ACD81543	Acd81543 Human CDN
18	1657	100.0	2372	7 ACA60365	Aca60365 Novel hum
19	1657	100.0	2372	7 ABX71612	Abx71612 Human CDN
20	1657	100.0	2372	7 ACH06944	Ach06944 Human sec
21	1657	100.0	2372	7 ACA58812	Aca58812 cDNA enco
22	1657	100.0	2372	7 ACA63988	Aca63988 cDNA enco
23	1657	100.0	2372	7 ACA91252	Aca91252 cDNA enco
24	1657	100.0	2372	7 ACD45151	Acd45151 Human sec
25	1657	100.0	2372	7 ABX96181	Abx96181 Human sec
26	1657	100.0	2372	7 ACA05502	Aca05502 cDNA enco
27	1657	100.0	2372	7 ACA93699	Aca93699 Human CDN
28	1657	100.0	2372	7 ACD20169	Acd20169 Human sec
29	1657	100.0	2372	7 ACA67273	Aca67273 cDNA enco
30	1657	100.0	2372	7 ACH66246	Ach66246 Novel hum
31	1657	100.0	2372	7 ACD02300	Acd02300 Novel hum
32	1657	100.0	2372	7 ACA89291	Aca89291 Novel hum
33	1657	100.0	2372	7 ACA68928	Aca68928 Novel hum
34	1657	100.0	2372	7 ACA54972	Aca54972 Novel hum
35	1657	100.0	2372	7 ACA98450	Aca98450 Human PRO
36	1657	100.0	2372	8 ACA63375	Aca63375 cDNA enco
37	1657	100.0	2372	8 ACD19807	Acd19807 Human sec
38	1657	100.0	2372	8 ADB29405	Adb29405 Human sec
39	1657	100.0	2372	8 ADB17062	Adb17062 Human CDN
40	1657	100.0	2372	8 ACH03578	Ach03578 Human sec
41	1657	100.0	2372	8 ADA18261	Ada18261 Human sec
42	1657	100.0	2372	8 ACD66954	Acd66954 Human CDN
43	1657	100.0	2372	8 ADA19867	Ada19867 Novel hum
44	1657	100.0	2372	8 ADB17250	Adb17250 Human CDN
45	1657	100.0	2372	8 ACD83115	Acd83115 Human PRO

checked.

ALIGNMENTS

RESULT 1
AAF93818
ID AAF93818 standard; cDNA; 1755 BP.
XX AAF93818;
AC AAF93818;
XX AAF93818;
DT 23-MAY-2001 (first entry)
XX Human cDNA encoding a membrane or secretory protein clone PSEC0135.
DE Human; secretory protein; membrane protein; vaccine; gene therapy;
XX Human; secretory protein; membrane protein; vaccine; gene therapy;
KW Human; secretory protein; membrane protein; vaccine; gene therapy;
KW Human; secretory protein; membrane protein; vaccine; gene therapy;
XX Human; secretory protein; membrane protein; vaccine; gene therapy;
OS Homo sapiens.
XX Homo sapiens.
PN EP1067182-A2.
XX EP1067182-A2.
PD 10-JAN-2001.
XX 10-JAN-2001.
PF 07-JUL-2000; 2000EP-00114090.
XX 07-JUL-2000; 2000EP-00114090.
PR 08-JUL-1999; 99JP-00194179.
PR 11-JAN-2000; 2000JP-00118775.
PR 02-MAY-2000; 2000JP-00183766.
XX (HELI-) HELIX RES INST.
XX Aaf93818 Human CDN
XX Ade71449 Human CDN
XX Aaz98172 Human sig
XX Ade71445 Human CDN
XX Aax52250 Protein P
XX Adc78520 Human PRO
XX Aaf72408 Human PRO
XX Aaf92060 Human PRO

PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT gene therapy or as candidate target molecules in drug development.
XX
PS Claim 1; SEQ ID NO 149; 609pp + Sequence Listing; English.
XX
CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC which encode human secretory or membrane proteins represented by AAB88317
CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
CC invention. The invention also includes methods for the production of
CC antibodies directed against the proteins, and cDNA sequences, which can
CC be used in vaccines. The polynucleotide sequences can be used in gene
CC therapy. The polynucleotide sequences and the proteins they encode may be
CC used in the prevention, treatment and diagnosis of diseases associated
CC with inappropriate secretory protein/membrane protein expression. The
CC nucleic acids and complementary sequences may also be used as DNA probes
CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
CC and quantitate the presence of similar nucleic acid sequences in samples.
CC They may also be used to study the expression and function of secretory
CC proteins/membrane polypeptides and their role in metabolism. The
CC polypeptides may be used as antigens in the production of antibodies
CC against them and in assays to identify modulators (agonists and
CC antagonists) of expression and activity. The antibodies and antagonists
CC may also be used as therapeutic agents to down regulate expression and
CC activity. The antibodies may also be used as diagnostic agents for
CC detecting the presence of the polypeptides in samples (e.g. by enzyme
CC linked immunosorbant assay (ELISA)). Examples of diseases which may be
CC treated include rheumatoid arthritis and diabetes
XX
SQ Sequence 1755 BP; 502 A; 422 C; 406 G; 425 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,66e-146 Length: 1755
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-079-111-1 (1-322) x AAF93818 (1-1755)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db ATGCCAGGCTCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 260
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db GTCCAAGGCTCTTTCGCTGCAGAGAGCTTCCATCCAGGTGTCATGCAGAATTATGGGG 320
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db ATCACCCTGTGTAGCAAAAAGGCGAACCAGCAGCTGAATTCACAGAAGCTAAGGAGGCC 380
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db TGTAGGCTGCTGGGACTAAGTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 440
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTGCTGGTGCATCTCTAGGATT 500
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db AGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTTGGAAGGTTCCAGTG 560
QY 121 SerArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAATCGTGCAAT 620
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db CCAGAAATATTACACCACCAAGATCCCATATTCAACACTCAAACACTGCAACAACAACA 680

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTTACAATACCTGCC 740
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db CCTACTACTACTCCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 800
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db TGTGTACAGAAAGTTTTTATGGAACTAGCACCATTGTCTACAGAAACTGAACCATTTGTT 860
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db GAAATATAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 920
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db CTAGTGGTTGCTCTCTCTTCTTTGGTGCTGCAGTGGTCTTTGGATTGCTATGTCAA 980
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAAGAAATGATCGAAACC 1040
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db AAAGTAGTAAAGGAGGAGAGGCAATGATAGCAACCTTAATGAGGAATCAAAGAAACT 1100
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db GATAAAAAACCCAGAGAGTCCAGAGTCCCAAGCAAACTACCGTGGATGCCTGGAAGCT 1160
QY 321 GluVal 322
Db 1161 GAAGTT 1166
RESULT 2
ADE71449
ID ADE71449 standard; cDNA; 2027 BP.
XX
AC ADE71449;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human cDNA encoding PDEBC #2.
XX
KW breast cancer; PDEBC; metastatic; human; ss; gene.
XX
OS Homo sapiens.
XX
PN US2003124543-A1.
XX
PD 03-JUL-2003.
XX
PF 20-FEB-2002; 2002US-00079111.
XX
PR 15-JAN-1999; 99US-00232160.
XX
PA (STUA/) STUART S G.
PA (STRE/) STREETER D G.
XX
PI Stuart SG, Streeter DG;
XX
DR WPI; 2004-009141/01.
DR P-PSDB; ADE71444.
XX
PT A new cDNA encoding a protein differentially expressed in breast cancer
PT designated PCEBC is useful to stage, treat, and monitor progression or
PT treatment of breast cancer, particularly an invasive, metastatic stage of
PT the disease.
XX
PS Claim 2; Fig 1; 31pp; English.
XX

CC The invention relates to an isolated cDNA encoding a protein that is
CC differentially expressed in breast cancer, designated PDEBC. The
CC invention is useful to diagnose breast cancer. The invention is also
CC useful to stage, treat, and monitor progression or treatment of breast
CC cancer, particularly an invasive, metastatic stage of the disease. The
CC present sequence represents cDNA encoding human PDEBC Incyte 3044710CB1.
CC Note: There are two sequences that have been assigned SEQ ID 2 in the
CC specification, the present sequence represents the sequence given in
CC figure 1.

XX
SQ Sequence 2027 BP; 612 A; 461 C; 445 G; 509 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.25e-146 Length: 2027
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x ADE71449 (1-2027)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 20
Db 181 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCATTCCATCTGGACCACGAGGCTCCTG 240
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 241 GTCCAAGGCTCTTTGCCGTGCAGAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 300
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 301 ATCACCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 360
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 361 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 420
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 421 AGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGGATTGCTGGTCATCTCTAGGATT 480
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 481 AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTCCTGATTTGGAAGGTTCCAGTG 540
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 541 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCAAT 600
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 601 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAAACAACA 660
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 661 GAAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACATACTGCTGCC 720
QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 721 CCTACTACTACTCTCTGCTGCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 780
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db 781 TGTGTACAGAAAGTTTTTATGAAACTAGCACCATGTCTACAGAAACTGAACATTGTGT 840
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 841 GAAAAATAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 900
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 901 CTAGTGCTTGCTCTCTCTTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGGCTATGTCAA 960

QY 261 ArgTyrValLysAlaPhePropheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 961 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC 1020
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1021 AAAGTAGTAAAGGAGGAGAGGCCAATGATGACCAACCCTAATGAGGAATCAAGAAACT 1080
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1081 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTCCGATGCCTGGAAGCT 1140

QY 321 GluVal 322
Db 1141 GAAGTT 1146

RESULT 3

AAZ98172
ID AAZ98172 standard; cDNA; 2029 BP.
XX
AC AAZ98172;
XX
DT 11-MAY-2000 (first entry)
XX

DE Human signal peptide containing protein HSPP-64 cDNA SEQ ID NO:198.

XX Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
KW reproductive disorder; developmental disorder; arteriosclerosis;
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW Parkinson's disease; Huntington's diseases; ovulatory defect;
KW muscular dystrophy; ss.

XX Homo sapiens.

XX WO200000610-A2.

XX 06-JAN-2000.

XX 25-JUN-1999; 99WO-US014484.

XX 26-JUN-1998; 98US-0090762P.

XX 31-JUL-1998; 98US-0094983P.

XX 01-OCT-1998; 98US-0102686P.

XX 11-DEC-1998; 98US-0112129P.

XX (INCY-) INCYTE PHARM INC.

XX Lal P. Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX
DR WPI; 2000-160673/14.
DR P-PSDB; AAY87287.

XX New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
PT disease.

XX Claim 9; Page 288-289; 327pp; English.

XX AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
CC anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
CC neuroprotective, cardiovascular and antiasthmatic activities, and can be
CC used in gene therapy. HSPPs can be used to treat or prevent disorders
CC associated with decreased activity or function of HSPP. Antagonists of
CC HSPP are used to treat or prevent disorders associated with increased
CC activity or function of HSPP. Such diseases include cell proliferation

CC (including cancer), inflammation, cardiovascular, neurological, reproductive or developmental disorders, (e.g. arteriosclerosis, cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia, asthma, Crohn's disease, microbial or other infections, congestive or ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP nucleic acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for diagnosis and monitoring), in gene therapy, as antisense, triplex-forming or ribozyme therapeutics, for detecting related sequences or genetic variations, and for chromosomal mapping. HSPP are also used to raise specific antibodies (Ab) and to screen for agonists and antagonists (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP -related diseases (in usual immunoassays), as therapeutic antagonists, in competitive drug screens, and for purification of HSPP from natural sources

XX
SQ Sequence 2029 BP; 612 A; 463 C; 445 G; 509 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.25e-146 Length: 2029
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-079-111-1 (1-322) x AAZ98172 (1-2029)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 183 ATGCCAGGTGCTTCAGCCTGGTGTCTTCTCACTTCATCTGGACCAGGCTCCTG 242
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 243 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCAGCAATTATGGGG 302
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 303 ATCACCTTGTGAGCAAAAAGGCGAACGACGAGCTGAATTTCCAGAAGCTAAGGAGCC 362
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 363 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCACCAAGTTGAACAGCCTTGAAAGCT 422
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 423 AGCTTTGAACACTTGACGCTATGGCTGGGTGGAGATGGATTTCGTGGTCATCTCTAGGATT 482
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 483 AGCCCCAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTGGAAGGTTCCAGTG 542
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 543 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACITGGACTAACTCGTGCAAT 602
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 603 CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAACAACA 662
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 663 GAATTATTGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 722
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 723 CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATTGATT 782
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 783 TGTGTACACAGAAGTTTTTATGGAACACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 842

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 843 GAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTTGCCCCACGGCTCTG 902
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 903 CTAGTGTCTGCTCTCCTCTTCTTTTGGTGTGCAGCTGGTCTTGGATTTCGTATGTCAA 962
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 963 AGGTATGTGAAGGCCTTCCCTTTTACAAAACAAGAATCAGCAGAAGAAATGATCGAAACC 1022
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1023 AAAGTAGTAAAGGAGGAGAGGCGCAATGATAGCAACCTAATGAGGAATCAAAGAAACT 1082
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1083 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAAGCT 1142
QY 321 GluVal 322
Db 1143 GAAGTT 1148
RESULT 4
ADE71445
ID ADE71445 standard; cDNA; 2029 BP.
XX
AC ADE71445;
XX 29-JAN-2004 (first entry)
DT
XX Human cDNA encoding PDEBC Incyte 3044710CB1.
DE
XX breast cancer; PDEBC; metastatic; human; ss; gene.
KW
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT CDS 183..1151
FT /*tag= a
FT /product= "PDEBC"
XX
PN US2003124543-A1.
XX
PD 03-JUL-2003.
XX
PF 20-FEB-2002; 2002US-00079111.
XX
PR 15-JAN-1999; 99US-00232160.
XX
PA (STUA/) STUART S G.
PA (STRE/) STREETER D G.
XX
PI Stuart SG, Streeter DG;
XX
DR WPI; 2004-009141/01.
DR P-PSDB; ADE71444.
XX
PT A new cDNA encoding a protein differentially expressed in breast cancer designated PDEBC is useful to stage, treat, and monitor progression or treatment of breast cancer, particularly an invasive, metastatic stage of the disease.
PT
PT
XX
PS Claim 2; SEQ ID NO 2; 31pp; English.
XX
CC The invention relates to an isolated cDNA encoding a protein that is differentially expressed in breast cancer, designated PDEBC. The invention is useful to diagnose breast cancer. The invention is also useful to stage, treat, and monitor progression or treatment of breast cancer, particularly an invasive, metastatic stage of the disease. The present sequence represents cDNA encoding human PDEBC Incyte 3044710CB1.
CC Note: There are two sequences that have been assigned SEQ ID 2 in the

CC specification, the present sequence represents the sequence given in the
CC sequence listing.

XX
SQ Sequence 2029 BP; 612 A; 463 C; 445 G; 509 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.25e-146 Length: 2029
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x ADE71445 (1-2029)

QY	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu	20
Db	183	ATGCCAGGTGCTCAGCCTGGTGTGTTGCTTCTCACTTCATCTGGACCAGAGGCTCCTG	242
QY	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	243	GTCCAAGGCTCTTTCGCTGCAGAGAGCTTTCATCCAGGTGTCTATGCAGAATTATGGGG	302
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	303	ATCACCCCTTGTGACAAAAGCGAACCCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC	362
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	363	TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT	422
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	423	AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGGTGCATCTCTAGGATT	482
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	483	AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTGATTTTGGAGGTTCCAGTG	542
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	543	AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATT	602
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	603	CCAGAAATTATCACACCAAGATCCCATATTTCACACTCAAACGTGCACACAAACAACA	662
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	663	GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	722
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	723	CCTACTACTACTCTCCTGCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT	782
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal	220
Db	783	TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	842
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	843	GAAAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTGGAGGTGTCCCCACGCTCTG	902
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	903	CTAGTGCTTGCTCTCCTCTCTCTTGTGGTGTGCAGCTGTCTGGATTTTGCATGTCAA	962
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr	280
Db	963	AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAATGATCGAAACC	1022
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300

Db	1023	AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCTAATAGGAATCAAGAAACT	1082
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1083	GATAAAACCAGAGAGTCCAAGAGTCCAAGCAAACTACCGTGCATGCCTGGAAGCT	1142
QY	321	GluVal 322	
Db	1143	GAAGTT 1148	
RESULT 5			
ID	AA52250	standard; DNA; 2372 BP.	
XX	AA52250;		
AC	AA52250;		
XX	25-JUN-1999	(first entry)	
DT	XX		
XX	Protein PRO263 cDNA clone DNA34431-1171.		
DE	XX		
XX	Secreted protein; transmembrane protein; human; enterocolitis;		
KW	Zollinger-Ellison syndrome; gastrointestinal ulceration;		
KW	congenital microvillus atrophy; skin disease; cell growth;		
KW	abnormal keratinocyte differentiation; psoriasis; epithelial cancer;		
KW	Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;		
KW	dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;		
KW	wound healing; tissue repair; ss.		
XX	Homo sapiens.		
OS	XX		
XX	WO9914328-A2.		
PD	25-MAR-1999.		
XX	16-SEP-1998;	98WO-US019330.	
PF	17-SEP-1997;	97US-0059113P.	
XX	17-SEP-1997;	97US-0059115P.	
PR	17-SEP-1997;	97US-0059117P.	
PR	17-SEP-1997;	97US-0059119P.	
PR	17-SEP-1997;	97US-0059121P.	
PR	17-SEP-1997;	97US-0059122P.	
PR	17-SEP-1997;	97US-0059184P.	
PR	18-SEP-1997;	97US-0059263P.	
PR	18-SEP-1997;	97US-0059266P.	
PR	15-OCT-1997;	97US-0062125P.	
PR	17-OCT-1997;	97US-0062285P.	
PR	17-OCT-1997;	97US-0062287P.	
PR	21-OCT-1997;	97US-0063486P.	
PR	24-OCT-1997;	97US-0062814P.	
PR	24-OCT-1997;	97US-0062816P.	
PR	24-OCT-1997;	97US-0063045P.	
PR	24-OCT-1997;	97US-0063120P.	
PR	24-OCT-1997;	97US-0063121P.	
PR	24-OCT-1997;	97US-0063127P.	
PR	24-OCT-1997;	97US-0063128P.	
PR	27-OCT-1997;	97US-0063327P.	
PR	27-OCT-1997;	97US-0063329P.	
PR	28-OCT-1997;	97US-0063541P.	
PR	28-OCT-1997;	97US-0063542P.	
PR	28-OCT-1997;	97US-0063544P.	
PR	28-OCT-1997;	97US-0063549P.	
PR	28-OCT-1997;	97US-0063550P.	
PR	28-OCT-1997;	97US-0063564P.	
PR	29-OCT-1997;	97US-0063435P.	
PR	29-OCT-1997;	97US-0063704P.	
PR	29-OCT-1997;	97US-0063732P.	
PR	29-OCT-1997;	97US-0063734P.	
PR	29-OCT-1997;	97US-0063735P.	
PR	29-OCT-1997;	97US-0063738P.	
PR	29-OCT-1997;	97US-0064215P.	
PR	31-OCT-1997;	97US-0063870P.	
PR	31-OCT-1997;	97US-0064103P.	

KW atherosclerosis; cardiac injury; infertility; premature aging; AIDS;
KW diabetes; stroke; gene therapy; transgenic; PRO; human; ss; Gene.
XX Homo sapiens.
OS
XX
PN WO200015796-A2.
XX
PD 23-MAR-2000.
XX
PF 15-SEP-1999; 99WO-US021090.
XX
PR 16-SEP-1998; 98WO-US019330.
XX
PA (GETH) GENENTECH INC.
XX
PI Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;
PI Yuan J;
XX
DR WPI; 2000-271434/23.
DR P-PSDB; ADC78521.
XX
PT Novel nucleic acids encoding secreted and transmembrane polypeptides with
PT homology, e.g. to growth and cancer-associated antigens.
XX
PS Claim 2; SEQ ID NO 200; 355pp; English.
XX
CC The invention relates to a novel nucleic acid encoding a PRO polypeptide.
CC The polypeptides and polynucleotides of the invention may be useful as
CC research tools and as therapeutics for treating enterocolitis, Zollinger-
CC Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,
CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal
CC scarring and wound healing, nerve repair, thrombosis, bone and/or
CC cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple
CC sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,
CC infertility, premature aging, AIDS, diabetes complications and stroke.
CC The molecules may also be utilised during gene therapy procedures and
CC transgenic animal production. The current sequence is that of the human
CC PRO cDNA of the invention.
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.04e-146 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-079-111-1 (1-322) x ADC78520 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCATTCCATCTGGACCACGAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAGCGCAACCAGCAGCTGAATTCACAGAAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAGTGAACAGCCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCTGTATTGGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACATCATCTGATCTTGGACTAATCGTGCAAT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTCTCCTCTGCTCCAGCTTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrSerMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTCTTGCCTCTCTCTTTTGGTGCTGCAGTGGTCTTTGGATTTTGCATGTCAAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGGAGGCCAATGATAGCAACCTTAATGAGGAATCAAGAAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTCGATGCCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125
RESULT 7
AAF72408
ID AAF72408 standard; cDNA; 2372 BP.
XX
AC AAF72408;
XX 24-APR-2001 (first entry)
XX Human PRO263 cDNA.
DE
XX Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW ischaemia; inflammation; ss.
OS Homo sapiens.
XX
PN WO200104311-A1.
XX
PD 18-JAN-2001.
XX
PF 22-FEB-2000; 2000WO-US004414.
XX
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.

PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy NA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
DR WPI; 2001-081051/09.
DR P-PSDB; AAB80247.
XX
PT Sixty one nucleic acids encoding PRO polypeptides which are useful in the
PT treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
PT cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
PT disease).
XX
PS Claim 2; Fig 73; 393pp; English.
XX
CC The present sequence is one of sixty one nucleic acids encoding novel
CC secreted and transmembrane PRO polypeptides. The PRO polypeptides are
CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
CC squamous cell carcinoma), gastrointestinal disorders (e.g.
CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,
CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.
CC endometrial bleeding, angiogenesis, ischaemia such as coronary ischaemia,
CC atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid
CC arthritis, multiple sclerosis), infertility, AIDS and diabetes and
CC retinal disorders such as retinitis pigmentosum. The PRO nucleic acids
CC have applications in molecular biology, including use as hybridization
CC probes, and in chromosome and gene mapping
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.04e-146 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-079-111-1 (1-322) x AAF72408 (1-2372)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219
Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCATCCAGGTGTCTATGCAGAAATTATGGG 279
Qy 41 IleThrLeuValSerLysLysAlaAAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC 339
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTGGCCGGCAAGGACCAAGTTGAACAGCCTTGAAAGCT 399

Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTTCGTGGTCATCTCTAGGATT 459
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAACCCCAAGTGTGGGAAATGGGTGGTGTCTCTGATTGGAGGTTCCAGTG 519
Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACCTTGGACTAACTCGTGCA 579
Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 639
Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTATTGTTCAGTGACAGTACCTACTCTCGGTGGCATCCCTTACTCTACAATACCTGCC 699
Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCTCTCTCGCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATTGATT 759
Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAAAGTTTTTATGGAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 819
Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879
Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTCTGCTCTCTCTCTTCTTTGGTGTGCAGCTGGTCTTGGATTTTGTATGTCAA 939
Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCCTTCCCTTTTACAAAACAAGAAATCAGCAGAAAGAAATGATCGAA 999
Qy 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGGAGCAATGATAGCAACCTTAATGAGGAATCAAAGAAACT 1059
Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCCTGGAAGCT 1119
Qy 321 GluVal 322
Db 1120 GAAGTT 1125
RESULT 8
AAF92060
ID AAF92060 standard; cDNA; 2372 BP.
XX
AC AAF92060;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human PRO263 cDNA.
XX
KW Human; PRO protein; mapping; ss.
XX
OS Homo sapiens.
XX
PN WO200116318-A2.
XX
PD 08-MAR-2001.
PF 24-AUG-2000; 2000WO-US023328.
XX

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PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 07-DEC-1999; 99US-0169495P.
PR 09-DEC-1999; 99US-0170262P.
PR 11-JAN-2000; 2000US-0175481P.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 03-MAR-2000; 2000US-0187202P.
PR 21-MAR-2000; 2000US-0191007P.
PR 30-MAR-2000; 2000WO-US008439.
PR 25-APR-2000; 2000US-0199397P.
PR 22-MAY-2000; 2000WO-US014042.
PR 05-JUN-2000; 2000US-0209832P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2001-183260/18.
DR P-PSDB; AAB87528.
XX
PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT biology, including use as hybridization probes, and in chromosome and
PT gene mapping.
XX
PS Claim 2; Fig 5; 278pp; English.
XX
CC The present sequence is the coding sequence for a human PRO polypeptide
CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
CC antagonists or anti-PRO antibodies are useful for preparation of a
CC medicament useful in the treatment of a condition which is responsive to
CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
CC protein may also be employed as molecular weight markers for protein
CC electrophoresis. The PRO coding sequence has applications in molecular
CC biology, including use as hybridisation probes, and in chromosome and
CC gene mapping
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.04e-146 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4

US-10-079-111-1 (1-322) x AAF92060 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCATCTCGACCCAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTTGTGAGCAAAAGCGGAACCCAGCAGCTGAATTCACAGAAGCTAAGGAGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGAAGGACCAAGTTGAAACAGCCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGCTGGGTGGAGATGGATTCGTGGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
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Db 460 AGCCCAACCCCAAGTGTGGAAAAAATGGGTGGTGTCTGTGATTTGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCA 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACGCAACACAAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACATACTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAAAGTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTGGAGGTGTCCCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCTCTCTTTGGTGGTGCAGCTGGTCTTGGATTTTGCTATGTCAAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAAATGATCGAA 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGAGAGAGGCCCAATGATAGCAACCTTAATGAGGAATCAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 9
ABS74380
ID ABS74380 standard; cDNA; 2372 BP.
XX
AC ABS74380;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO263.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;
KW antiarthritic; osteopathic; sports-related joint problem;
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN US2002119130-A1.
XX
PD 29-AUG-2002.
XX
PF 06-DEC-2001; 2001US-00006867.
XX
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0064215P.
PR 22-APR-1998; 98US-0082797P.
PR 29-APR-1998; 98US-0083495P.
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Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAGGCTCTTTGCGTGCAGAGAGCTTTCCATCCAGGTTGCATGCAGAAATTATGGGG 279
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTGTGAGCAAAAAGGCGAACCCAGCAGCTGAAATTCACAGAAGCTAAGGAGGCC 339
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAACCTTGACGCTATGGCTGGGTTGGAGATGGATTCTGGTCTATCTCTAGGATT 459
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTGGAGGTTCCAGTG 519
Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACCTGGACTAACTCGTGCAAT 579
Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCATATTCAACACTCAAACTGCAACACAAACA 639
Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699
Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATTGATT 759
Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAAAGTTTATTGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879
Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCCTCTTCTTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAA 939
Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC 999
Qy 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT 1059
Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAACTACCGTGGATGCCTGGAAGCT 1119
Qy 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 10
ABL88087

ID ABL88087 standard; cDNA; 2372 BP.

XX ABL88087;

AC ABL88087;

XX 16-MAY-2002 (first entry)

DT Human PRO263 cDNA sequence SEQ ID NO:31.

XX Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping; gene; ss.
XX Homo sapiens.
XX WO200200690-A2.
XX 03-JAN-2002.
XX 20-JUN-2001; 2001WO-US019692.
XX 23-JUN-2000; 2000US-0213637P.
XX 20-JUL-2000; 2000US-0219556P.
XX 25-JUL-2000; 2000US-0220624P.
XX 25-JUL-2000; 2000US-0220664P.
XX 28-JUL-2000; 2000WO-US020710.
XX 02-AUG-2000; 2000US-0222695P.
XX 17-AUG-2000; 2000US-00643657.
XX 23-AUG-2000; 2000WO-US023522.
XX 24-AUG-2000; 2000WO-US023328.
XX 07-SEP-2000; 2000US-0230978P.
XX 18-SEP-2000; 2000US-00664610.
XX 18-SEP-2000; 2000US-00665350.
XX 24-OCT-2000; 2000US-0242922P.
XX 08-NOV-2000; 2000US-00709238.
XX 08-NOV-2000; 2000WO-US030952.
XX 10-NOV-2000; 2000WO-US030873.
XX 01-DEC-2000; 2000WO-US032678.
XX 20-DEC-2000; 2000US-00747259.
XX 20-DEC-2000; 2000WO-US034956.
XX 22-JAN-2001; 2001US-00767609.
XX 28-FEB-2001; 2001US-00796498.
XX 28-FEB-2001; 2001WO-US006520.
XX 01-MAR-2001; 2001WO-US006666.
XX 09-MAR-2001; 2001US-00802706.
XX 14-MAR-2001; 2001US-00808689.
XX 22-MAR-2001; 2001US-00816744.
XX 05-APR-2001; 2001US-00828366.
XX 10-MAY-2001; 2001US-00854208.
XX 10-MAY-2001; 2001US-00854280.
XX 25-MAY-2001; 2001US-00866028.
XX 25-MAY-2001; 2001US-00866034.
XX 25-MAY-2001; 2001WO-US017092.
XX 30-MAY-2001; 2001US-00870574.
XX 30-MAY-2001; 2001WO-US017443.
XX 01-JUN-2001; 2001WO-US017800.
XX (GETH) GENENTECH INC.
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI; 2002-090516/12.
DR P-PSDB; ABB84832.
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX Claim 2; Fig 31; 565pp; English.
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC antiangiogenic, hypotensive, vulnery and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
DE

CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The PRO polynucleotides have applications in molecular biology,
CC including use as hybridisation probes, and in chromosome and gene
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC exemplification of the present invention
XX

SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.04e-146 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-079-111-1 (1-322) x ABL88087 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCTGGTGTTCCTCACTCCATCTGGACCACGAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTCACAGAAAGCTAAGGAGGCC 339
QY 61 CysArgLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGACCAAGTTGAAACAGCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTGCAGCTATGGCTGGGTTGGAGATGGATTCTGTGGTCATCTTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAACCCCAAGTGTGGAAAAATGGGTGGGTGCTCCTGATTTGGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCAAT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACCTGCACACAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db 760 TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCACCGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260

Db 880 CTAGTGCTTGCTCTCCTCTTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGCATGTCAAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAAAGGCCCAATGATGAGCAACCTTAATGAGGAATCAAGAAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGAGTCCAAGAAAACTACCGTGCATGCGTGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125
RESULT 11
ABL95576
ID ABL95576 standard; cDNA; 2372 BP.
XX
AC ABL95576;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related cDNA PRO263 SEQ ID NO: 31.
XX
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
XX
OS Homo sapiens.
XX
PN WO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US021735.
XX
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.

XX 18-JUL-2001; 2001US-00909088.
PF 17-SEP-1997; 97US-0059113P.
XX 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.

PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX (GETH) GENENTECH INC.
PA
XX
XX PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-328338/31.
DR P-PSDB; ABU71625.
XX
PT Isolated nucleic acid useful for e.g., treating pathological disorders
PT encodes a secreted or transmembrane protein.
XX
PS Claim 2; Fig 73; 473pp; English.
XX
CC The invention relates to human PRO polypeptides (secreted or
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC PRO polypeptides and polynucleotides can be used in treating pathological
CC disorders and tumors, in therapeutic treatment of cardiac insufficiency
CC disorders and in therapeutic treatment of disorders involving protein
CC secretion by the pancreas, including diabetes. They can also be used in
CC treating disorders associated with the preservation and maintenance of
CC gastrointestinal mucosa and the repair of acute and chronic mucosal
CC lesions, and skin diseases associated with abnormal keratinocyte
CC differentiation (e.g., psoriasis, epithelial cancers such as lung
CC squamous cell carcinoma, epidermoid carcinoma of the vulva and gliomas).
CC The sequences can be used as molecular markers for protein
CC electrophoresis purposes and can be utilised in protein-protein binding
CC assays, biochemical screening assays, immunoassays and cell-based assays.
CC This sequence represents a human PRO polynucleotide of the invention
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.04e-146 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACA59060 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAACAGACTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTGTGAGCAAAAGGCCAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCCGCAAGGCCAACCAAGTTGAAACAGCCTTTGAAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGTCATCTCTAGGATT 459

QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120	PR	17-SEP-1997;	97US-0059117P.
				PR	17-SEP-1997;	97US-0059119P.
Db	460	AGCCAAACCCCAAGTGTGGAAAAATGGGTGGTGCTGATTTGGAAGTTCCAGTG	519	PR	17-SEP-1997;	97US-0059121P.
				PR	17-SEP-1997;	97US-0059122P.
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140	PR	17-SEP-1997;	97US-0059184P.
				PR	18-SEP-1997;	97US-0059263P.
Db	520	AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCAAT	579	PR	18-SEP-1997;	97US-0059266P.
				PR	15-OCT-1997;	97US-0062125P.
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160	PR	17-OCT-1997;	97US-0062285P.
				PR	17-OCT-1997;	97US-0062287P.
Db	580	CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA	639	PR	21-OCT-1997;	97US-0063486P.
				PR	24-OCT-1997;	97US-0062814P.
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180	PR	24-OCT-1997;	97US-0062816P.
				PR	24-OCT-1997;	97US-0063045P.
Db	640	GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	699	PR	24-OCT-1997;	97US-0063120P.
				PR	24-OCT-1997;	97US-0063121P.
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeulle	200	PR	24-OCT-1997;	97US-0063127P.
				PR	24-OCT-1997;	97US-0063128P.
Db	700	CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATTGATT	759	PR	27-OCT-1997;	97US-0063327P.
				PR	27-OCT-1997;	97US-0063329P.
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220	PR	28-OCT-1997;	97US-00633541P.
				PR	28-OCT-1997;	97US-0063542P.
Db	760	TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCAATTTGTT	819	PR	28-OCT-1997;	97US-0063544P.
				PR	28-OCT-1997;	97US-0063549P.
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240	PR	28-OCT-1997;	97US-0063550P.
				PR	28-OCT-1997;	97US-0063564P.
Db	820	GAATAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGTCTG	879	PR	29-OCT-1997;	97US-0063435P.
				PR	29-OCT-1997;	97US-0063704P.
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260	PR	29-OCT-1997;	97US-0063732P.
				PR	29-OCT-1997;	97US-0063734P.
Db	880	CTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA	939	PR	29-OCT-1997;	97US-0063735P.
				PR	29-OCT-1997;	97US-0063738P.
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr	280	PR	29-OCT-1997;	97US-0064215P.
				PR	31-OCT-1997;	97US-0063870P.
Db	940	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGATCAGCAGAAGGAATGATCGAAACC	999	PR	31-OCT-1997;	97US-0064103P.
				PR	03-NOV-1997;	97US-0064248P.
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300	PR	07-NOV-1997;	97US-0064809P.
				PR	12-NOV-1997;	97US-0065186P.
Db	1000	AAAGTAGTAAAGGAGGAGAGAGCCAAATGATAGCAACCTTAATGAGGAATCAAAGAAAACT	1059	PR	17-NOV-1997;	97US-0065846P.
				PR	18-NOV-1997;	97US-0065693P.
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320	PR	21-NOV-1997;	97US-0066120P.
				PR	21-NOV-1997;	97US-0066364P.
Db	1060	GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCT	1119	PR	24-NOV-1997;	97US-0066453P.
				PR	24-NOV-1997;	97US-0066466P.
QY	321	GluVal 322		PR	24-NOV-1997;	97US-0066511P.
Db	1120	GAAGTT 1125		PR	24-NOV-1997;	97US-0066770P.
				PR	24-NOV-1997;	97US-0066772P.
RESULT 13				PR	10-SEP-1998;	98WO-US018824.
ACA58457				PR	14-SEP-1998;	98WO-US019177.
ID ACA58457 standard; cDNA; 2372 BP.				PR	16-SEP-1998;	98WO-US019330.
XX				PR	17-SEP-1998;	98WO-US019437.
AC ACA58457;				PR	01-DEC-1998;	98WO-US025108.
XX				PR	08-SEP-1999;	99WO-US020594.
DT 10-JUN-2003 (first entry)				PR	13-SEP-1999;	99WO-US020944.
XX				PR	15-SEP-1999;	99WO-US021090.
DE cDNA encoding human PRO polypeptide #36.				PR	15-SEP-1999;	99WO-US021547.
XX				PR	05-OCT-1999;	99WO-US023089.
KW Human; secreted and transmembrane protein; PRO polypeptide; cancer;				PR	29-NOV-1999;	99WO-US028214.
KW Alzheimer's disease; ischaemia; cytostatic; nootropic; vasotropic;				PR	30-NOV-1999;	99WO-US028313.
KW neuroprotective; gene; ss.				PR	01-DEC-1999;	99WO-US028301.
OS Homo sapiens.				PR	02-DEC-1999;	99WO-US028564.
XX				PR	02-DEC-1999;	99WO-US028565.
PN US2002192659-A1.				PR	16-DEC-1999;	99WO-US030095.
XX				PR	20-DEC-1999;	99WO-US030911.
PD 19-DEC-2002.				PR	20-DEC-1999;	99WO-US030999.
XX				PR	05-JAN-2000;	2000WO-US000219.
PF 10-JUL-2001; 2001US-00902853.				PR	11-FEB-2000;	2000WO-US003565.
XX				PR	22-FEB-2000;	2000WO-US004414.
PR 17-SEP-1997; 97US-0059113P.				PR	24-FEB-2000;	2000WO-US005004.
PR 17-SEP-1997; 97US-0059115P.				PR	02-MAR-2000;	2000WO-US005841.
				PR	20-MAR-2000;	2000WO-US007377.
				PR	30-MAR-2000;	2000WO-US008439.
				PR	22-MAY-2000;	2000WO-US014042.

PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-361832/34.
DR P-PSDB; ABU71480.
XX
PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or
PT PRO1868, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
PS Claim 2; Fig 73; 474pp; English.
XX
CC The present invention relates to the isolation of novel human secreted
CC and transmembrane proteins (PRO polypeptides), and the polynucleotide
CC sequences encoding them. The polynucleotide sequences are useful in
CC molecular biology, as hybridisation probes, in chromosome and gene
CC mapping, in generating antisense RNA and DNA, and in gene therapy. The
CC polynucleotide sequences may also be used in preparing PRO polypeptides
CC by recombinant techniques, and in generating either transgenic animals or
CC knock-out animals which, in turn, are useful in the development and
CC screening of therapeutically useful reagents. The PRO polypeptides or
CC their antibodies are useful in preparing a medicament for treating a
CC condition responsive to the polypeptide or antibody, such as cancer,
CC Alzheimer's disease or ischaemia, and in various diagnostic assays. The
CC present sequence encodes a human PRO polypeptide of the invention
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.04e-146 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACA58457 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCTGGTGTTGCTTCTCACTTCCATCTGGACCAGAGGTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAAGGCGAACACAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAACACAGCCTTGAAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAAACCTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGGTCACTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCCAACCCCAAGTGTGGGAAAAAATGGGTGGGTGCTCCTGATTGGAAGGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCystyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAAATAAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879

QY 241 LeuValLeuAlaLeuLeuPhePheGlyValAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTCTGCTCTCCTCTCTTTTGGTGTGCAGCTGGTCTTGGATTGTGTCATAA 939

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAATGATCGAAACC 999

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGGAGGCCCATGATAGCAACCTAATAGGAATCAAAGAAACT 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCT 1119

QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 14
ACA60164
ID ACA60164 standard; cDNA; 2372 BP.
XX
AC ACA60164;
XX
DT 12-JUN-2003 (first entry)
XX
DE Human cDNA for secreted/transmembrane protein PRO263.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO;
XX gene therapy; chromosome identification; chromosome marker.
OS Homo sapiens.
XX
PN US2003003530-A1.
XX
PD 02-JAN-2003.
XX
PF 11-JUL-2001; 2001US-00904011.
XX
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.

PR	15-OCT-1997;	97US-0062125P.	PI	Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PR	17-OCT-1997;	97US-0062285P.	PI	Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen MB, Goddard A;
PR	17-OCT-1997;	97US-0062287P.	PI	Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PR	21-OCT-1997;	97US-0063486P.	PI	Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PR	24-OCT-1997;	97US-0062814P.	PI	Williams PM, Wood WI;
PR	24-OCT-1997;	97US-0063045P.	XX	WPI; 2003-329602/31.
PR	24-OCT-1997;	97US-0063120P.	DR	P-PSDB; ABU71926.
PR	24-OCT-1997;	97US-0063121P.	DR	
PR	24-OCT-1997;	97US-0063127P.	XX	
PR	24-OCT-1997;	97US-0063128P.	PT	New transmembrane polypeptides and nucleic acids encoding the
PR	24-OCT-1997;	97US-0063128P.	PT	polypeptides, useful in gene therapy, in chromosome identification, as
PR	27-OCT-1997;	97US-0063327P.	PT	chromosome markers, in generating probes and in tissue typing.
PR	27-OCT-1997;	97US-0063329P.	XX	
PR	28-OCT-1997;	97US-0063541P.	PS	Claim 2; Fig 73; 484pp; English.
PR	28-OCT-1997;	97US-0063542P.	XX	
PR	28-OCT-1997;	97US-0063544P.	CC	The invention relates to an isolated nucleic acid with at least 80%
PR	28-OCT-1997;	97US-0063549P.	CC	nucleic acid sequence identity to a nucleotide sequence encoding one of
PR	28-OCT-1997;	97US-0063550P.	CC	61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a
PR	28-OCT-1997;	97US-0063564P.	CC	PRO protein extracellular domain. Also included are a vector comprising a
PR	29-OCT-1997;	97US-0063435P.	CC	the PRO nucleic acid, a host cell comprising the vector, producing a PRO
PR	29-OCT-1997;	97US-0063704P.	CC	polypeptide (by culturing the host cell for the expression of the PRO
PR	29-OCT-1997;	97US-0063732P.	CC	polypeptide, and recovering the PRO polypeptide from the cell culture),
PR	29-OCT-1997;	97US-0063734P.	CC	an isolated PRO polypeptide (having at least 80% sequence identity to: (
PR	29-OCT-1997;	97US-0063735P.	CC	a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino
PR	29-OCT-1997;	97US-0063738P.	CC	acid sequence encoded by a nucleic acid molecule deposited with an ATCC
PR	29-OCT-1997;	97US-0064215P.	CC	number (detailed in the specification); or (c) an extracellular domain of
PR	31-OCT-1997;	97US-0063870P.	CC	a PRO polypeptide or to a PRO polypeptide lacking its associated signal
PR	31-OCT-1997;	97US-0064103P.	CC	peptide), a chimaeic molecule comprising a PRO polypeptide of fused to a
PR	03-NOV-1997;	97US-0064248P.	CC	heterologous amino acid sequence, an anti-PRO antibody, detecting a
PR	07-NOV-1997;	97US-0064809P.	CC	PRO245 or PRO1868 in a sample suspected of containing the polypeptide,
PR	12-NOV-1997;	97US-0065186P.	CC	linking a bioactive molecule to a cell expressing a PRO245 or PRO1868 and
PR	17-NOV-1997;	97US-0065846P.	CC	modulating at least one biological activity of a cell expressing a PRO245
PR	18-NOV-1997;	97US-0065693P.	CC	or PRO1868. Nucleic acids which encode PRO can be used to generate either
PR	21-NOV-1997;	97US-0066120P.	CC	transgenic animals or knock-out animals which may be used in the
PR	21-NOV-1997;	97US-0066364P.	CC	development and screening of therapeutically useful reagents. The nucleic
PR	24-NOV-1997;	97US-0066453P.	CC	acids may also be used in gene therapy, in chromosome identification, as
PR	24-NOV-1997;	97US-0066466P.	CC	chromosome markers, or in generating probes. The PRO polypeptides are
PR	24-NOV-1997;	97US-0066511P.	CC	useful as molecular markers for protein electrophoresis, and the isolated
PR	24-NOV-1997;	97US-0066770P.	CC	nucleic acids may be used for recombinantly expressing those markers. The
PR	24-NOV-1997;	97US-0066772P.	CC	PRO polypeptides and nucleic acids may also be used in tissue typing.
PR	10-SEP-1998;	98WO-US018824.	CC	Anti-PRO antibodies are useful in diagnostic assays for PRO, and in
PR	14-SEP-1998;	98WO-US019177.	CC	affinity purification of PRO from recombinant cell culture or natural
PR	16-SEP-1998;	98WO-US019330.	CC	sources. The present sequence encodes a PRO protein
PR	17-SEP-1998;	98WO-US019437.	XX	
PR	01-DEC-1998;	98WO-US025108.	SQ	Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
PR	08-SEP-1999;	99WO-US020594.		
PR	13-SEP-1999;	99WO-US020944.		
PR	15-SEP-1999;	99WO-US021090.		
PR	15-SEP-1999;	99WO-US021547.		
PR	05-OCT-1999;	99WO-US023089.		
PR	29-NOV-1999;	99WO-US028214.		
PR	30-NOV-1999;	99WO-US028313.		
PR	01-DEC-1999;	99WO-US028301.		
PR	02-DEC-1999;	99WO-US028564.		
PR	02-DEC-1999;	99WO-US028565.		
PR	16-DEC-1999;	99WO-US030095.		
PR	20-DEC-1999;	99WO-US030911.		
PR	20-DEC-1999;	99WO-US030999.		
PR	05-JAN-2000;	2000WO-US000219.		
PR	11-FEB-2000;	2000WO-US003565.		
PR	22-FEB-2000;	2000WO-US004414.		
PR	24-FEB-2000;	2000WO-US005004.		
PR	02-MAR-2000;	2000WO-US005841.		
PR	20-MAR-2000;	2000WO-US007377.		
PR	30-MAR-2000;	2000WO-US008439.		
PR	22-MAY-2000;	2000WO-US014042.		
PR	02-JUN-2000;	2000WO-US015264.		
PR	28-JUL-2000;	2000WO-US020710.		
PR	24-AUG-2000;	2000WO-US023328.		
PR	18-SEP-2000;	2000US-00665350.		
XX				
PA	(GETH) GENENTECH INC.			
XX				

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

4.04e-146

1657.00

100.00%

100.00%

100.00%

7

Length:

Matches:

Conservative:

Mismatches:

Indels:

Gaps:

2372

322

0

0

0

0

US-10-079-111-1 (1-322) x ACA60164 (1-2372)

QY

1

MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu

20

Db

160

ATGGCCAGGTGCTTCAGCCTGGTGTGTTCTTCTCACTTCCATCTGGACCACGAGGCTCCTG

219

QY

21

ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly

40

Db

220

GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCATCCAGGTGTCTATGCAGAAATTATGGGG

279

QY

41

IleThrLeuValSerIlyLysAlaAasnGlnGlnLeuAsnPheThrGluAlaLysGluAla

60

Db

280

ATCACCCCTTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTTCACAGAAGCTAAGGAGGCC

339

QY

61

CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla

80

Db

340

TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAGGACCAAGTTGAAACAGCCTTGAAAGCT

399

QY

81

SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle

100

Db 400 ||| AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCTCGTGCATCTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

Db 460 AGCCCAAACCCCAAGTGTGGAAAAATGGGTGGGTGTCTGATTGGGAAGGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCAAT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

Db 580 CCAGAAATTTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACACAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

Db 640 GAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTTACAATACCTGCC 699

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

Db 760 TGTGTACACAGAAGTTTTTATGGAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240

Db 820 GAAATATAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260

Db 880 CTAGTGCTTGCTTCCTCTTCTTTGGTGTGCAGCTGGTCTTGGATTGTCTATGTCAA 939

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280

Db 940 AGGTATGTGAAGGCTTCCCTTTTACAACAAGAATCAGCAGAGGAATGATCGAAACC 999

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300

Db 1000 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACT 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320

Db 1060 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCT 1119

QY 321 GluVal 322

Db 1120 GAAGTT 1125

RESULT 15

ACD07564

ID ACD07564 standard; cDNA; 2372 BP.

XX

AC ACD07564;

XX

DT 07-AUG-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO263 cDNA.

XX

KW Human; secreted and transmembrane protein; PRO; pharmaceutical;

KW diagnostic; biosensor; bioreactor; Parkinson's disease;

KW Alzheimer's disease; inflammation; nephritis; wound healing;

KW nerve repair; collateral blood vessel formation; cancer;

KW colorectal cancer; haemorrhage; rheumatoid arthritis; diabetes;

KW cirrhosis; fibrosis; restenosis; dermal fibrotic condition; keloid;

KW scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis;

KW infertility; gene therapy; gene; ss.

XX

OS Homo sapiens.

XX

PN US2002197671-A1.

XX

PD 26-DEC-2002.

XX

PF 17-JUL-2001; 2001US-00907824.

XX

PR 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059115P.

PR 17-SEP-1997; 97US-0059117P.

PR 17-SEP-1997; 97US-0059119P.

PR 17-SEP-1997; 97US-0059121P.

PR 17-SEP-1997; 97US-0059122P.

PR 17-SEP-1997; 97US-0059184P.

PR 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 15-OCT-1997; 97US-0062125P.

PR 17-OCT-1997; 97US-0062285P.

PR 17-OCT-1997; 97US-0062287P.

PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0062814P.

PR 24-OCT-1997; 97US-0062816P.

PR 24-OCT-1997; 97US-0063045P.

PR 24-OCT-1997; 97US-0063120P.

PR 24-OCT-1997; 97US-0063121P.

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PR 24-OCT-1997; 97US-0063128P.

PR 27-OCT-1997; 97US-0063327P.

PR 27-OCT-1997; 97US-0063329P.

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PR 28-OCT-1997; 97US-0063542P.

PR 28-OCT-1997; 97US-0063544P.

PR 28-OCT-1997; 97US-0063549P.

PR 28-OCT-1997; 97US-0063550P.

PR 28-OCT-1997; 97US-0063564P.

PR 29-OCT-1997; 97US-0063435P.

PR 29-OCT-1997; 97US-0063704P.

PR 29-OCT-1997; 97US-0063732P.

PR 29-OCT-1997; 97US-0063734P.

PR 29-OCT-1997; 97US-0063735P.

PR 29-OCT-1997; 97US-0063738P.

PR 29-OCT-1997; 97US-0064215P.

PR 31-OCT-1997; 97US-0063870P.

PR 31-OCT-1997; 97US-0064103P.

PR 03-NOV-1997; 97US-0064248P.

PR 07-NOV-1997; 97US-0064809P.

PR 12-NOV-1997; 97US-0065186P.

PR 17-NOV-1997; 97US-0065846P.

PR 18-NOV-1997; 97US-0065693P.

PR 21-NOV-1997; 97US-0066120P.

PR 21-NOV-1997; 97US-0066364P.

PR 24-NOV-1997; 97US-0066453P.

PR 24-NOV-1997; 97US-0066466P.

PR 24-NOV-1997; 97US-0066511P.

PR 24-NOV-1997; 97US-0066770P.

PR 24-NOV-1997; 97US-0066772P.

PR 10-SEP-1998; 98WO-US018824.

PR 14-SEP-1998; 98WO-US019177.

PR 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98WO-US019437.

PR 01-DEC-1998; 98WO-US025108.

PR 08-SEP-1999; 99WO-US020594.

PR 13-SEP-1999; 99WO-US020944.

PR 15-SEP-1999; 99WO-US021090.

PR 15-SEP-1999; 99WO-US021547.

PR 05-OCT-1999; 99WO-US023089.

PR 29-NOV-1999; 99WO-US028214.

PR 30-NOV-1999; 99WO-US028313.

PR 01-DEC-1999; 99WO-US028301.

PR 02-DEC-1999; 99WO-US028564.

PR 02-DEC-1999; 99WO-US028565.

PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.

PR 20-DEC-1999; 99WO-US030999.

PR 05-JAN-2000; 2000WO-US000219.

PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
PA (GETH) GENENTECH INC.
XX

PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-370793/35.
DR P-PSDB; ABO01809.
XX

PT New genes and secreted and transmembrane polypeptides (e.g. PRO245 or
PT PRO335), useful for treating or diagnosing e.g. Alzheimer's disease,
PT cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia
PT or strokes.

XX Claim 2; Fig 73; 482pp; English.

XX The invention describes a new isolated nucleic acid molecule comprising
CC the full length coding sequence of the DNA deposited with the American
CC Type Culture Collection (e.g. ATCC Deposit No. 209258) , or a sequence
CC with at least 80% identity to a DNA encoding a PRO polypeptide comprising
CC any of 61 sequences having 164-1119 amino acids fully defined in the
CC specification. The PRO polypeptides or polynucleotides are useful as
CC pharmaceuticals, diagnostics, biosensors or bioreactors. These are
CC particularly useful for detecting or treating e.g. Parkinson's disease,
CC Alzheimer's disease, inflammations, nephritis, wound healing, nerve
CC repair, collateral blood vessel formation, cancers (e.g. colorectal
CC cancer), haemorrhage (or reduce risk for haemorrhage), rheumatoid
CC arthritis, diabetes, cirrhosis of the liver, fibrosis of the lungs,
CC restenosis, dermal fibrotic conditions (e.g. keloids or scarring),
CC ischaemia, strokes, hypertension, heart attacks, atherosclerosis, or
CC infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep,
CC pigs, goats, or rabbits) The PRO polypeptides are useful as targets for
CC therapeutic intervention in these diseases, and diagnostic determination
CC of the presence of these diseases. The PRO polypeptides are also useful
CC as molecular weight markers, or for chromosome identification. The PRO
CC genes are useful as hybridisation probes, or for screening libraries of
CC human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
CC therapy, particularly for replacing a defective gene. This sequence
CC encodes a novel human secreted and transmembrane PRO polypeptide
XX

SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:
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Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
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US-10-079-111-1 (1-322) x ACD07564 (1-2372)

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QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
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QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
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QY 121 SerArgGlnPheAlaIaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
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QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
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QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTCACAGAAGTTTTTTATGGAAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAAAATAAAGCAGCATTCAGAAGATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
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Job time : 515 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 15, 2004, 21:04:16 ; Search time 3065 Seconds
(without alignments)
3137.234 Million cell updates/sec

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Word size: 12

Total number of hits satisfying chosen parameters: 101

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	280	87.0	1201	9	AL546669	AL546669 AL546669
4	265	82.3	1201	9	AL551020	AL551020 AL551020
5	237	73.6	839	9	AL546217	AL546217 AL546217
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13	225	69.9	1201	13	BX366718	BX366718 BX366718
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15	219	68.0	1151	9	AL550829	AL550829 AL550829
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17	191	59.3	972	9	AL549512	AL549512 AL549512
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22	136	42.2	802	14	CB994314	CB994314 AGENCOURT
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C 53	53	16.5	1073	9	AL552625	AL552625 AL552625
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ALIGNMENTS

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ACCESSION  AL550279
VERSION     AL550279.2 GI:31272096
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 1154)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On Feb 15, 2001 this sequence version replaced gi:12887098.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 5952.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI039DE03QP1&cluster=5952.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
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digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.:      7.84e-289      Length:      1154
Score:          322.00         Matches:    322
Percent Similarity: 100.00%     Conservative: 0
Best Local Similarity: 100.00%  Mismatches:  0
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DB:              9            Gaps:       0

US-10-079-111-1 (1-322) x AL550279 (1-1154)

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QY      21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
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QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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Db      302 TGTAGGCTGCTGGGACTAAGTTTGGCCGGAAGGACCAAGTTGAAACAGCCTTGAAAGCT 361

QY      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
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Db      362 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTGCTGGTCACTCTTAGGATT 421

QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
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Db      662 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 721

QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
        |||||||
Db      722 TGTGTCAACAGAAAGTTTTTATGGAAACTAGACCCATGTCTACAGAAACTGAACCATTTGTT 781

QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
        |||||||
Db      782 GAAATAAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTTGTCCTCCACGGCTCTG 841

QY      241 LeuValLeuAlaLeuLeuPhePheGlyValAlaAlaGlyLeuGlyPheCysTyrValLys 260
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Db      842 CTAGTGTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTTGTATGTCAAA 901
```


COMMENT On Feb 15, 2001 this sequence version replaced gi:12880008.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI029CE05QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVtroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI029CE05QP1.

FEATURES

source
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI029YJ09"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 1.01e-249 Length: 1201
Score: 280.00 Matches: 280
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 86.96% Indels: 0
DB: 9 Gaps: 0

US-10-079-111-1 (1-322) x AL546669 (1-1201)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 126 ATGCCAGGTGCTTCAGCCTGGTGTTCCTTCTCACTTCCATCTGGACCAGGCTCCTG 185
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 186 GTCCAAGGCTCTTTGGGTGCAGAAGAGCTTCCATCCAGGTGTCATGCAGAATTATGGGG 245
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 246 ATCACCCCTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTACAGAAGCTTAAGGAGGCC 305
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 306 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAAACAGCCTTGAAAGCT 365
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 366 AGCTTTGAAAACCTTGCACTATGGCTGGGTGGAGATGGATTTCGTGGTCATCTCTAGGATT 425
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 426 AGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCCTGAATTGGAAGGTTCCAGTG 485
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 486 AGCCGCAGCTTTCAGCCCTATTGTTACAACCTCATCTGATACITGGACTAACTCGTGCATT 545
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 546 CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 605
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 606 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC 665

QY

181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 666 CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 725

QY

201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 726 TGTGTCACAGAAAGTTTATGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 785

QY

221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 786 GAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 845

QY

241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 846 CTAGTGTGCTCTCCTCTTCTTTGGTGTGCAGCTGGTCTTGGATTTTGGTATGTCAAA 905

QY

261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 906 AGGTATGTGAAGCCTTCCCTTTTACAAACAGAAATCAGCAGAAGGAATGATCGAAACC 965

RESULT 4

AL551020

LOCUS AL551020 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI066YL13 5-PRIME, mRNA sequence.
ACCESSION AL551020
VERSION AL551020.2 GI:31272837
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12888564.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI066CF07QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVtroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI066CF07QP1.

FEATURES

source

1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI066YL13"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.: 9.19e-236 Length: 1201
Score: 265.00 Matches: 280
Percent Similarity: 99.64% Conservative: 0
Best Local Similarity: 99.64% Mismatches: 1
Query Match: 82.30% Indels: 1
DB: 9 Gaps: 0

US-10-079-111-1 (1-322) x AL551020 (1-1201)


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QY      1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrrpThrThrArgLeuLeu 20
      |||
Db      98 ATGCCAGGTCCTTCAGCCTGGTGTCTCTCACTTCCATCTGGACCCAGAGGCTCCTG 157

QY      21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
      |||
Db      158 GTCCAAGGCTCTTTGCGTGCAGAGAGCTTTCCATCCAGGTGTCAAGCAATATATGGG 217

QY      41 IleThrLeuValSerLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
      |||
Db      218 ATCACCCCTTGTAGCAAAAAGGCGAACCCAGCAGCTGAATTTACAGAGCTAAGGAGGCC 277

QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
      |||
Db      278 TGTAGGCTGCTGGGACTAAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGACT 337

QY      81 SerPheGluThrCysSerTyrGlyTrrpValGlyAspGlyPheValValIleSerArgIle 100
      |||
Db      338 AGCTTTGAAACTTCAGACTATGGCTGGGTGGAGATGGATTTCGTGGTCACTCTAGGATT 397

QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrrpLysValProVal 120
      |||
Db      398 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTGATTTGGAGGTTCCAGTG 457

QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrrpThrAsnSerCysIle 140
      |||
Db      458 AGCCGACAGTTTGCAGCCTATTTGTACAACTCATCTGATACTTGGACTAACTCGTGCATT 517

QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
      |||
Db      518 CCAGAAATTATCACCAAAAGATCCCATATTCAACACTCAAACTGCAACACAAAAACA 577

QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
      |||
Db      578 GAATTATTGTTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAAATACCTGCC 637

QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
      |||
Db      638 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT 697

QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
      |||
Db      698 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 757

QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
      |||
Db      758 GAAAAATAAGCAGCATTCAGAATGAAGCTGTGGGTTTGGAGGTGTCCCCACGGCTCTG 817

QY      241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
      |||
Db      818 CTAGTGCTTGCTCTCCTCTCTCTTTGGTGTCTGCAGCTGGTCTGGATTTTGTATGTCAAA 877

QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
      |||
Db      878 AGGTATGTGAAGGC-TTCCCTTTTACAAACAAGAATCAGCAGAGGAAATGATCGAAACC 936

QY      281 Lys 281
      |||
Db      937 AAG 939
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RESULT 5
AL546217
LOCUS      AL546217      839 bp      mRNA      linear      EST 31-MAY-2003
DEFINITION AL546217 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0D1025YP16 5-PRIME, mRNA sequence.
ACCESSION  AL546217
VERSION     AL546217.2  GI:31268051
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1  (bases 1 to 839)
```

```
AUTHORS      Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE        Full-length cDNA libraries and normalization
JOURNAL      Unpublished (2001)
COMMENT      On Feb 15, 2001 this sequence version replaced gi:12879120.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 5952.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0D1025DH08QP1&cluster=5952.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0D1025DH08QP1.
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FEATURES
source      Location/Qualifiers
            1..839
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="CS0D1025YP16"
               /tissue_type="PLACENTA COT 25-NORMALIZED"
               /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
               /note="1st strand cDNA was primed with a NotI-oligo(dT)
               primer. Five prime end enriched, double-strand cDNA was
               digested with Not I and cloned into the Not I and EcoR V
               sites of the pCMVSPORT 6 vector. Library was normalized."
```

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ORIGIN
Alignment Scores:
Pred. No.:      7.27e-210      Length:      839
Score:          237.00         Matches:    237
Percent Similarity: 100.00%     Conservative: 0
Best Local Similarity: 100.00%  Mismatches:   0
Query Match:    73.60%         Indels:     0
DB:             9              Gaps:       0

US-10-079-111-1 (1-322) x AL546217 (1-839)
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QY      1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrrpThrThrArgLeuLeu 20
      |||
Db      125 ATGCCAGGTCCTTCAGCCTGGTGTCTCTCACTTCCATCTGGACCCAGAGGCTCCTG 184

QY      21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
      |||
Db      185 GTCCAAGGCTCTTTGCGTGCAGAGAGCTTTCCATCCAGGTGTCAATGCAGAAATATGGGG 244

QY      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
      |||
Db      245 ATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTACAGAGACTAAGAGGCC 304

QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
      |||
Db      305 TGTAGGCTGCTGGGACTAAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGACT 364

QY      81 SerPheGluThrCysSerTyrGlyTrrpValGlyAspGlyPheValValIleSerArgIle 100
      |||
Db      365 AGCTTTGAAACTTCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCACTCTAGGATT 424

QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrrpLysValProVal 120
      |||
Db      425 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTCTGATTTGGAAGGTTCCAGTG 484

QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrrpThrAsnSerCysIle 140
      |||
Db      485 AGCCGACAGTTTGCAGCCTATTTGTACAACTCATCTGATACTTGGACTAACTCGTGCATT 544

QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
      |||
Db      545 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAAAACA 604

QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
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http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DE011DG10QP1.
FEATURES
source
1. .913
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE011YN20"
/tissue type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN

Alignment Scores:
Pred. No.: 7.94e-210 Length: 913
Score: 237.00 Matches: 260
Percent Similarity: 99.62% Conservative: 0
Best Local Similarity: 99.62% Mismatches: 1
Query Match: 73.60% Indels: 1
DB: 13 Gaps: 0

US-10-079-111-1 (1-322) x BX459046 (1-913)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu 20
|||||
DB 132 ATGCCAGGTGCTTCAGCCCTGGTGTGCTTCTCACITCCATCTGGACCACGAGGCTCTG 191

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
|||||
DB 192 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGG 251

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
|||||
DB 252 ATCACCCCTTGTGAGCAAAAGGCGAAACACGAGCTGAATTTACAGAAAGCTAAGGAGGCC 311

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
|||||
DB 312 TGTAGGCTGCTGGACTAAGTTGGCCGGCAAGGACCAGTGAACAGCCTTGAAGGCT 371

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
|||||
DB 372 AGCTTTGAAACTTGCAGCTATGCTGGGTGGAGATGGATTGCTGTCATCTCTAGGATT 431

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
|||||
DB 432 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGTGTCTGATTGGAAGTTCCAGTG 491

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
|||||
DB 492 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTTAACCTCGTGCA 551

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
|||||
DB 552 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 611

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
|||||
DB 612 GAATTTATTGTGAGTACAGTACCTACTCGTGGCATCCCTTACTCTACAATACCTGCC 671

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
|||||
DB 672 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 731

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
|||||
DB 732 TGTGTACAGAAAGTTTATTGGAACCTAGCACCATGTCTACAGAAACTGAACCATTTTGT 791

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
|||||

DB 792 GAAATAAAGCAGCATTCAAGATGAAGCTGCTGGTTGGAGGTGT-CCCACGCTCTG 850

QY 241 LeuValLeuAlaLeuLeuPheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
|||||
DB 851 CTAGTGCTTGCTCTCTCTCTTTTGGTGTGCAGCTGGTCTTGGATTTGCTATGTCAA 910

QY 261 Arg 261
|||
DB 911 AGG 913

RESULT 8
AL553858 1014 bp mRNA linear EST 31-MAY-2003
LOCUS AL553858 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI077YJ17 5-PRIME, mRNA sequence.
ACCESSION AL553858
VERSION AL553858.2 GI:31275672
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1014)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12894087.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI077CE09QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI077CE09QP1.
FEATURES
source
1. .1014
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI077YJ17"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 8.85e-210 Length: 1014
Score: 237.00 Matches: 259
Percent Similarity: 99.62% Conservative: 0
Best Local Similarity: 99.62% Mismatches: 1
Query Match: 73.60% Indels: 1
DB: 9 Gaps: 0

US-10-079-111-1 (1-322) x AL553858 (1-1014)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu 20
|||||
DB 162 ATGCCAGGTGCTTCAGCCCTGGTGTGCTTCTCACITCCATCTGGACCACGAGGCTCTG 221

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
|||||
DB 222 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGG 281

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
|||||

Db	282	ATCACCCCTTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAAGGAGGCC	341
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	342	TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT	401
QY	81	SerPheGluThrCysSerTyrGlyTrrpValGlyAspGlyPheValValIleSerArgIle	100
Db	402	AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCACTCTAGGATT	461
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	462	AGCCCAACCCCAAGTGTGGGAAAAATGGGTGGTGTCTGATTTGGAGGTTCCAGTG	521
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	522	AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATT	581
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	582	CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACAACA	641
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	642	GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC	701
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	702	CCTACTACTCTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	761
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal	220
Db	762	TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	821
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	822	GAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTTGGAGGTGT-CCCACGGCTCTG	880
QY	241	LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	881	CTAGTGCTTGCTCTCCTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGGTATGTCAAA	940

RESULT 9	AL544430	AL544430	1201 bp	mRNA	linear	EST 31-MAY-2003
LOCUS	AL544430	Homo sapiens	PLACENTA	COT 25-NORMALIZED	Homo sapiens	cdna
DEFINITION	clone CS0DI018YG12	5-PRIME, mRNA	sequence.			

FEATURES
source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI018YG12"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

```

ORIGIN

Alignment Scores:		
Pred. No.:	1.05e-209	1201
Score:	237.00	237
Percent Similarity:	100.00%	Matches:
Best Local Similarity:	100.00%	Conservative:
Query Match:	73.60%	Mismatches:
DB:	9	Indels:
		Gaps:

US-10-079-111-1 (1-322) x AL544430 (1-1201)

[illegible]

RESULT 10
AL547774
LOCUS


```
DB: 13 Gaps: 0
US-10-079-111-1 (1-322) x BX402505 (1-1201)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 212 ATGCCAGGTCCTCAGCCTGGTGTTCCTCATTCCATCTGGACCACGAGGTCCTG 271

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 272 GTCCAAGGCTCTTTGCCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGG 331

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 332 ATCACCCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 391

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 392 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 451

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 452 AGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGGATTTCGTGGTCATCTTAGGATT 511

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 512 AGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGTGCTCCTGATTTGGAAAGGTTCCAGTG 571

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 572 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCAATT 631

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 632 CCAGAAATTATCACCAACCAAGATCCCATATTTCACACACTCAAACCTGCAACACAAACAACA 691

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 692 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 751

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 752 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 811

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 812 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 871

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValPro 237
Db 872 GAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCA 922
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RESULT 12
AL550615
LOCUS
DEFINITION AL550615 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI058YJ19 5-PRIME, mRNA sequence.
ACCESSION AL550615
VERSION AL550615.2 GI:31272432
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 970)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12887757.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
```

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r For more information about this cluster, see <http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI058CE10QP1&cluster=5952.r>. Contact : Feng Liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/InvitrogenCorporation1600FaradayAvenueGenoscopeSequenceID:CS0DI058CE10QP1>.

FEATURES
source

1..970
/location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI058YJ19"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 1.71e-200 Length: 970
Score: 227.00 Matches: 227
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 70.50% Indels: 0
DB: 9 Gaps: 0
US-10-079-111-1 (1-322) x AL550615 (1-970)

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QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 249 ATGGCCAGGTGCTTCAGCCTGGTGTTCCTCATTCCATCTGGACCACGAGGTCCTG 308

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 309 GTCCAAGGCTCTTTCGTGCAGAAGAGCTTTCATCCAGGTGTATGCAGAAATTATGGGG 368

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 369 ATCACCCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAGAAAGCTAAGGAGCC 428

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 429 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 488

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 489 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGGTCATCTTAGGATT 548

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 549 AGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGTGCTCCTGATTTGGAAGGTTCCAGTG 608

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 609 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGGACTAACTCGTGCAATT 668

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 669 CCAGAAATTATCACCAACCAAGATCCCATATTCACACTCAAACCTGCAACACAAACAACA 728

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 729 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 788

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 789 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 848

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
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|||||
849 TGTGTCACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAACTGAACATTGTT 908

221 GluAsnLysAlaAlaPheLys 227
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909 GAAATAAAGCAGCATTC AAG 929

RESULT 13
BX366718                               1201 bp      mRNA      linear      EST 08-MAY-2003
LOCUS
DEFINITION
BX366718 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI040YD03 5-PRIME, mRNA sequence.
ACCESSION
BX366718
VERSION
BX366718.1 GI:30451557
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
AUTHORS
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished (2001)
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0AI040CB02QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0AI040CB02QP1.

FEATURES
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CS0DI040YD03"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 1.55e-198 Length: 1201
Score: 225.00 Matches: 225
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 69.88% Indels: 0
DB: 13 Gaps: 0

US-10-079-111-1 (1-322) x BX366718 (1-1201)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
|||||
Db 212 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCATTCCATCTGGACCACGAGGCTCCTG 271
|||||
Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
|||||
Db 272 GTCCAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 331
|||||
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
|||||
Db 332 ATCACCCCTGTGAGCAAAAAGCGAACCAGCAGCTGAATTTTCAGAAAGCTAAGAGGCC 391
|||||
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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Db 392 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 451
Qy 81 SerPheGluThrCysSerTyrGlyTipValGlyAspGlyPheValValIleSerArgIle 100
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Db 452 AGCTTTGAAACITGCAGCTATGGCTGGTTGGAGATGGATTCTGGTCACTCTAGGATT 511
|||||
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTipLysValProVal 120
|||||
Db 512 AGCCCAAACCCCAAGTGTGGGAAAAATGGGTGGTGCTCTGATTTTGGAAGGTTCAGTG 571
|||||
Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
|||||
Db 572 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCA 631
|||||
Qy 141 ProGluIleIleThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
|||||
Db 632 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 691
|||||
Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
|||||
Db 692 GAATTATTGTGAGTACAGTACCTACTCGTGGCATCCCTTACTCTACAATACCTGCC 751
|||||
Qy 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
|||||
Db 752 CCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTTCCACGGAGAAAAAATTGATT 811
|||||
Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
|||||
Db 812 TGTGTCACAGAAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 871
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Qy 221 GluAsnLysAlaAla 225
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Db 872 GAAATAAAGCAGCA 886
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RESULT 14
AL546623                               1201 bp      mRNA      linear      EST 31-MAY-2003
LOCUS
DEFINITION
AL546623 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI029YM23 5-PRIME, mRNA sequence.
ACCESSION
AL546623
VERSION
AL546623.2 GI:31268456
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
AUTHORS
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished (2001)
COMMENT
On Feb 15, 2001 this sequence version replaced gi:12879917.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI029AG12QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI029AG12QP1.

FEATURES
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CS0DI029YM23"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 1.55e-198 Length: 1201
Score: 225.00 Matches: 225
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 69.88% Indels: 0
DB: 13 Gaps: 0

US-10-079-111-1 (1-322) x BX366718 (1-1201)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
|||||
Db 212 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCATTCCATCTGGACCACGAGGCTCCTG 271
|||||
Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
|||||
Db 272 GTCCAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 331
|||||
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
|||||
Db 332 ATCACCCCTGTGAGCAAAAAGCGAACCAGCAGCTGAATTTTCAGAAAGCTAAGAGGCC 391
|||||
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	303	TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT	362
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	363	AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTGGTGCATCTCTAGGATT	422
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	423	AGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCCTGATTGGAAAGTTCCAGTG	482
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	483	AGCCGACAGTTTGCAGCCCTATGTTACAACCTCATCTGATACTTGGACTAACTCGTGCAAT	542
QY	141	ProGluIleIleThrTrpLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	543	CCAGAAATATTATCACCCAAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA	602
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	603	GAATTTATTGTCAGTGACAGTACCTACTCGTGGCATCCCTTACTCTACAATACCTGCC	662
QY	181	Pro	181
Db	663	CCT	665
RESULT 19			
AL550621			
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DEFINITION	clone CS0DI058YN14	5-PRIME, mRNA sequence.	
ACCESSION	AL550621		
VERSION	AL550621.2	GI:31272438	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 1201)		
JOURNAL	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.		
COMMENT	Full-length cDNA libraries and normalization		
	Unpublished (2001)		
	On Feb 15, 2001 this sequence version replaced gi:12887768.		
	Contact: Genoscope		
	Genoscope - Centre National de Sequencage		
	BP 191 91006 EVRY cedex - France		
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr		
	Library was constructed by Life Technologies, a division of		
	Invitrogen. This sequence belongs to sequence cluster 5952.r For		
	more information about this cluster, see		
	http://www.genoscope.cns.fr/		
	cgi-bin/cluster.cgi?seq=CS0DI058DG07QPl&cluster=5952.r. Contact :		
	Feng Liang Email : fliang@lifetech.com URL :		
	http://fulllength.invitrogen.com/ InvitroGen Corporation 1600		
	Faraday Avenue Genoscope sequence ID : CS0DI058DG07QP1.		
FEATURES	Location/Qualifiers		
Source	1. .1201		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="CS0DI058YN14"		
	/tissue_type="PLACENTA COT 25-NORMALIZED"		
	/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"		
	/note="1st strand cDNA was primed with a NotI-oligo(dT)		
	primer. Five prime end enriched, double-strand cDNA was		
	digested with Not I and cloned into the Not I and EcoR V		
	sites of the pCMVSPORT 6 vector. Library was normalized."		
ORIGIN			
Alignment Scores:			

Pred. No.:	1.75e-145	Length:	1201
Score:	168.00	Matches:	268
Percent Similarity:	99.26%	Conservative:	0
Best Local Similarity:	99.26%	Mismatches:	1
Query Match:	52.17%	Indels:	2
DB:	9	Gaps:	0
US-10-079-111-1 (1-322) x AL550621 (1-1201)			
QY	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu	20
Db	158	ATGCCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG	217
QY	21	ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	218	GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCAATGAGGCTATGGGG	277
QY	41	IleThrLeuValSerLysLysAlaAasnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	278	ATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC	337
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	338	TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT	397
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	398	AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTGCTGTCATCTCTAGGATT	457
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	458	AGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTGATTGGAAGGTTCCAGTG	517
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	518	AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGACTTGGACTAATCGTGCAAT	577
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	578	CCAGAAATATTACACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA	637
QY	161	Glu-PheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAl	180
Db	638	AA-ATTATTGTGAGTGACAGTACCTACTCGTGGCATCCCTTACTCTACAATACCTGC	696
QY	180	aProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuI	200
Db	697	CCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGAT	756
QY	200	eCysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVa	220
Db	757	TTGTGTCACAGAAAGTTTTTATGGAAACTAGACCAATGTCTACAGAAACTGAACCATTTGT	816
QY	220	lGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLe	240
Db	817	TGAAAAATAAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTGGAGGTGTCCCCACGGCTCT	876
QY	240	uLeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrVally	260
Db	877	GCTAGTGCTTGCTCTCCTCTCTTTGGTGTGCTGCAGCTGGTCTTTGGATTTTGTATGTCAA	936
QY	260	sArgTyrValLysAlaPheProPheThr	269
Db	937	AAGGTATGTGAAGGCCCTTCCCTTTTACA	964
RESULT 20			
CB959809			
LOCUS	CB959809	760 bp	linear
DEFINITION	AGENCOURT_13889469 NIH_MGC_147 Homo sapiens cDNA clone		EST 29-APR-2003
	IMAGE:30345878 5', mRNA sequence.		
ACCESSION	CB959809		
VERSION	CB959809.1	GI:30215925	
KEYWORDS	EST.		

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 760)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDAM384 row: h column: 15
High quality sequence stop: 545.
FEATURES
source Location/Qualifiers
1..760
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30345878"
/tissue_type="Human Placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC_147"
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
ali-XhoI; Site_2: BamH; Oligo-dT primed using primer
5'-TTTTTCTTTTCTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: This is
a NIH_MGC library."
ORIGIN
Alignment Scores:
Pred. No.: 1.37e-133 Length: 760
Score: 155.00 Matches: 155
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 48.14% Indels: 0
DB: 14 Gaps: 0
US-10-079-111-1 (1-322) x CB959809 (1-760)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 99 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCAGGCTCCTG 158
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 159 GTCCAAGGCTCTTTCGTCGTCAGAGAGCTTCCATCCAGGTGTCATGCAGAATTATGGGG 218
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 219 ATCACCCCTTGTCAGCAAAAAGGCGAACCCAGAGCTGAATTTACAGAAAGCTAAGGAGGCC 278
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 279 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 338
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 339 AGCTTTGAAACITGCAGCTATGGCTGGGTTGAGATGGATTTCGTGGTCATCTCTAGGATT 398
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 399 AGCCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCCTGATTTCGAAGGTTCCAGTG 458

QY 121 SerArgGlnPheAlaTyrCysTyrAsnSerAspThrTrpThrThrAsnSerCysIle 140
Db 459 AGCCGACAGTTTGACGCCTATTGTTACAACCTCATCTGATACTTGGACTAATCGTGCAAT 518
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThr 155
Db 519 CCAGAAATTATCACCACCAAGATCCCATATTCACAACTCAAACT 563
RESULT 21
AL545331
LOCUS
DEFINITION AL545331 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI027YD19 5-PRIME, mRNA sequence.
ACCESSION AL545331
VERSION AL545331.2 GI:31267167
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 864)
Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12877812.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
[http://www.genoscope.cns.fr/](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI027CB10QP1&cluster=5952.r)
Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/InvitrogenCorporation1600>
Faraday Avenue Genoscope sequence ID : CS0DI027CB10QP1.
FEATURES
source Location/Qualifiers
1..864
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI027YD19"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Alignment Scores:
Pred. No.: 1.13e-131 Length: 864
Score: 153.00 Matches: 226
Percent Similarity: 99.56% Conservative: 0
Best Local Similarity: 99.56% Mismatches: 1
Query Match: 47.52% Indels: 1
DB: 9 Gaps: 0
US-10-079-111-1 (1-322) x AL545331 (1-864)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 183 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 242
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 243 GTCCAAGGCTCTTTGCGTGCAGAGAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG 302
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 303 ATCACCCCTTGTCAGCAAAAAGGCGAACCCAGAGCTGAATTTTCAGAAAGCTAAGGAGGCC 362

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
|||||
Db 363 TGTAGCTGCTGGACTAAGTTTGGCCGGAAGGACCAAGTTGAAAACAGCCTTGAAAGCT 422

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
|||||
Db 423 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGAATCGTGGTCATCTCTAGGATT 482

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
|||||
Db 483 AGCCCAAAACCCCAAGTGTGGAA-AATGGGGTGGGTGTCTGATTGGGAAGGTTCCAGTG 541

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
|||||
Db 542 AGCCGACAGTTTGCAGCCTATTGTACAACCTCATCTGATACTTGGACTAACTCGTGCAAT 601

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
|||||
Db 602 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 661

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
|||||
Db 662 GAATTATTGTGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 721

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
|||||
Db 722 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 781

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
|||||
Db 782 TGTGTACAGAGAAGTTTTTATGGAAGCTAGCACCATGTCTACAGAAACTGAACCATTTGTT 841

QY 221 GluAsnLysAlaAlaPheLys 227
|||||
Db 842 GAAATAAAGCAGCATTTCAAG 862

RESULT 22
CB994314

LOCUS CB994314 802 bp mRNA linear EST 01-MAY-2003

DEFINITION AGENCOURT 13620505 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30335820 5', mRNA sequence.

ACCESSION CB994314 GI:30288834

VERSION CB994314.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 802)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDAM358 row: e column: 13
High quality sequence stop: 646.

FEATURES
source Location/Qualifiers
1..802
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30335820"
/tissue_type="pre-eclamptic placenta"
/lab_host="DH10B TonA"

/clone_lib="NIH_MGC_148"
/note="Organ: placenta; Vector: pBluescriptR; Site 1:
ali-XhoI; Site 2: BamH; Library is oligo-dT primed and
directionally cloned using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert
size 2.3 kb and normalized to ROT 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."

ORIGIN

Alignment Scores:
Pred. No.: 6.97e-116 Length: 802
Score: 136.00 Matches: 167
Percent Similarity: 98.82% Conservative: 0
Best Local Similarity: 98.82% Mismatches: 1
Query Match: 42.24% Indels: 2
DB: 14 Gaps: 0

US-10-079-111-1 (1-322) x CB994314 (1-802)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
|||||
Db 231 ATGCCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTCCATCTGGACCACGAGGTCCTG 290

QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
|||||
Db 291 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGG 350

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
|||||
Db 351 ATCACCCCTTGTGAGCAAAAGCGAACCCAGCAGCTGAATTCACAGAAGCTAAGGAGGCC 410

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
|||||
Db 411 TGTAGGCTGCTGGGACTAAGTTTGGCCGGAAGGACCAAGTTGAAACAGCCTTGAAAGCT 470

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
|||||
Db 471 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGAATTCGTGGTCATCTCTAGGATT 530

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
|||||
Db 531 AGCCCAAAACCCCAAGTGTGGAAAAAATGGGTGGGTGGTGTGATTGGGAAGGTTCCAGTG 590

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsn-SerCysIle 140
|||||
Db 591 ACCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAG-CTCGTGCAT 649

QY 140 eProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrTh 160
|||||
Db 650 TCCAGAAATTATCACCAACCAAGATCCCATATTTCACACTCAAACTGCAACACACAACAAC 709

QY 160 rGluPheIleValSerAspSerThr 168
|||||
Db 710 AGAATTATTGTGAGTGACAGTACC 734

RESULT 23
AL552661

LOCUS AL552661 1116 bp mRNA linear EST 31-MAY-2003

DEFINITION AL552661 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI067YG15 5-PRIME, mRNA sequence.

ACCESSION AL552661

VERSION AL552661.2 GI:31274476

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1116)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12891779.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI067AD08QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI067AD08QP1.

FEATURES
source 1..1116
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI067YG15"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 4.42e-111 Length: 1116
Score: 131.00 Matches: 231
Percent Similarity: 99.14% Conservative: 0
Best Local Similarity: 99.14% Mismatches: 1
Query Match: 40.68% Indels: 2
DB: 9 Gaps: 0

US-10-079-111-1 (1-322) x AL552661 (1-1116)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
|||||
249 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCAGAGGTCCTG 308
21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
|||||
309 GTCCAAGGCTCTTTGCGTGCAGAGAGCTTCCATCCAGGTGCATGCAGAATTATGGGG 368
41 ileThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
|||||
369 ATCACCCCTTGAGCAAAAAGCGAACCAGCAGCTGAATTCACAGAAGCTAAGGAGGCC 428
61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
|||||
429 TGTAGGCTGCTGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 488
81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
|||||
489 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCATCTCTAGGATT 548
101 SerProAsnProLysCysGlyLysAsn-GlyValGlyValLeuIleTrpLysValProVa 120
|||||
549 AGCCCAACCCCAAGTGTGGGAAMA-TGGGGTGGGTGTCCTGATTTCGAAGGTTCCAGT 607
120 lSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIl 140
|||||
608 GAGCCGACAGTTTCAGGCCTATTGTTACAACTCATCTGATCTTGGACTAACTCGTGCA 667
140 eProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrTh 160
|||||
668 TCCAGAAATTATCACCCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAAC 727
160 rGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAl 180
|||||

Db 728 AGAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGC 787
QY 180 aProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIl 200
|||||
Db 788 CCCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGAT 847
QY 200 eCysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVa 220
|||||
Db 848 TTGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGT 907
QY 220 lGluAsnLysAlaAlaPheLysAsnGluAlaAlaGly 232
|||||
Db 908 TGAATAATAAGCAGCATTCAAGAATGAAGCTGCTGGG 944

RESULT 24
AA046671 596 bp mRNA linear EST 06-SEP-1996
LOCUS zfl2d09.r1 Soares fetal_heart_NbHH19W Homo sapiens cDNA clone
DEFINITION IMAGE:376721 5' similar to PIR:A38745 A38745 cell adhesion molecule
CD44 precursor - rat [1] ;, mRNA sequence.
ACCESSION AA046671
VERSION AA046671.1 GI:1524772
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 596)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 419.
Location/Qualifiers
1..596
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1284977"
/db_xref="taxon:9606"
/clone="IMAGE:376721"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal_heart_NbHH19W"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site1: Not I; Site2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCCGATCTTTTGTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbHL19W."

ORIGIN

Alignment Scores:
Pred. No.: 8.86e-106 Length: 596
Score: 125.00 Matches: 181

Percent Similarity:	98.91%	Conservative:	0
Best Local Similarity:	98.91%	Mismatches:	2
Query Match:	38.82%	Indels:	2
DB:	9	Gaps:	0

US-10-079-111-1 (1-322) x AA046671 (1-596)

41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
3	ATCACCCCTTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTCCAGAGAGCTAAGGAGGCC	62
61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
63	TGTAGGTG-CTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACACGCTTGAAAGCT	121
81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
122	AGCTTTGAAACCTTGACGCTATGGCTGGGTGGAGATGGATTTCGTGGTCATCTCTAGGATT	181
101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
182	AGCCCCAACCCCAAGTGTGGGAAAAAATGGGTGGTGTCTCTGATTTCGGAAGGTTCCAGTG	241
121	SerArgGlnPheAlaLaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
242	AGCGACAGTTTGACGCTATTGTTACAACCTCATCTGATACCTTGGACTAACTCGTGCATT	301
141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
302	CCAGAAATTTATCACCAACCAAGATCCCATATTTCAACACTCAAACCTGCAACACAAACAACA	361
161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
362	GAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC	421
181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
422	CCTACTACTACTCCTCTGCTCCAGT-TCCACCTTCTATTCCACGGAGAAAAAATTGATT	480
201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal	220
481	TGTGTACACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	540
221	GluAsnLys	223
541	GAARATAAG	549

RESULT 25
CB988195
LOCUS CB988195 974 bp mRNA linear EST 01-MAY-2003
DEFINITION AGENCOURT_13892970 NIH_MGC_147 Homo sapiens cDNA clone
IMAGE:30345877 5', mRNA sequence.

CB988195
CB988195.1
EST.
Homo sapiens (human)

ORGANISM

REFERENCE 1 (bases 1 to 974)

AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

```

Plate: NDAM384 row: h column: 14
High quality sequence stop: 456.
FEATURES
      Location/Qualifiers
      source
      1..974

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/note="Organ: placenta; Vector: pBluescriptR; Site_1: ali-XhoI; Site_2: BamH; Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: This is a NIH MGC library."

ORIGIN

Alignment Scores:	
Pred. NO.:	5.66e-100
Score:	119.00
Length:	974
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Matches:	119
Mismatches:	0
Query Match:	36.96%
Indels:	0
Gaps:	0
DB:	14

US-10-079-111-1 (1-322) x CB988195 (1-974)

Qy	1	Met	Ala	Arg	Cys	Phe	Ser	Leu	Val	Leu	Leu	Leu	Leu	Thr	Ser	Ile	Trp	Thr	Arg	Leu	Leu	20
Db	99	ATG	CCC	AGG	TGCTT	CAG	CTT	GGT	TGT	TGCTT	TCT	CACTT	CCAT	TTC	GAC	CCAC	GAG	GC	TCT	CTG	158	
Qy	21	Val	Gln	Gly	Ser	Leu	Arg	Ala	Glu	Glu	Leu	Ser	Ile	Gln	Val	Ser	Cys	Arg	Ile	Met	Gly	40
Db	159	GTCC	AAG	GCTCTT	TGCGT	GCAG	AAG	AGCTT	TCC	ATCC	AGGTG	TCA	TCC	AGGTG	TCA	TGC	AGA	ATT	TAT	GGG	218	
Qy	41	Ile	Thr	Leu	Val	Ser	Lys	Lys	Ala	Asn	Gln	Gln	Leu	Asn	Phe	Thr	Glu	Ala	Lys	Glu	Ala	60
Db	219	ATC	ACCC	CTTG	GAG	CAAAA	AGG	CGA	ACC	CAG	CAG	CTGA	ATT	TCA	CAG	AAG	CTA	AGG	AGG	CC	278	
Qy	61	Cys	Arg	Leu	Leu	Gly	Leu	Ser	Leu	Ala	Gly	Lys	Asp	Gln	Val	Glu	Thr	Ala	Leu	Lys	Ala	80
Db	279	TGT	AGG	CTG	TGG	ACTA	AGTTT	TGG	CCG	CAAG	GAC	CAAG	TTC	GAA	AC	CAG	CTT	GAAA	AGCT	338		
Qy	81	Ser	Phe	Glu	Thr	Cys	Ser	Tyr	Gly	Trp	Val	Gly	Asp	Gly	Phe	Val	Val	Ile	Ser	Arg	Ile	100
Db	339	AGC	TTT	GAA	ACTT	GCAG	CTAT	GGCT	GGGT	TGG	AGAT	TGG	ATT	TCT	GGT	CA	TCT	CTA	GGATT	398		
Qy	101	Ser	Pro	Asn	Pro	Lys	Cys	Gly	Lys	Asn	Gly	Val	Gly	Val	Leu	Ile	Trp	Lys	Val	Pro	119	
Db	399	AGC	CCA	AA	CCCC	AA	GTG	TGG	AAAA	AAAT	TGGG	TGGG	TGCT	CTGA	TTT	GGA	AGG	TTT	CCA	455		

RESULT 26
AL552777

LOCUS	AL552777	1074 bp	mRNA	linear	EST 31-MAY-2003
DEFINITION	AL552777 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI068YF16 5-PRIME, mRNA sequence.				

ACCESSION AL552777
VERSION AL552777.2 GI:31274592

KEYWORDS EST.

SOURCE	Homo sapiens (human)
1	
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ORGANISM

REFERENCE 1 (bases 1 to 1074)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Li, W.B.; Gruber, C.; Jessee, J. and Polaves, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL: Unpublished (2007)

COMMENT
On Feb 15, 2001 this sequence version replaced qi:12892000.
Unpublished (2001)

DB: 14 Gaps: 0

US-10-079-111-1 (1-322) x H69328 (1-465)

QY 142 GluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThrGlu 161
|||||
Db 1 GAATATATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAGAA 60

QY 162 PheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAlaPro 181
|||||
Db 61 TTTATTGTGAGTGACAGTACTCTCGGTGGCATCCCCTTACTCTACAATACCTGCCCT 120

QY 182 ThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIleCys 201
|||||
Db 121 ACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTGT 180

QY 202 ValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheValGlu 221
|||||
Db 181 GTCACAGAAGTTTTTATGGAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAA 240

QY 222 AsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeuLeu 241
|||||
Db 241 AATAAAGCAGCATTCAAGAATGAAGCTGCTGGTTTGGAGGTGTCCCCACGGCTCTGCTA 300

QY 242 ValLeuAlaLeuLeuPhePheGlyAlaAlaAlaAlaGlyLeuGly 255
|||||
Db 301 GTGCTTGCTCTCCTCTCTTTGTTGGTGTGCAGCTGGTCTTGGG 342

RESULT 28
BG012717

LOCUS BG012717 368 bp mRNA linear EST 24-JAN-2001

DEFINITION IL5-GN0239-141200-341-c05 GN0239 Homo sapiens cDNA, mRNA sequence.

ACCESSION BG012717

VERSION BG012717.1 GI:12462184

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 368)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=IL5&t2=IL5-GN0239-141200-341-c05&t3=2000-12-14&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 339.
Location/Qualifiers
1. .368
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="GN0239"
/note="Organ: placenta_normal; Vector: puc18; Site_1:

FEATURES
source

SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:
Pred. No.: 7.92e-95 Length: 368
Score: 113.00 Matches: 113
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 35.09% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x BG012717 (1-368)

QY 22 GlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGlyIle 41
|||||
Db 2 CAAGGCTCTTTGCGTGCAGAGAGCTTTCCATCCAGGTGCATGCAGAAATTATGGGGATC 61

QY 42 ThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAlaCys 61
|||||
Db 62 ACCCTTGTGAGCAAAAAGCGAACCAAGCAGCTGAATTTACAGAAAGCTAAGGAGCCTGT 121

QY 62 ArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAlaSer 81
|||||
Db 122 AGGCTGTGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGC 181

QY 82 PheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIleSer 101
|||||
Db 182 TTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCACTCTCTAGGATTAGC 241

QY 102 ProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProValSer 121
|||||
Db 242 CCAAAACCCCAAGTGTGGGAAAATGGGTGGTGTCTCTGATTGGAGGTTCCAGTGAGC 301

QY 122 ArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThr 134
|||||

Db 302 CGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACT 340

RESULT 29
BG541447

LOCUS BG541447 872 bp mRNA linear EST 03-APR-2001

DEFINITION 602570880F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4695427 5', mRNA sequence.

ACCESSION BG541447

VERSION BG541447.1 GI:135333680

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 872)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1520 row: p column: 20
High quality sequence stop: 669.
Location/Qualifiers
1. .872
/organism="Homo sapiens"
/mol_type="mRNA"

FEATURES
source

/db_xref="taxon:9606"
/clone="IMAGE:4695427"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgcctcgcc); Site_2: SfiI (ggcattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGGCACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 1.65e-93 Length: 872
Score: 112.00 Matches: 112
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.78% Indels: 0
DB: 12 Gaps: 0

US-10-079-111-1 (1-322) x BG541447 (1-872)

QY 211 ThrMetSerThrGluThrGluProPheValGluAsnLysAlaAlaPheLysAsnGluAla 230
|||||
Db 2 ACCATGCTCTACAGAAACTGAACCATTTGTTGAAAATAAAGCAGCATTCAGAATGAAGCT 61
QY 231 AlaGlyPheGlyGlyValProThrAlaLeuLeuValLeuAlaLeuPhePheGlyAla 250
|||||
Db 62 GCTGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGTGCTCTCCCTCTCTTTGGTGCT 121
QY 251 AlaAlaGlyLeuGlyPheCysTyrValLysArgTyrValLysAlaPheProPheThrAsn 270
|||||
Db 122 GCAGCTGGTCTTGGAATTTTGCTATGTCAAAGGTATGTGAAGGCCTTCCCTTTTACAAAC 181
QY 271 LysAsnGlnGlnLysGluMetIleGluThrLysValLysGluGluLysAlaAsnAsp 290
|||||
Db 182 AAGAATCAGCAGAGGAATGATCGAAACCAAGTAGTAAAGGAGGAGGCCAATGAT 241
QY 291 SerAsnProAsnGluSerLysLysThrAspLysAsnProGluGluSerLysSerPro 310
|||||
Db 242 AGCAACCTAATGAGGAATCAAAGAAAACTGATAAAACCCAGAAAGTCCAAGAGTCCA 301
QY 311 SerLysThrThrValArgCysLeuGluAlaGluVal 322
|||||
Db 302 AGCAAAACTACCGTGCATGCCTGGAAAGCTGAAGTT 337

RESULT 30
BG483354
LOCUS 602504223F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4617797 5',
DEFINITION mRNA sequence.
ACCESSION BG483354
VERSION BG483354.1 GI:13415633
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 801)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM1374 row: n column: 06
High quality sequence stop: 630.

FEATURES

source

Location/Qualifiers
1..801
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4617797"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgcctcgcc); Site_2: SfiI (ggcattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGGCACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 6.81e-89 Length: 801
Score: 107.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 33.23% Indels: 0
DB: 12 Gaps: 0

US-10-079-111-1 (1-322) x BG483354 (1-801)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
|||||
Db 47 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCCTCATCTCCATCTGGACCACGAGGCTCCTG 106
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
|||||
Db 107 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTCCATCCAGGTGTCTATGCAGAAATTATGGG 166
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
|||||
Db 167 ATCACCCCTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTCAACAGAAAGCTAAGAGGCC 226
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
|||||
Db 227 TGTAGGCTGCTGGACTAAGTTTGGCCGGAAGGACCAAGTTGAAACAGCCTTGAAAGCT 286
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
|||||
Db 287 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCATCTCTAGGATT 346
QY 101 SerProAsnProLysCysGly 107
|||||
Db 347 AGCCCAAAACCCCAAGTGTGGG 367

RESULT 31

CA407758
LOCUS CA407758 487 bp mRNA linear EST 07-NOV-2002
DEFINITION 1003907 Human Fat Cell 5'-Stretch Plus cDNA Library Homo sapiens
CDNA 5', mRNA sequence.
ACCESSION CA407758
VERSION CA407758.1 GI:24772629
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 487)
REFERENCE Yang,R.-Z.; Shuldiner,A. and Gong,D.-W.
AUTHORS EST analysis of human adipose gene expression
TITLE

JOURNAL COMMENT Unpublished (2002)
Contact: Gong Da-Wei
Division of Endocrinology, Diabetes and Nutrition
University of Maryland
660 Redwood St, HH497, Baltimore, MD 21201, USA
Tel: 410 706 1672
Fax: 410 706 1622
Email: dgong@medicine.umaryland.edu
PCR Primers
FORWARD: CTCGGGAAGCGCGCCATTGTGTGGT
BACKWARD: AATACGACTCACTATAGGGCGAATTGG
Seq primer: GTTGGTACCGGGAATTC
Location/Qualifiers
1. .487
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="Male and Female"
/tissue_type="Adipose"
/clone_lib="Human Fat Cell 5'-Stretch Plus cDNA Library"
/note="Vector: lambdaTriplex"

ORIGIN

Alignment Scores:
Pred. No.: 2.96e-87 Length: 487
Score: 105.00 Matches: 105
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 32.61% Indels: 0
DB: 14 Gaps: 0

US-10-079-111-1 (1-322) x CA407758 (1-487)

QY 86 SerTyrGlyTrpValGlyAspGlyPheValIleSerArgIleSerProAsnProLys 105
|||||
Db 21 AGCTATGGCTGGGTTGGAGATGGATTCTCTAGGATTAGCCCAACCCCAAG 80
|||||

QY 106 CysGlyLysAsnGlyValGlyValIleLeuTrpLysValProValSerArgGlnPheAla 125
|||||

Db 81 TGTGGGAAAAATGGGGTGGGTGCTCTGATTGGAAAGTTCCAGTGAGCCGACAGTTTGCA 140
|||||

QY 126 AlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIleProGluIleIleThr 145
|||||

Db 141 GCCTATTGTTACAACCTCATCTGATACTTGGACTTAACTCGTGCTTCCAGAAATTATCACC 200
|||||

QY 146 ThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThrGluPheIleValSer 165
|||||

Db 201 ACCAAGATCCCATATTCAACACTCAAACACTGCAACACAAACACAGAAATTATTGTCACT 260
|||||

QY 166 AspSerThrTyrSerValAlaSerProTyrSerThrIleProAlaProThrThrThrPro 185
|||||

Db 261 GACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTACTCCT 320
|||||

QY 186 ProAlaProAlaSer 190
|||||

Db 321 CCTGCTCCAGCTTCA 335
|||||

RESULT 32
AL598709
LOCUS AL598709 743 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp313B2422.r1.313 (synonym: hlcc2) Homo sapiens cDNA clone
ACCESSION DKFZp313B2422.5', mRNA sequence.
AL598709
VERSION AL598709.1 GI:15161400
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 743)
AUTHORS Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Duesterhoeft, et al.)

JOURNAL COMMENT Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No s1 sequence available.
This clone (DKFZp313B2422) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1. .743
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp313B2422"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="313 (synonym: hlcc2)"
/note="Vector: pTriplex2; Site_1: SfilA; Site_2: SfilB;
cDNA-collection"

ORIGIN

Alignment Scores:
Pred. No.: 4.58e-87 Length: 743
Score: 105.00 Matches: 188
Percent Similarity: 96.91% Conservative: 0
Best Local Similarity: 96.91% Mismatches: 3
Query Match: 32.61% Indels: 6
DB: 9 Gaps: 0

US-10-079-111-1 (1-322) x AL598709 (1-743)

QY 1 MetAlaArgCysPheSerLeuValIleLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
|||||

Db 158 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGTCCTG 217
|||||

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
|||||

Db 218 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG 277
|||||

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
|||||

Db 278 ATCACCTTGTGAGCAAAAGCGCAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 337
|||||

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
|||||

Db 338 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGACCAAGTTGAAACAGCCTTGAAAGCT 397
|||||

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
|||||

Db 398 AGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGGATTCTGTAGGATT 457
|||||

QY 101 SerProAsnProLysCys-GlyLysAsnGlyValGlyValLeu-IleTrpLysValProV 120
|||||

Db 458 AGCCCAAAACCCCAAGCG-TGGGAAAAATGGGGTGGGTGTCCA-GATTTGGAAGGTTCCAG 515
|||||

QY 120 alSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysI 140
|||||

Db 516 TGAGCCGACAGTTTGCAGCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCA 575
|||||

QY 140 leProGluIleIleThrLysAspProIlePhe-AsnThrGlnThrAlaThrGlnThr 159
|||||

Db 576 TTCCAGAAATTATCACCAACCAAGATCCCATACT-CAACACTCAAACCTGCAACACAAACA 634
|||||

QY 160 ThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIlePro 179
|||||

Db 635 ACAGAAATTATTGTGTCAGTGACAGTACCTACTCTCGGTGGCATCCCTTACTCTACATACCT 694
|||||

QY 180 AlaProThrThrThrProProAlaProAlaSerThr 191
|||||

QY 153 hr 153
Db 592 CT 593

RESULT 35
CB269023
LOCUS
DEFINITION 1007930 Human Fat Cell 5'-Stretch Plus cDNA Library Homo sapiens
cdNA 5', mRNA sequence.
CB269023
CB269023.1 GI:28443608
EST.
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 473)
Yang, R.-Z., Shuldiner, A. and Gong, D.-W.
EST analysis of human adipose gene expression
Unpublished (2002)
Contact: Gong Da-Wei
Division of Endocrinology, Diabetes and Nutrition
University of Maryland
660 Redwood St, HH497, Baltimore, MD 21201, USA
Tel: 410 706 1672
Fax: 410 706 1622
Email: dgong@medicine.umaryland.edu
PCR Primers
FORWARD: CTCGGAAGCGGCCATTGTTGGT
BACKWARD: AATACGACTCACTATAGGCGGAATTGG
Seq primer: GTTGGTACCCGGGAATTC.
Location/Qualifiers
1. .473
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="Male and Female"
/tissue type="Adipose"
/clone_lib="Human Fat Cell 5'-Stretch Plus cDNA Library"
/note="Vector: lambdaTriplex"

FEATURES
source

ORIGIN

Alignment Scores:
Pred. No.: 5.82e-78 Length: 473
Score: 95.00 Matches: 95
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 29.50% Indels: 0
DB: 14 Gaps: 0

US-10-079-111-1 (1-322) x CB269023 (1-473)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 127 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 186

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 187 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 246

QY 41 IleThrLeuValSerLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 247 ATCACCTTGTGAGCAAAAGGCGAACCAGCAGCTGAATTCACAGAAAGCTAAGGAGGCC 306

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 307 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAACAGCCTTGAAAGCT 366

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheVal 95
Db 367 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTG 411

RESULT 36

BX366589
LOCUS
DEFINITION BX366589 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI024YP17 5-PRIME, mRNA sequence.
BX366589
BX366589.1 GI:30437038
EST.
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0AI024CH09QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0AI024CH09QP1.
Location/Qualifiers
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI024YP17"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
source

ORIGIN

Alignment Scores:
Pred. No.: 1.53e-77 Length: 1201
Score: 95.00 Matches: 222
Percent Similarity: 97.80% Conservative: 0
Best Local Similarity: 97.80% Mismatches: 2
Query Match: 29.50% Indels: 5
DB: 13 Gaps: 0

US-10-079-111-1 (1-322) x BX366589 (1-1201)

QY 14 IleTrpThrThrArgLeuLeuValGlnGlySerLeuArgAlaGluLeuSerIleGln 33
Db 203 ATCTGGACCACGAGGCTCCTGTGTCGAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAG 262

QY 34 ValSerCysArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnLeuAsn 53
Db 263 GTGTCATGCAGAAATTATGGGGATCACCTTGTGAGCAAAAGCGAACCCAGCAGCTGAAT 322

QY 54 PheThrGluAlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGln 73
Db 323 TTCACAGAAAGCTAAGGAGGCTGTAGGCTGTGGGACTTAAGTTTGGCCGCAAGGACCAA 382

QY 74 ValGluThrAlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGly 93
Db 383 GTTGAACACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGA 442

QY 94 PheValValIleSerArgIleSerProAsnProLysCysGlyLysAsn-GlyValGlyVa 113
Db 443 TTCGTGGTTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAWA-TGGGGTGGGTGT 501

QY 113 lleuIleTrpLysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAs 133

Db 502 CCTGATTGGAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGA 561

QY 133 pThrTrpThrAsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnTh 153

Db 562 TACTTGGACTAACTCGTGCAATCCAGAAATTATCACCAACAAAGATCCCATATTCAACAC 621

QY 153 rGlnThrAlaThrGlnThrThrGluPheIleValSerAspSerThr-TyrSerValAlaS 173

Db 622 TCAAACCTGCACACAAACAACAGAAATTTATTGTCAGTGACAGTTC-CTACTCGGTGGCAT 680

QY 173 erProTyrSerThrIleProAlaProThrThrProAlaProAlaSerThrSerI 193

Db 681 CCCCTTACTCTACAATACTGCCCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTA 740

QY 193 leProArgArgLysLysLeuIleCysValThrGluValPheMetGluThrSerThrMets 213

Db 741 TTCCACGGAGAAAAAATGATTGTGTACAGAAAGTTTATTATGGAAACTAGCACCATGT 800

QY 213 erThrGluThrGluPro-PheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGly 232

Db 801 CTACAGAAACTGAACCATTTTGTGTAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGG 860

QY 233 PheGlyGlyValPro 237

Db 861 TTTGGAGGTGTCCCM 875

RESULT 37

H02823

LOCUS

DEFINITION yj41h11.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151365 5', mRNA sequence.

ACCESSION H02823

VERSION H02823.1 GI:865756

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 411)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Insert Size: 2127 High quality sequence stops: 326 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 2127 Std Error: 0.00 Seq primer: M13Rp1 High quality sequence stop: 326. Location/Qualifiers 1. .411 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:563454" /db_xref="taxon:9606" /clone="IMAGE:151365" /sex="Female" /dev_stage="placenta obtained at birth (full term)" /lab_host="DH10B (ampicillin resistant)" /clone_lib="Soares placenta Nb2HP" /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st

FEATURES source

strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGAAGAATTCGGCCGACGAAATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. "

ORIGIN

Alignment Scores: 4.29e-77 Length: 411

Pred. No.: 94.00 Matches: 94

Score: 100.00% Conservative: 0

Percent Similarity: 100.00% Mismatches: 0

Best Local Similarity: 29.19% Indels: 0

Query Match: 14 Gaps: 0

DB:

US-10-079-111-1 (1-322) x H02823 (1-411)

QY 114 LeuIleTrpLysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAsp 133

Db 1 CTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGAT 60

QY 134 ThrTrpThrAsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThr 153

Db 61 ACTTGGACTAACTCGTGCATTCAGAAATTATCACCAAGATCCCATATTCAACACT 120

QY 154 GlnThrAlaThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSer 173

Db 121 CAAACTGCAACACAAACAACAGAAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCC 180

QY 174 ProTyrSerThrIleProAlaProThrThrProAlaProAlaSerThrSerIle 193

Db 181 CCTTACTCTACAATACTGCCCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATT 240

QY 194 ProArgArgLysLysLeuIleCysValThrGluValPheMet 207

Db 241 CCACGGAGAAAAAATGATTGTGTGCACAGAGTTTATTATG 282

RESULT 38

BI763579

LOCUS

DEFINITION BI763579 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5190393 5', mRNA sequence.

ACCESSION BI763579

VERSION BI763579.1 GI:15755157

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 877)

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11475 row: p column: 10 High quality sequence stop: 715. Location/Qualifiers 1. .877 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5190393" /lab_host="DH10B"

FEATURES source

Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVtroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI030AB05QP1.
Location/Qualifiers
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI030YC09"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a Noti-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
source

ORIGIN

Alignment Scores:
Pred. No.: 2.64e-67 Length: 1201
Score: 84.00 Matches: 84
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.09% Indels: 0
DB: 9 Gaps: 0

US-10-079-111-1 (1-322) x AL546565 (1-1201)

QY 77 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 96
|||||
Db 434 GCCTGAAAGCTAGCTTTGAAACTGTCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTC 493

QY 97 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 116
|||||
Db 494 ATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAATGGGGTGGTGTCTGATTGG 553

QY 117 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 136
|||||
Db 554 AAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGACT 613

QY 137 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 156
|||||
Db 614 AACTCGTGCATTCCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCA 673

QY 157 ThrGlnThrThr 160
|||||
Db 674 ACACAAACAACA 685

RESULT 43
T96904
LOCUS
DEFINITION
T96904.1 GI:735528
T96904.1 GI:735528
EST.
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 444)
Hallier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Wilson,R.

TITLE
JOURNAL
COMMENT
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

Insert Size: 1301
High quality sequence stops: 254 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1301 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 254.
Location/Qualifiers
1. .444
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:473953"
/db_xref="taxon:9606"
/clone="IMAGE:121408"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen INFLS"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5', AACTGGAAGAATTAAATGAAGATCTTTTCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

FEATURES
source

ORIGIN

Alignment Scores:
Pred. No.: 8.03e-67 Length: 444
Score: 83.00 Matches: 83
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 25.78% Indels: 0
DB: 14 Gaps: 0

US-10-079-111-1 (1-322) x T96904 (1-444)

QY 213 SerThrGluThrGluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaGly 232
|||||
Db 13 TCTACAGAAACTGAACCATTTGTTGAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGG 72

QY 233 PheGlyGlyValProThrAlaLeuLeuValLeuAlaLeuLeuPhePheGlyAlaAla 252
|||||
Db 73 TTGGAGGTGTCCCCACGGCTCTGCTAGTGTCTTCTCTCTCTCTCTCTCTCTCTCT 132

QY 253 GlyLeuGlyPheCysTyrValLysArgTyrValLysAlaPheProPheThrAsnLysAsn 272
|||||
Db 133 GGTCTTGGATTTTGCATGTCAAAAGGTATGTGAAGCCTTCCCTTTTACAAACAAGAA 192

QY 273 GlnGlnLysGluMetIleGluThrLysValLysGluGluLysAlaAsnAspSerAsn 292
|||||
Db 193 CAGCAGAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGGAGGAGGAGGAGGAG 252

QY 293 ProAsnGlu 295
|||||
Db 253 CCTAATGAG 261

RESULT 44
BG566260
LOCUS
DEFINITION
BG566260.1 GI:13573913
EST.
ACCESSION
BG566260
VERSION
BG566260.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 794)
NIH-MGC http://mgc.nci.nih.gov/.

RESULT 48
AY411058
LOCUS
DEFINITION
AY411058
Pan troglodytes XLKD1 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY411058
VERSION
AY411058.1 GI:39767026
KEYWORDS
GSS.
SOURCE
ORGANISM
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.
REFERENCE
1 (bases 1 to 790)
AUTHORS
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 790)
AUTHORS
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Direct Submission
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
source
1..790
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
gene
<1..>790
/gene="XLKD1"
/locus_tag="HCM4097"
ORIGIN
Alignment Scores:
Pred. No.: 2.7e-43 Length: 790
Score: 58.00 Matches: 58
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 18.01% Indels: 0
DB: 29 Gaps: 0
US-10-079-111-1 (1-322) x AY411058 (1-790)
QY 63 LeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAlaSerPhe 82
Db 8 CTGCTGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCCAGCTTT 67
QY 83 GluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIleSerPro 102
Db 68 GAGACTTGCAGCTATGGCTGGTTGGAGATGGATTGGTGCATCTCTAGGATTAGCCCA 127
QY 103 AsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 128 AACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTCTGATTGTGAAAGTTCCAGTG 181
RESULT 49
CD671330
LOCUS
DEFINITION
CD671330
Human Iris cDNA (Normalized): fg Homo sapiens cdna clone
fg03c09 5', mRNA sequence.
ACCESSION
CD671330
VERSION
CD671330.1 GI:32173061
KEYWORDS
EST.
SOURCE
Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 529)
AUTHORS
Wistow,G., Bernstein,S.L., Ray,S., Wyatt,M.K., Behal,A.,
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
TITLE
Expressed sequence tag analysis of adult human iris for the NEIBank
Project: steroid-response factors and similarities with retinal
pigment epithelium
JOURNAL
Mol. Vis. 8 (4), 185-195 (2002)
MEDLINE
22103462
PUBMED
12107412
COMMENT
Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 03 row: c column: 09
Seq primer: M13RP1 reverse primer (ABI).
FEATURES
Location/Qualifiers
source
1..529
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="fg03c09"
/tissue_type="Iris"
/dev_stage="Adult"
/lab_host="EMDH108"
/clone_lib="Human Iris cDNA (Normalized): fg"
/note="Organ: Eye; Vector: pCMVSPORT6; A human iris
library (bx) was normalized by self-subtraction. One
portion of double stranded plasmid DNA representing the
library was linearized by NotI. This NotI digested library
was used as a template for biotinylated RNA synthesis
using SP6 RNA polymerase. Another portion of the double
stranded plasmid library was converted to single-stranded
circles in vitro using Gene II and Exonuclease III (Life
Technologies). Single-stranded DNA (1 mg) was hybridized
(Cot 500) with 41 mg of Bio-RNA and vector blocking
oligonucleotides. The hybridized Bio-RNA/ss-circles were
removed by streptavidin:phenol extraction. EST analysis
was performed on the library at the NIH Intramural
Sequencing Center(NISC)."
ORIGIN
Alignment Scores:
Pred. No.: 1.3e-41 Length: 529
Score: 56.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 17.39% Indels: 0
DB: 14 Gaps: 0
US-10-079-111-1 (1-322) x CD671330 (1-529)
QY 267 ProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThrLysValLysGluGlu 286
Db 2 CCTTTTACAAACAAGAATCAGCAGAAAGGAATGATCGAAACCAAGTAGTAAGGAGGAG 61
QY 287 LysAlaAsnAspSerAsnProAsnGluGluSerLysLysThrAspLysAsnProGluGlu 306
Db 62 AAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAAGAAACCTGATAAAACCCAGAAGAG 121
QY 307 SerLysSerProSerLysThrThrValArgCysLeuGluAlaGluVal 322
Db 122 TCCAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCTGAAGTT 169
RESULT 50
AA463325
LOCUS
DEFINITION
AA463325
415 bp mRNA linear EST 10-JUN-1997
zx71f04.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cdna clone

IMAGE:796927 5', mRNA sequence.
AA463325
VERSION AA463325.1 GI:2188209
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 415)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE WashU-Merck EST Project 1997
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 272.
FEATURES
source
1..415
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:6041595"
/db_xref="taxon:9606"
/clone="IMAGE:796927"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/clone_lib="Soares total_fetus_Nb2HF8 9w"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from pooled 8-9 week (total) fetus material with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGACGGCGCTTAATTTTTTTTTTTT 3'] . Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN
Alignment Scores:
Pred. No.: 8.59e-41 Length: 415
Score: 55.00 Matches: 83
Percent Similarity: 98.81% Conservative: 0
Best Local Similarity: 98.81% Mismatches: 1
Query Match: 17.08% Indels: 1
DB: 9 Gaps: 0
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QY 7 LeuValLeuLeuThrSerIleTrpThrThrArgLeuLeuValGlnGlySerLeuArg 26
Db 136 CTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGT 195
QY 27 AlaGluGluLeuSerIleGlnValSerCysArgIleMetGlyIleThrLeuValSerLys 46
Db 196 GCAGAGAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGATCACCCCTTGAGCAAA 255
QY 47 LysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAlaCysArgLeuLeuGlyLeu 66
Db 256 AAGGCGAACACAGCAGCTGAATTTACAGAAGCTAAGGAGGCCTGTAG-CTGCTGGGACTA 314
QY 67 SerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAlaSerPheGluThrCysSer 86
Db 315 AGTTTGCCGGCAAGGACCAAGTTGAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGC 374
QY 87 TyrGlyTrpVal 90
Db 375 TATGGCTGGGTT 386
Search completed: September 16, 2004, 04:48:42
Job time : 3107 secs

BP/ant

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 15, 2004, 21:13:40 ; Search time 97 Seconds
(without alignments)
1842.208 Million cell updates/sec

Title: US-10-079-111-1
Perfect score: 322
Sequence: 1 MARCFSLVLLLTISIWTRLL.....NPESKSPSKTTVRCLEAEV 322

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Word size: 12

Total number of hits satisfying chosen parameters: 14

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10079111/runat 13092004_102226 14021/app_query_fasta_1.519
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=olig.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=100 -DOCALIGN=200 -THR SCORE=quality -THR_MIN=12 -ALIGN=50 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10079111@CGN 1 1 69 @runat 13092004 102226 14021 -NCPU=6 -ICPU=3
-NO_MMAL -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length DB ID	Description	
1	322	100.0	2029 4	US-09-232-160-13	Sequence 13, Appl
2	322	100.0	2372 4	US-09-907-794A-200	Sequence 200, App
3	322	100.0	2372 4	US-09-905-125A-200	Sequence 200, App
4	322	100.0	2372 4	US-09-902-775A-200	Sequence 200, App
5	322	100.0	2404 4	US-09-833-381-849	Sequence 849, App
6	322	100.0	2404 4	US-09-833-381-853	Sequence 853, App
7	239	74.2	2313 2	US-08-892-880-1	Sequence 1, Appli
8	60	18.6	492 2	US-08-892-880-12	Sequence 12, Appl
9	46	14.3	466 2	US-08-892-880-13	Sequence 13, Appl
10	36	11.2	498 2	US-08-892-880-15	Sequence 15, Appl
11	29	9.0	1896 4	US-09-724-864-28	Sequence 28, Appl
12	16	5.0	50 4	US-09-907-794A-205	Sequence 205, App

ALIGNMENTS

RESULT 1
US-09-232-160-13
; Sequence 13, Application US/09232160
; Patent No. 6368794
; GENERAL INFORMATION:
; APPLICANT: Steve Daniel
; APPLICANT: James Gilmore
; APPLICANT: Susan G. Stuart
; APPLICANT: Laura Stuve
; TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: PA-0003 US
; CURRENT APPLICATION NUMBER: US/09/232,160
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 2029
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 3044710
US-09-232-160-13

Alignment Scores:					
Pred. No.:	7.42e-316	Length:	2029		
Score:	322.00	Matches:	322		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	100.00%	Indels:	0		
DB:	4	Gaps:	0		
US-10-079-111-1 (1-322) x US-09-232-160-13 (1-2029)					
Qy	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrTrpArgLeuLeu	20		
Db	183	ATGCCAGGTGCTTCAGCCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG	242		
Qy	21	ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly	40		
Db	243	GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG	302		
Qy	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60		
Db	303	ATCACCCCTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTCACAGAAGCTAAGGAGGCC	362		
Qy	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80		
Db	363	TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAGTTGAAACAGCCTTGAAGCT	422		
Qy	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle	100		
Db	423	AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCGTGGTCATCTCTAGGATT	482		
Qy	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValIleTrpLysValProVal	120		
Db	483	AGCCCAAAACCCCAAGTGTGGAAAAAATGGGTGGGTGCTCTGATTTGAAGGTTCCAGTG	542		
Qy	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140		
Db	543	AGCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGACTACTGGACTAATCGTGCAAT	602		
Qy	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160		
Db	603	CCAGAAATTATCACCCACCAAGATCCCATATTCAACACTCAAACTGCAACACAACA	662		
Qy	161	GlupheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180		

Db 663 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAAATACCTGCC 722

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

Db 723 CCTACTACTACTCCTCGTCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT 782

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220

Db 783 TGTGTACAGAAAGTTTTTATGGAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 842

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240

Db 843 GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 902

QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260

Db 903 CTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGGCTATGTCAA 962

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280

Db 963 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGATCAGCAGAAGGAAATGATCGAAACC 1022

QY 281 LysValValLysGluGluLysAlaAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300

Db 1023 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCTAATGAGGAATCAAGAAAAACT 1082

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320

Db 1083 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAAACTACCGTGCGATGCTGGAAGCT 1142

QY 321 GluVal 322

Db 1143 GAAGTT 1148

RESULT 2

US-09-907-794A-200

; Sequence 200, Application US/09907794A

; Patent No. 6635468

GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/907,794A

; CURRENT FILING DATE: 2001-07-17

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29

; PRIOR APPLICATION NUMBER: PCT/US99/28313

; PRIOR FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: PCT/US99/28564

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/28565

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/30095

; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: PCT/US99/30911

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US99/30999

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US00/00219

; PRIOR FILING DATE: 2000-01-05

; NUMBER OF SEQ ID NOS: 423

; SEQ ID NO 200

; LENGTH: 2372

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-907-794A-200

Alignment Scores:

Pred. No.:	8.62e-316	Length:	2372
Score:	322.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-079-111-1 (1-322) x US-09-907-794A-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20

Db 160 ATGGCCAGGTCTTTCAGCCTGGTGTTCCTTCTCATCTCCATCTGGACCAGAGGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

Db 220 GTCCAAGGCTCTTTCGTGCAGAAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnLysLeuAsnPheThrGluAlaLysGluAla 60

Db 280 ATCACCCCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTTCACAGAGCTAAGGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTTCGTGGTCACTCTTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

Db 460 AGCCCCAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTGGAGGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

Db ||||| 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTCATT 579

Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

Db ||||| 580 CCAGAAATTATCACCCAAAAGATCCCATATTCAACACTCAAACGTGCAACACAAAACAACA 639

Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

Db ||||| 640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699

Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

Db ||||| 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATGATT 759

Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

Db ||||| 760 TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCAATTGTT 819

Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240

Db ||||| 820 GAAAATAAAGCAGCAATTCAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879

Qy 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260

Db ||||| 880 CTAGTGCTTGCTCTCCTCTCTTTGTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA 939

Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280

Db ||||| 940 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAATGATCGAAACC 999

Qy 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300

Db ||||| 1000 AAAGTAGTAAAGGAGGAGAGAGGCCAATGATAGCAACCTTAATGAGGAATCAAAGAAAACT 1059

Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320

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Qy 321 GluVal 322

Db ||||| 1120 GAAGTT 1125

RESULT 3

US-09-905-125A-200
; Sequence 200, Application US/09905125A

; Patent No. 6664376

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/905,125A

; CURRENT FILING DATE: 2001-07-12

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29

; PRIOR APPLICATION NUMBER: PCT/US99/28313

; PRIOR FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: PCT/US99/28564

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/28565

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/30095

; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: PCT/US99/30911

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US99/30999

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US00/00219

; PRIOR FILING DATE: 2000-01-05

; NUMBER OF SEQ ID NOS: 423

; SEQ ID NO 200

; LENGTH: 2372

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-905-125A-200

Alignment Scores:

Pred. No.: 8.62e-316 Length: 2372

Score: 322.00 Matches: 322

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 4 Gaps: 0

US-10-079-111-1 (1-322) x US-09-905-125A-200 (1-2372)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20

Db 160 ATGCCCAGGTGCTTCAGCCCTGGTGTGTTCTTCACITCCATCTGGACCACGAGGCTCTG 219

Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

Db 220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG 279

Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60

Db 280 ATCACCCCTTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 339

Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATCGATTTCGTGGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTGATTGTGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCAAT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db 760 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATATAAGCAGCATTTCAAGAATGAAGCTGTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrVallys 260
Db 880 CTAGTGCTTGCTCTCCTCTTCTTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAA 939
QY 261 ArgTyrVallysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAAGGAATGATCGAAACC 999
QY 281 LysValVallysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAAAGAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 4

US-09-902-775A-200
; Sequence 200, Application US/09902775A
; Patent No. 6686451

GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/902,775A

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29

; PRIOR APPLICATION NUMBER: PCT/US99/28313

; PRIOR FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: PCT/US99/28564

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/28565

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/30095

; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: PCT/US99/30911

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US99/30999

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US00/00219

; PRIOR FILING DATE: 2000-01-05

; NUMBER OF SEQ ID NOS: 423

; SEQ ID NO 200

; LENGTH: 2372

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-902-775A-200

Alignment Scores:

Pred. No.: 8.62e-316 Length: 2372

Score: 322.00 Matches: 322

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 4 Gaps: 0

US-10-079-111-1 (1-322) x US-09-902-775A-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACACGAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuLeuAsnPheThrGluAlaLysGluAla 60

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|||||
280 ATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 339
QY CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db TGTAGGCTGCTGGACTAAGTTTGGCCGGCAGGACCAAGTTGAAACACAGCCTTGAAAGCT 399
QY SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db AGCTTTGAAACITGCAGCTATGGCTGGTTGGAGATGGATTCGTGGTCACTCTAGGATT 459
QY SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTGATTGTGGAAAGTTCCAGTG 519
QY SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT 579
QY ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db CCAGAAATATTACCAACCAAAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639
QY GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db GAATTTATTGTAGTGACAGTACCTACTCGTGGCATCCCCCTTACTCTACAAATACCTGCC 699
QY ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db CCTACTACTACTCCTCCTCTGCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT 759
QY CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCAATTGTT 819
QY GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db GAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCCCCACGGCTCTG 879
QY LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db CTAGTGCTTGCTCTCCTCTTCTTGGTGTGCTGCAGCTGGTCTTGGATTTTGTATGTCAAA 939
QY ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAAGGAAATGATCGAAACC 999
QY LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db AAAGTAGTAAAGGAGGAGAGGCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACT 1059
QY AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCTGGAAAGCT 1119
QY GluVal 322
Db GAAGT 1125
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RESULT 5

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US-09-833-381-849
; Sequence 849, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186e1 Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 849
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-849

Alignment Scores:
Pred. No.:      8.76e-316      Length:      2404
Score:          322.00        Matches:    322
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:     100.00%      Indels:       0
DB:              4           Gaps:         0

US-10-079-111-1 (1-322) x US-09-833-381-849 (1-2404)

QY      1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db      190 ATGGCCAGGTGCTTCAGCCTGGTGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 249
QY      21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      250 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCAATGCAGAAATATGGGG 309
QY      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      310 ATCACCCCTTGTGAGCAAAAAGGCAACCCAGCAGCTGAATTTTCACAGAAGCTAAGAGGCC 369
QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      370 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCITTGAAAGCT 429
QY      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db      430 AGCTTTGAAACTTGCAGCTATGGCTGGTGGATGGATTCGTGGTCATCTTAGGATT 489
QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      490 AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTTGGAAGGTTCCAGTG 549
QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerSerAspThrTrpThrAsnSerCysIle 140
Db      550 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATT 609
QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      610 CCAGAAATTTATCACCAACCAAGATCCCATAATTCAACACTCAAACTGCAACACACAACAACA 669
QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      670 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTTGCC 729
QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      730 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 789
QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      790 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCAATTGTT 849
QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db      850 GAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 909
QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      910 CTAGTGCTTGTCTCTCTCTTCTTGGTGTGCGAGCTGGTCTTGGATTTTGTCTATGTCAAA 969
QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      970 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAATCAGCAGAAAGGAAATGATCGAAACC 1029
QY      281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
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RESULT 11
US-09-724-864-28
; Sequence 28, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1896
; TYPE: DNA
; ORGANISM: Mouse
US-09-724-864-28

Alignment Scores:
Pred. No.: 1.09e-19 Length: 1896
Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.01% Indels: 0
DB: 4 Gaps: 0

US-10-079-111-1 (1-322) x US-09-724-864-28 (1-1896)
QY 224 AlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeuValLeu 243
Db 719 GCAGCATTCAAGAACGACGAGCTGGGTTTGGAGGTGTCCCAACCGCCCTGCTGGTGTG 778
QY 244 AlaLeuLeuPhePheGlyAlaAlaAla 252
Db 779 GCTCTCCTCTTCTTTGGTGCTGCCGCT 805

RESULT 12
US-09-907-794A-205
; Sequence 205, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
```

```
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 205
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-907-794A-205

Alignment Scores:
Pred. No.: 4.39e-08 Length: 50
Score: 16.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.97% Indels: 0
DB: 4 Gaps: 0

US-10-079-111-1 (1-322) x US-09-907-794A-205 (1-50)
QY 59 GluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnVal 74
Db 3 GAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTT 50

RESULT 13
US-09-905-125A-205
; Sequence 205, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
```



```

; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 205
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-905-125A-205
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Alignment Scores:
Pred. No.: 4.39e-08 Length: 50
Score: 16.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.97% Indels: 0
DB: 4 Gaps: 0
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US-10-079-111-1 (1-322) x US-09-905-125A-205 (1-50)

QY      59 GluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnVal 74
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Db      3 GAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTT 50

RESULT 14
US-09-902-775A-205
; Sequence 205, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
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; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 205
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-902-775A-205

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Alignment Scores:	
Pred. No.:	4.39e-08
Score:	16.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	4.97%
DB:	4
Length:	50
Matches:	16
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-079-111-1 (1-322) x US-09-902-775A-205 (1-50)

	Glu	Ala	Cys	Arg	Leu	Leu	Gly	Leu	Ser	Leu	Ala	Gly	Lys	Asp	Gln	Val	74
Qy																	
D6																	
	3	GAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCCGCAAGGCCAAAGTT	50														

Search completed: September 16, 2004, 04:50:06
Job time : 109 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 15, 2004, 16:31:46 ; Search time 4676 Seconds
(without alignments)
2984.700 Million cell updates/sec

Title: US-10-079-111-1
Perfect score: 322
Sequence: 1 MARCFSLVLLTISIWTRLL.....NPESKSPSKTTVRCLEAEV 322

Scoring table: OLIGO
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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Word size: 12
Total number of hits satisfying chosen parameters: 43

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO spool/US10079111/runat_13092004_102224_13988/app_query.fasta_1.519
-DB=GenEmbl -QFMT=fastap -SUFFIX=olig.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=100
-DOCALIGN=200 -THR SCORE=quality -THR MIN=12 -ALIGN=50 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10079111@cgn_1_1_3731@runat_13092004_102224_13988 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
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33: em_htg_mus:*
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35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
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40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	322	100.0	1285	9	AF127670	AF127670 Homo sapi
2	322	100.0	1755	6	AX136227	AX136227 Sequence
3	322	100.0	1755	6	BD123566	BD123566 Secretory
4	322	100.0	1755	9	AK075443	AK075443 Homo sapi
5	322	100.0	2029	6	AR204700	AR204700 Sequence
6	322	100.0	2029	6	BD222718	BD222718 Human sig
7	322	100.0	2372	6	AR410761	AR410761 Sequence
8	322	100.0	2372	6	AX092274	AX092274 Sequence
9	322	100.0	2372	6	AX454446	AX454446 Sequence
10	322	100.0	2372	6	AX490924	AX490924 Sequence
11	322	100.0	2372	6	AX697609	AX697609 Sequence
12	322	100.0	2372	6	BD075532	BD075532 Secretory
13	322	100.0	2372	6	BD172392	BD172392 Secreted
14	322	100.0	2372	6	BD172711	BD172711 Secreted
15	322	100.0	2372	6	BD173030	BD173030 Secreted
16	322	100.0	2372	6	BD173349	BD173349 Secreted
17	322	100.0	2372	6	BD175383	BD175383 Secretory
18	322	100.0	2372	9	AY358925	AY358925 Homo sapi
19	221	68.6	2282	9	BC026231	BC026231 Homo sapi
20	183	56.8	2313	9	AF118108	AF118108 Homo sapi
21	125	38.8	716	6	AX136529	AX136529 Sequence
22	125	38.8	716	6	BD123769	BD123769 Secretory
23	116	36.0	451	6	BD076146	BD076146 5' EST of
24	103	32.0	165698	9	AC009532	AC009532 Homo sapi
25	39	12.1	363	6	BD077623	BD077623 5'EST of
26	37	11.5	373	6	BD073800	BD073800 5'EST of
27	32	9.9	1613	4	AY372937	AY372937 Bos tauru
28	29	9.0	1516	10	MMU311501	AJ311501 Mus muscu
29	29	9.0	2027	10	BC038653	BC038653 Mus muscu
30	29	9.0	2027	10	BC038892	BC038892 Mus muscu
31	28	8.7	59529	2	AC110451_3	Continuation (4 of
32	28	8.7	235382	2	AC130104	AC130104 Rattus no
33	28	8.7	239307	2	AC129402	AC129402 Rattus no
34	22	6.8	603	4	AY304537	AY304537 Sus scrof
35	16	5.0	50	6	AR410765	AR410765 Sequence
36	16	5.0	50	6	AX697614	AX697614 Sequence
37	16	5.0	50	6	BD075536	BD075536 Secretory
38	16	5.0	50	6	BD172396	BD172396 Secreted
39	16	5.0	50	6	BD172715	BD172715 Secreted
40	16	5.0	50	6	BD173034	BD173034 Secreted
41	16	5.0	50	6	BD173353	BD173353 Secreted
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ALIGNMENTS

RESULT 1
AF127670
LOCUS

AF127670 1285 bp mRNA linear PRI 13-OCT-2000

DEFINITION Homo sapiens hyaluronic acid receptor (HAR) mRNA, complete cds.
ACCESSION AF127670
VERSION AF127670.2 GI:10800121
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1285)
AUTHORS Winkelman,J.C., Basu,S., Ozdemir,E. and Blough,R.I.
TITLE HAR: a novel homolog of CD44 and putative hyaluronic acid receptor encoded by a gene on human chromosome 11p15
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1009)
AUTHORS Winkelman,J.C., Basu,S., Ozdemir,E. and Blough,R.I.
TITLE Direct Submission
JOURNAL Submitted (11-FEB-1999) Hematology-Oncology, University of Cincinnati, 231 Bethesda Avenue, Cincinnati, Ohio 45267-0508, USA
REFERENCE 3 (bases 1 to 1285)
AUTHORS Winkelman,J.C., Basu,S., Ozdemir,E. and Blough,R.I.
TITLE Direct Submission
JOURNAL Submitted (12-OCT-1999) Hematology-Oncology, University of Cincinnati, 231 Bethesda Avenue, Cincinnati, Ohio 45267-0508, USA
REMARK Sequence update by submitter
COMMENT On Oct 13, 2000 this sequence version replaced gi:5732667.
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ORIGIN

Alignment Scores:
Pred. No.: 0 Length: 1285
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-10-079-111-1 (1-322) x AF127670 (1-1285)
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Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 181 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTCCATCCAGGTGTCATGCAGAATTATGGGG 240
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 241 ATCACCCCTTGTGAGCAAAAAGCGAACCCAGAGCTGAATTCACAGAAGCTAAGGAGGCC 300
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

Db 301 TGTAGGCTGCTGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 360
Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 361 AGCTTTGAAACTTGACGCTATGGCTGGTTGGAGATGGATTCTGGTTCATCTCTAGGATT 420
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
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Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 601 GAATTTATTGTCAGTGACAGTACCTACTCGTGGCATCCCCCTTACTTACAATACCTGCC 660
Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 661 CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 720
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Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
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Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
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Qy 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
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RESULT 2
AX136227
LOCUS AX136227 1755 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 149 from Patent EP1067182.
ACCESSION AX136227
VERSION AX136227.1 GI:14272635
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
TITLE Secretory protein or membrane protein
JOURNAL Patent: EP 1067182-A 149 10-JAN-2001;
FEATURES Helix Research Institute (JP)
source Location/Qualifiers
1..1755

QY	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
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QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
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QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
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QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	621	CCAGAAATTTATCACCAACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACA	680
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	681	GAATTTATTGTCAGTGACGTACCTACTCGGTGGCATCCCTTACTCTACATACCTGCC	740
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	741	CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	800
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	801	TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	860
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	861	GAAATAAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCGCCACGGCTCTG	920
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	921	CTAGTGCTTGCTCTCCTCTTCTTTGGTGTGCAGCTGGTCTTGATTTTGCTATGTCAA	980
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	981	AGGTATGTGAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAATGATCGAAACC	1040
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1041	AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAAGAAACT	1100
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1101	GATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAAACTACCGTGCATGCGCTGGAAGCT	1160
QY	321	GluVal	322
Db	1161	GAAGTT	1166
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AK075443			
LOCUS			
DEFINITION	Homo sapiens cDNA PSEC0135 fis, clone PLACE1004850, highly similar to Homo sapiens lymphatic endothelium-specific hyaluronan receptor LYVE-1 mRNA.	1755 bp	linear
ACCESSION	AK075443		
VERSION	AK075443.1	GI:22761535	

oligo capping; fis (full insert sequence).

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

Ota,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayashi,K., Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T., Nakamura,Y., Nagahari,K., Sugano,S. and Isogai,T.

HRI human cDNA sequencing project

Unpublished

2 (bases 1 to 1755)

Isogai,T. and Yamamoto,J.

Direct Submission

Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass sequencing, clone selection and full insert sequencing: Helix Research Institute (supported by Japan Key Technology Center etc.); cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center.

Location/Qualifiers

1..1755

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ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-10-079-111-1 (1-322) x AK075443 (1-1755)

QY

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20

Db

201

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260

QY

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40

Db

261

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320

QY

41

IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla

60

Db

321

ATCACCCCTGTGAGCAAAAGCGGAACCAAGCTGAATTTACAGAAAGCTAAGGAGGCC

380

QY

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CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla

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Db

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QY

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Db

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QY

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QY

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140

Db

561

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620

QY

141

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160

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QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	681	GAATTATTGTGAGTACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	740
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeulle	200
Db	741	CCTACTACTCTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATTGATT	800
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	801	TGTGTCACAGAAAGTTTTTATGGAAGTAGCACCATGTCTACAGAAACTGAACCATTTGTT	860
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu	240
Db	861	GAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGCCACGGCTCTG	920
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrVallys	260
Db	921	CTAGTGCTTGCTCTCCTCTCTTTGGTGCTGCAGCTGGTCTTGATTTTGCTATGTCAAA	980
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
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QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1041	AAAGTAGTAAGGAGGAGAGGCCAATGATAGCAACCTTAATGAGGAATCAAAGAAACT	1100
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1101	GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAACTACCGTGCATGCCCTGGAAGCT	1160
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Db	1161	GAAGTT 1166	
RESULT 5			
AR204700		2029 bp	DNA
LOCUS	AR204700		linear
DEFINITION	Sequence 13 from patent US 6368794.		
ACCESSION	AR204700		
VERSION	AR204700.1	GI:21502094	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 2029)		
AUTHORS	Daniel,S., Gilmore,J., Stuart,S.G. and Stuve,L.L.		
TITLE	Detection of altered expression of genes regulating cell proliferation		
JOURNAL	Patent: US 6368794-A 13 09-APR-2002;		
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ORIGIN			

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Best Local Similarity:	100.00%	Mismatches:	0
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US-10-079-111-1 (1-322) x AR204700 (1-2029)

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QY	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	243	GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTATGCAGAATTATGGGG	302
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
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Db	363	TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT	422
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
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QY	121	SerArgGlnPheAlaAlaIaIyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	543	AGCCGACAGTTTGCAGCCTATGTTACAACCTCATCTGATACTTGGACTAACTCGTGCAAT	602
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	603	CCAGAAATTATCACCCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA	662
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	663	GAATTTATTGTCAGTGACAGTACTACTCGGTGGCAATCCCTTACTCTACAATACCTGCC	722
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	723	CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	782
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	783	TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	842
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu	240
Db	843	GAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG	902
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Db	963	AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAAATGATCGAAACC	1022
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Db	1023	AAAGTAGTAAGGAGGAGAGGCCCAATGATAGCAACCTTAATGAGGAATCAAAGAAACT	1082
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
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RESULT 6			
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LOCUS	BD222718		linear
DEFINITION	Human signal peptide-containing protein.		
ACCESSION	BD222718		
VERSION	BD222718.1	GI:33032488	
KEYWORDS	JP 2002519030-A/64.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 2029)
AUTHORS Lal,P., Tang,Y.T., Gorgone,G.A., Corley,N.C., Guegler,K.J., Baughn,M.R., Akerblom,I.E., Young,J.A., Yue,H., Patterson,C., Reddy,R., Hillman,J.L. and Bandman,O.
Human signal peptide-containing protein
Patent: JP 2002519030-A 64 02-JUL-2002;
INCYTE PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002519030-A/64
PD 02-JUL-2002
PF 25-JUN-1999 JP 2000557363
PR 26-JUN-1998 US 60/090762,31-JUL-1998 US 60/094983 PR 01-OCT-1998 US 60/102686,11-DEC-1998 US 60/112129 PI PREETI LAL,Y TOM TANG,GINA A GORGONE,NEIL C CORLEY,KARL J PI GUEGLER, PI MARIAH R BAUGHN,INGRID E AKERBLOM,JANICE AU YOUNG,HENRY YUE, PI CHANDRA PATTERSON,ROOPA REDDY,JENNIFER L HILLMAN,OLGA BANDMAN PC C12N15/09,A61K38/00,A61K39/395,A61K45/00,A61P9/00,A61P15/00, PC A61P25/00, PC A61P29/00,A61P35/00,A61P43/00,C07K14/47,C07K16/18,C12N1/15, PC C12N1/19, PC C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/68//C12P21/08, PC C12N15/00, PC A61K37/02,C12N5/00 CC Incyte Clone No: 3044710 FH Key Location/Qualifiers FT source 1..2029 /organism='Homo sapiens (human)'. FT Location/Qualifiers 1..2029 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
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QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
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DEFINITION Sequence 200 from patent US 6635468.
ACCESSION AR410761
VERSION AR410761.1 GI:40162261
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Ashkenazi,A., Botstein,D., Desnovers,L., Eaton,D.L., Ferrara,N., Filvaroff,E., Fong,S., Gao,W.-Q., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Hillan,K.J., Kljavin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A., Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: US 6635468-A 200 21-OCT-2003;
FEATURES Location/Qualifiers
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/organism="unknown"
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DEFINITION AX092274					
ACCESSION AX092274					
VERSION AX092274.1	GI:13444451				
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and Wood,W.I.				
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same				
JOURNAL	Patent: WO 0116318-A 5 08-MAR-2001; Genentech, Inc. (US)				
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KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I. and Ye,W.
TITLE Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis
JOURNAL Patent: WO 0200690-A 31 03-JAN-2002; Genentech, Inc. (US)
FEATURES
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Best Local Similarity: 100.00% Mismatches: 0
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RESULT 11
AX697609
LOCUS AX697609 2372 bp DNA linear PAT 02-APR-2003
DEFINITION Sequence 200 from Patent WO0104311.
ACCESSION AX697609
VERSION AX697609.1 GI:29498705
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ashkenazi,A.J., Botstein,D., Desnoyers,L., Eaton,D.L., Ferrara,N., Filvaroff,E., Fong,S., Gao,W.Q., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Hillan,K.J., Kljavin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A., Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: WO 0104311-A 200 18-JAN-2001; Genentech Inc. (US)
FEATURES
source Location/Qualifiers
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Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Db 880 CTAGTGCTTGCTCTCCTCTTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAA 939

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280

Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAAATGATCGAAACC 999

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300

Db 1000 AAAGTAGTAAAGGAGGAGAGGCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAAC 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320

Db 1060 GATAAAACCCAGAGAGTCCAGAGTCCAAGCTCCAAGCAAAACTACCGTGCATGCGAAGCT 1119

QY 321 GluVal 322

Db 1120 GAAGTT 1125

RESULT 12

BD075532

LOCUS BD075532 2372 bp DNA linear PAT 27-AUG-2002

DEFINITION Secretory and transmembrane polypeptide and nucleic acid encoding the same.

ACCESSION BD075532

VERSION BD075532.1 GI:22621135

KEYWORDS JP 2001516580-A/165.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2372)

AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Penica,D., Chen,J. and Yuan,J.

TITLE Secretory and transmembrane polypeptide and nucleic acid encoding the same

JOURNAL Patent: JP 2001516580-A 165 02-OCT-2001; GENENTECH INC

COMMENT OS Homo sapiens (human)

PN JP 2001516580-A/165

PD 02-OCT-2001

PF 16-SEP-1998 JP 2000511867

PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR

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17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR

18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR

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24-OCT-1997 US 60/063045,24-OCT-1997 US 60/063128 PR

27-OCT-1997 US 60/063329,27-OCT-1997 US 60/063327 PR

28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR

28-OCT-1997 US 60/063550,28-OCT-1997 US 60/063542 PR

28-OCT-1997 US 60/063544,28-OCT-1997 US 60/063564 PR

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29-OCT-1997 US 60/064103,31-OCT-1997 US 60/063870 PR

03-NOV-1997 US 60/064248,07-NOV-1997 US 60/064809 PR

12-NOV-1997 US 60/065186,17-NOV-1997 US 60/065846 PR

18-NOV-1997 US 60/065693,21-NOV-1997 US 60/066120 PR

21-NOV-1997 US 60/066364,24-NOV-1997 US 60/066772 PR

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24-NOV-1997 US 60/066511,24-NOV-1997 US 60/066453 PR

25-NOV-1997 US 60/066840

PI WILLIAM I WOOD,AUSTIN L GURNEY,AUDLEY GODDARD,DIANE PENICA, PI JEAN CHEN,

PI JEAN YUAN

PC C12N15/09,C07K14/47,C07K14/705,C07K16/18,C07K16/28,C07K19/00,

PC C12N1/19,

PC C12N1/21,C12N5/10,C12P21/02,C12P21/08,C12Q1/02//(C12P21/08, PC C12R1:91),

PC C12N15/00,C12N5/00

CC Secretory and transmembrane polypeptide and nucleic acid CC encoding the same

Location/Qualifiers

1..2372

1..2372

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

FEATURES

source

1..2372

ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 2372

Score: 322.00 Matches: 322

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-079-111-1 (1-322) x BD075532 (1-2372)

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Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

Db 220 GTCCAAGGCTCTTGGCTGCAGAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60

Db	280	ATCACCCCTTGTGAGCAAAAAGGCGAACACGACGCTGAATTTACAGAAAGCTAAGGAGGCC	339
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGGCTGCTGGGACTAAGTTTGGCCGGAAGGACCAAGTTGAAACAGCCTTGAAAGCT	399
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	400	AGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGGATTCTGTGTCATCTCTAGGATT	459
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	460	AGCCCAAACCCCAAGTGTGGGAAAAATGGGTGGTGCTGATTTGGAAGGTTCCAGTG	519
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	520	AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATT	579
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACA	639
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	699
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	700	CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	759
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTACAGAAAGTTTTTATGGAACACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGTTTGGAGGTGTCCCCACGGCTCTG	879
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGCTTGCTCTCCTCTTCTTTGGTGTGCAGCTGGTCTTGGATTTTGTATGTCAA	939
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAAGGAATGATCGAAACC	999
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1000	AAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAAGAAAACT	1059
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAAAGCT	1119
QY	321	GluVal	322
Db	1120	GAAGTT	1125
RESULT 13			
BD172392			
LOCUS	BD172392		
DEFINITION	Secreted and transmembrane polypeptides and nucleic acids encoding the same.		
ACCESSION	BD172392		
VERSION	BD172392.1 GI:284113692		
KEYWORDS	JP 200223786-A/165.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 2372) Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.		

TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: JP 2002223786-A 165 13-AUG-2002; GENENTECH INC		
COMMENT	OS Homo sapiens (human) PN JP 200223786-A/165 PD 13-AUG-2002 PF 18-DEC-2001 JP 2001385135 PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR 17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR 17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR 17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR 18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR 17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR 21-OCT-1997 US 60/063486,24-OCT-1997 US 60/062816 PR 24-OCT-1997 US 60/062814,24-OCT-1997 US 60/063127 PR 24-OCT-1997 US 60/063120,24-OCT-1997 US 60/063121 PR 24-OCT-1997 US 60/063045,24-OCT-1997 US 60/063128 PR 27-OCT-1997 US 60/063329,27-OCT-1997 US 60/063327 PR 28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR 28-OCT-1997 US 60/063550,28-OCT-1997 US 60/063542 PR 28-OCT-1997 US 60/063544,28-OCT-1997 US 60/063564 PR 29-OCT-1997 US 60/063734,29-OCT-1997 US 60/063738 PR 29-OCT-1997 US 60/063704,29-OCT-1997 US 60/063435 PR 29-OCT-1997 US 60/064215,29-OCT-1997 US 60/063735 PR 29-OCT-1997 US 60/063732,31-OCT-1997 US 60/064103 PR 31-OCT-1997 US 60/063870,03-NOV-1997 US 60/064248 PR 07-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR 17-NOV-1997 US 60/065846,18-NOV-1997 US 60/065693 PR 21-NOV-1997 US 60/066120,21-NOV-1997 US 60/066364 PR 24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066466 PR 24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR 24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI JIAN ZHENG, PI JEAN YUAN PC C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC C12N5/10, PC C12P21/02//C12P21/08,(C12P21/02,C12R1:19),(C12P21/02,C12R1:91), PC (C12P21/02,C12R1:645),C12N15/00,C12N5/00 CC Secreted and transmembrane polypeptides and nucleic CC acids encoding the same FH Key Location/Qualifiers FT source 1..2372 FT /organism='Homo sapiens (human)'. FEATURES source Location/Qualifiers 1..2372 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" ORIGIN Alignment Scores: Pred. No.: 0 Length: 2372 Score: 322.00 Matches: 322 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 6 Gaps: 0 US-10-079-111-1 (1-322) x BD172392 (1-2372) QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20 Db 160 ATGCCCAGGTGCTTCAGCCTGGTGTGTTCTTCTCACTTCCATCTGGACCACGAGGTCCTG 219 QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40 Db 220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG 279 QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60 		

Db 280 ATCACCCTTGTGACAAAAAGGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
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Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGGATTCTGTGTCATCTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
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Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCCTGATTTGGAAAGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
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Db 640 GAATTTATTGTGAGTACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699

QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
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Db 700 CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
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Db 760 TGTGTACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
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Db 820 GAAATATAAGCAGCATTCGAAGTCAAGCTGCTGGTTTGGAGGTGTCCCCACGGCTCTG 879

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
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Db 880 CTAGTGCTTGCTCTCTCTCTCTTTGGTGTGCTGAGCTGGTCTTGGATTTTGTATGTCAA 939

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
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Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAGAATCAGCAGAAAGGAATGATCGAAACC 999

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
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Db 1000 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAAACT 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
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RESULT 14
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LOCUS

DEFINITION

2372 bp DNA linear PAT 18-FEB-2003

Secreted and transmembrane polypeptides and nucleic acids encoding the same.

BD172711

ACCESSION

BD172711

VERSION

BD172711.1 GI:28414015

KEYWORDS

JP 2002238586-A/165.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 2372)

AUTHORS

Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.

TITLE

Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL

Patent: JP 2002238586-A 165 27-AUG-2002;

GENENTECH INC

COMMENT

OS Homo sapiens (human)

PN JP 2002238586-A/165

PD 27-AUG-2002

PF 18-DEC-2001 JP 2001385205

PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR

17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR

17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR

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31-OCT-1997 US 60/063870,03-NOV-1997 US 60/064248 PR

07-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR

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24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR

24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI

WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI

JIAN ZHENG,

PI JEAN YUAN

PC C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC C12N5/10,

PC C12P21/02//C12P21/08,(C12N1/19,C12R1:645),(C12N1/21,C12R1:19), PC (C12N5/10,C12R1:91),(C12P21/02,C12R1:91),(C12P21/02,C12R1:645), PC (C12P21/02,C12R1:19),(C12P21/08,C12R1:91),C12N15/00,C12N5/00, PC (C12N5/00,C12R1:91)

CC Secreted and transmembrane polypeptides and nucleic CC acids encoding the same

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source

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Location/Qualifiers

/organism='Homo sapiens (human)'. /mol_type="genomic DNA" /db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 2372

Score: 322.00 Matches: 322

Percent Similarity: 100.00% Conservative: 0

Best local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-079-111-1 (1-322) x BD172711 (1-2372)

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QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
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Db 220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCATCCAGGTGTCAATGAGAAATATGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTTGAGCAAAAAGCGAACCCAGCAGCTGAATTCACAGAACTAAGGAGGCC 339

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QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
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QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTCAGTGACAGTACCTACTCGTGGCATCCCCCTTACTCTACAATACCTGCC 699

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
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QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db 760 TGTGTACAGAAGTTTTTTATGGAAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATATAAGCAGCATTTCAAGAATGAAGCTGTGGGTTTGGAGGTGTCCCCACGGCTCTG 879

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCCTCTTCTTTGGTGTGCAGCTGGTCTTGATTTTGTATGTCAAA 939

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAACAAGAATCAGCAGAAAGGAATGATCGAAACC 999

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCCCTAATGAGGAATCAAAAGAACT 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCAGAAAGAGTCCAAGAGTCCAAGCAAAAACCTACCGTGCATGCCTGGAAGCT 1119

QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 16
BD173349
LOCUS BD173349 2372 bp DNA linear PAT 18-FEB-2003
DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding the same.
ACCESSION BD173349
VERSION BD173349.1 GI:28414660
KEYWORDS JP 2002238588-A/165.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2372)

AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL
COMMENT Patent: JP 2002238588-A 165 27-AUG-2002;
GENENTECH INC
OS Homo sapiens (human)
PN JP 200238588-A/165
PD 27-AUG-2002
PF 18-DEC-2001 JP 2001385315
PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR
17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR
17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR
17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR
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17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR
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21-NOV-1997 US 60/066120,21-NOV-1997 US 60/066364 PR
24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066466 PR
24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR
24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09, C07K14/435, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC C12N5/10,
PC C12P21/02//C12P21/08, (C12N1/19, C12R1:645), (C12N1/21, C12R1:19), PC (C12N5/10, C12R1:91), (C12N15/00, C12N5/00, (C12N5/00, C12R1:91) CC
Secreted and transmembrane polypeptides and nucleic CC acids encoding the same
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Score: 322.00 Matches: 322
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QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAGAGACTTTCATCCAGGTGTGATGCAGAAATTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60

Db 280 ATCACCCCTTGAGCAAAAGCGGAACACGAGCTGAATTTACAGAAAGCTAAGAGGCC 339

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QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

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QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

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QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260

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QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280

Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAATGATCGAAACC 999

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QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320

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QY 321 GluVal 322

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LOCUS

DEFINITION

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ACCESSION

BD175383

VERSION

BD175383.1 GI:29121079

KEYWORDS

JP 2002253280-A/165.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 2372)

AUTHORS

Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and

Yuan,J.

Secretory and transmembrane polypeptide and nucleic acid encoding the same

Patent: JP 2002253280-A 165 10-SEP-2002;

GENENTECH INC

OS Homo sapiens (human)

PN JP 2002253280-A/165

PD 10-SEP-2002

PF 18-DEC-2001 JP 2001385319

PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR

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24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI

WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI

JIAN ZHENG,

PI JEAN YUAN

PC C12N15/09,A61K45/00,A61P1/00,A61P13/12,A61P17/00,A61P17/06, PC

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PC C07K19/00,

PC C12N1/19,C12N1/21,C12N5/10//A61K38/00,A61K39/395,A61K39/395,

PC A61P43/00,

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PC C12R1:91),

PC C12N15/00,C12N5/00,A61K37/02,(C12N5/00,C12R1:91) CC

Secretory and transmembrane polypeptide and nucleic acid CC

encoding the same

PH Key

FT source

Location/Qualifiers

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FEATURES

source

Location/Qualifiers

1..2372

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Alignment Scores:

Pred. No.: 0 Length: 2372

Score: 322.00 Matches: 322

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-079-111-1 (1-322) x BD175383 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20

Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

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Qy	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
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ACCESSION			
AY358925			
VERSION			
AY358925.1 GI:37182967			
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SOURCE			
Homo sapiens (human)			
ORGANISM			
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	1 (bases 1 to 2372) Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.		
TITLE	The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment		
JOURNAL	Genome Res. 13 (10), 2265-2270 (2003)		
PUBMED	12975309		
REFERENCE	2 (bases 1 to 2372)		
AUTHORS	Clark,H.F.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA		
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Db	106	GTCCAAGGCTCTTTGCGTGCAGAGAGCTTCCATCCAGGTGTCATGCAGAAATTATGGG	165
QY	41	IleThrLeuValSerLysLysAlaAsnGlnLeuAsnPheThrGluAlaLysGluAla	60
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QY	140	eProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrTh	160
Db	465	TCCAGAAATTATCACCCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA	524
QY	160	rGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAl	180
Db	525	AGAAATTTATGTGCAGTGACAGTACCTACTCGGTGGCATCCCTTTACTCTACAATAC	584
QY	180	aProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIl	200
Db	585	CCCTACTACTCTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGAT	644
QY	200	eCysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVa	220
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QY	220	lGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLe	240
Db	705	TGAAATAAAGCAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCT	764
QY	240	uLeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrVally	260
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DEFINITION	Homo sapiens lymphatic endothelium-specific hyaluronan receptor				
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ACCESSION	AF118108				
VERSION	AF118108.1	GI:5359672			
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 2313)				
AUTHORS	Banerji,S., Ni,J., Wang,S.X., Clasper,S., Su,J., Tammi,R., Jones,M. and Jackson,D.G.				
TITLE	LYVE-1, a new homologue of the CD44 glycoprotein, is a lymph-specific receptor for hyaluronan				
	J. Cell Biol. 144 (4), 789-801 (1999)				
JOURNAL	99156989				
MEDLINE	10037799				
PUBMED					
REFERENCE	2 (bases 1 to 2313)				
AUTHORS	Jackson,D.G., Banerji,S. and Ni,J.				
TITLE	Direct Submission				
JOURNAL	Submitted (06-JAN-1999) MRC Human Immunology Unit, Univ. of Oxford, John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK				
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	/translation="MARCSLVLLLTISIWTRLLVQSLRAEELSIQVSCRIMGITLV SKKANQQLNFTEAKEACRLGLSLAGKDQVDTALKASFETCSYGWVGDFVVISRISP NPKCGKNGVGLIWKVPVSRQFGAYCYNSSDTWNSRIPEIITTKDPIFNTQTATQTT EPIVSDSTYSVASPYSTIPAPTTTPAPASTSIPRRKKLICVTEVFMETSTMSTETEP FVENKAAFKEAAAGFGVPTALLVLALLFFGAAAGLFCYVKRYVKAFFPTNKNOOKE MIETKVVEEKANDSNNEESKTKDNPEESKSPSKTIVRCLEAEV"				
	247. .480				
misc_feature	/note="Region: Link domain"				
ORIGIN					
Alignment Scores:					
Pred. No.:	5.64e-185	Length:	2313		
Score:	183.00	Matches:	319		
Percent Similarity:	98.15%	Conservative:	0		
Best Local Similarity:	98.15%	Mismatches:	3		
Query Match:	56.83%	Indels:	6		
DB:	9	Gaps:	0		
US-10-079-111-1 (1-322) x AF118108 (1-2313)					
QY	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu	20		
Db	91	ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCATCTCGACTACGAGGCTCCTG	150		
QY	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40		
Db	151	GTCCAAGGCTCTTTGCGTGCAGAGAGCTTTCATCCAGGTGTCATGCAGAATTATGGG	210		
QY	41	IleThrLeuValSerLysLysAlaAsnGlnLeuAsnPheThrGluAlaLysGluAla	60		
Db	211	ATCACCCCTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTTCAGAAAGCTAAGGAGGCC	270		
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGlu-ThrAlaLeuLysAl	80		

Db 271 TGTAGGCTGCTGGGACTAAGTTTGGCCGGAAGGACCAAGTTGA-CACAGCCTTGAAAGC 329

QY 80 aSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIl 100
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Db 330 TAGCTTTGAAACTTGACGCTATGGCTGGTTGGAGATGGATTCTGGTCACTCTAGGAT 389
|||||

QY 100 eSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVa 120
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Db 390 TAGCCCCAAACCCCAAGTGTGGAAAAAATGGGTGGTCTCTGATTGTGAAGGTTCCAGT 449
|||||

QY 120 lSerArgGlnPheAla-AlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCys- 139
|||||

Db 450 GAGCCGACAGTTTGG-AGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGCG-C 507
|||||

QY 140 ileProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThr 159
|||||

Db 508 ATTCAGAAATTATCACCAACAAAGATCCCATATTCCAACACTCAAACGACACAAACA 567
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QY 160 ThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIlePro 179
|||||

Db 568 ACAGAAATTATTGTAGTGACAGTACCTACTCGGTGGATCCCTTACTCTACATACT 627
|||||

QY 180 AlaProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeu 199
|||||

Db 628 GCCCTACTACTACTCTCTCTCTCCAGCTTCCACITCTATTCACGGAGAAAAAATTG 687
|||||

QY 200 ileCysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPhe 219
|||||

Db 688 ATTTGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTT 747
|||||

QY 220 ValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAla 239
|||||

Db 748 GTTGAAAAATAAAGCAGCAATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCT 807
|||||

QY 240 LeuLeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrVal 259
|||||

Db 808 CTGCTAGTGCTTGCTCTCTCTCTTTTGGTGCTGCAGCTGCTCTGGATTTTGTATGTC 867
|||||

QY 260 LysArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGlu 279
|||||

Db 868 AAAAGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAAATCAGACAAGGAATGATCGAA 927
|||||

QY 280 ThrLysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLys 299
|||||

Db 928 ACCAAAGTAGTAAAGGAGGAGGAGGCCAATGATAGCAACCTAATGAGGAATCAAAGAA 987
|||||

QY 300 ThrAspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGlu 319
|||||

Db 988 ACTGATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCGCTGGAA 1047
|||||

QY 320 AlaGluVal 322
|||||

Db 1048 GCTGAAGTT 1056
|||||

RESULT 21

AX136529

LOCUS AX136529 716 bp DNA linear PAT 30-MAY-2001

DEFINITION Sequence 451 from Patent EP1067182.

ACCESSION AX136529

VERSION AX136529.1 GI:14272933

KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.

TITLE Secretory protein or membrane protein

JOURNAL Patent: Ep 1067182-A 451 10-JAN-2001;

FEATURES

source Location/Qualifiers

1. .716

/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN

Alignment Scores:

Pred. No.: 1.8e-123 Length: 716

Score: 125.00 Matches: 125

Percent Similarity: 100.00% Conservatives: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 38.82% Indels: 0

DB: 6 Gaps: 0

US-10-079-111-1 (1-322) x AX136529 (1-716)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
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Db 201 ATGGCCAGGTGCTTCAGCCTGGTGTGTTCTTCTCATCTCCATCTGGACCACGAGGCTCCTG 260
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QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
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Db 261 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCAATGCAGAAATTATGGGG 320
|||||

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
|||||

Db 321 ATCACCCCTTGTGAGCAAAAAGCGCAACCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 380
|||||

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
|||||

Db 381 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 440
|||||

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
|||||

Db 441 AGCTTTGAAACTTGACGCTATGGCTGGTGGAGATGGATTCTGGTCACTCTTAGGATT 500
|||||

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
|||||

Db 501 AGCCCAACCCCAAGTGTGGAAAAAATGGGTGGGTGCTCTGTGATTGTGAAGGTTCCAGTG 560
|||||

QY 121 SerArgGlnPheAla 125
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Db 561 AGCCGACAGTTTGCA 575
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RESULT 22

BD123769

LOCUS BD123769 716 bp DNA linear PAT 18-SEP-2002

DEFINITION Secretory protein or membrane protein.

ACCESSION BD123769

VERSION BD123769.1 GI:23218714

KEYWORDS JP 2002017376-A/278.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 716)

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.

TITLE Secretory protein or membrane protein

JOURNAL Patent: JP 2002017376-A 278 22-JAN-2002;

COMMENT HELIX RESEARCH INSTITUTE

OS Homo sapiens (human)

PN JP 2002017376-A/278

PD 22-JAN-2002

PF 07-JUL-2000 JP 2000253173

PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,TOMOYASU

PI SUGIYAMA,

PI KOJI HAYASHI

PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC

10, 10,

PC C12P21/02,C12Q1/68//C12P21/08,C12N15/00,C12N5/00 CC

Secretory protein or membrane protein

FH Key Location/Qualifiers

FT source 1. .716 /organism='Homo sapiens (human)'.
FT Location/Qualifiers
1. .716
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 1.8e-123 Length: 716
Score: 125.00 Matches: 125
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 38.82% Indels: 0
DB: 6 Gaps: 0
US-10-079-111-1 (1-322) x BD123769 (1-716)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db ATGGCCAGGTGCTTCAGCCTGGTGTCTCTCACTTCCATCTGGACACGAGGCTCCTG 260
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db GTCCAAGGCTCTTTGCGTGCAGAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGG 320
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db ATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTACAGAACTAAGGAGGCC 380
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db TGTAGGCTGTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 440
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCGTGGTCATCTCTAGGATT 500
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db AGCCCAACCCCAAGTGTGGGAAAAATGGGTGGTGTCTGATTTCGAAGGTTCCAGTG 560
QY 121 SerArgGlnPheAla 125
Db AGCCGACAGTTTGCA 575
RESULT 23
BD076146
LOCUS BD076146 451 bp DNA linear PAT 27-AUG-2002
DEFINITION 5' EST of tissue-nonspecific secretory protein.
ACCESSION BD076146
VERSION BD076146.1 GI:22621749
KEYWORDS JP 2001512011-A/94.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 451)
AUTHORS Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
TITLE 5' EST of tissue-nonspecific secretory protein
JOURNAL Patent: JP 2001512011-A 94 21-AUG-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001512011-A/94
PD 21-AUG-2001
PF 31-JUL-1998 JP 2000505289
PR 01-AUG-1997 US 08/905135
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT,BRUNO PI
LACROIX
PC C12N15/09,C12N15/09,C07K14/47,C12Q1/68,C12N15/00,C12N15/00 CC
blastn
CC identity 100

CC region 1. .133
CC id AA081350
CC est
CC blastn
CC identity 99
CC region 133. .240
CC id AA081350
CC est
CC blastn
CC identity 90
CC region 269. .300
CC id AA081350
CC est
CC blastn
CC identity 99
CC region 67. .231
CC id AA046671
CC est
CC blastn
CC identity 100
CC region 1. .68
CC id AA046671
CC est
CC Von Heijne matrix
CC score 6.7
CC seq CFSLVLLLTISIWT/TR
FH Key Location/Qualifiers
FT misc_feature 156. .288
FT misc_feature 289. .396
FT misc_feature 422. .453
FT misc_feature 289. .453
FT misc_feature 222. .289
FT sig_peptide 104. .151.
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1. .451
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 4.85e-114 Length: 451
Score: 116.00 Matches: 116
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 36.02% Indels: 0
DB: 6 Gaps: 0
US-10-079-111-1 (1-322) x BD076146 (1-451)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db ATGGCCAGGTGCTTCAGCCTGGTGTCTCTCACTTCCATCTGGACACGAGGCTCCTG 163
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGG 223
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db ATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTACAGAACTAAGGAGGCC 283
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db TGTAGGCTGTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 343
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCGTGGTCATCTCTAGGATT 403
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 116
Db AGCCCAACCCCAAGTGTGGGAAAAATGGGTGGTGGTGTCTCTAGGATT 451

repeat_region /rpt family="FLAM C"
complement(21661. .22039)
/rpt family="MLT1E2"
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/rpt family="AluJb"
repeat_region complement(22164. .22466)
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/rpt family="MLT1E2"
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repeat_region 28304. .28472
/rpt family="MERSB"
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repeat_region complement(34584. .34690)
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/rpt family="MIR"
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/rpt family="L2"
repeat_region complement(38043. .38343)
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repeat_region 39508. .39692
/rpt family="MIR"
repeat_region complement(39968. .40274)
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repeat_region 40393. .40477
/rpt family="L2"
repeat_region 41047. .41067
/rpt family=" (TTTA)n"

Alignment Scores:
Pred. No.: 9.91e-98 Length: 165698
Score: 103.00 Matches: 103
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 31.99% Indels: 0
DB: 9 Gaps: 0

US-10-079-111-1 (1-322) x AC009532 (1-165698)

QY 133 AspThrTrpThrAsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsn 152
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Db 12427 GATAC TTGGACTA ACTCGTGCAT TCCAGAAATTATCACCACCAAGATCCCATATTTCAAC 12368
QY 153 ThrGlnThrAlaThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAla 172

Db 12367 ACTCAAACTGCAACACAAACACAGAAATTTATTGTTCAGTGACAGTACCTACTCGGTGGCA 12308
QY 173 SerProTyrSerThrIleProAlaProThrThrThrProProAlaProAlaSerThrSer 192
|||||
Db 12307 TCCCCTTACTCTACAATACTACCTGCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCT 12248
QY 193 IleProArgArgLysLysLeuIleCysValThrGluValPheMetGluThrSerThrMet 212
|||||
Db 12247 ATTCCACGGAGAAAAAATTGATTTGTGTGCACAGAAAGTTTTTATGGAAACTAGCACCATG 12188
QY 213 SerThrGluThrGluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGly 232
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Db 12187 TCTACAGAAACTGAACCATTTGTTGAAATAAAGCAGCATTTCAAGATGAAGCTGCTGGG 12128
QY 233 PheGlyGly 235
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Db 12127 TTTGGAGGT 12119
RESULT 25
BD077623
LOCUS
DEFINITION 5'EST of secreted protein expressed in muscles and other mesodermal tissues.
ACCESSION BD077623
VERSION BD077623.1 GI:22623226
KEYWORDS JP 2001512016-A/209.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 363)
AUTHORS Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
TITLE 5'EST of secreted protein expressed in muscles and other mesodermal tissues
JOURNAL Patent: JP 2001512016-A 209 21-AUG-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001512016-A/209
PD 21-AUG-2001
PF 31-JUL-1998 JP 2000505295
PR 01-AUG-1997 US 08/905134
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT,BRUNO PI LACROIX
PC C12N15/09,C12N15/09,C07K14/47,C12M1/00,C12N15/00,C12N15/00 CC
blastn
CC identity 97
CC region 1. .116
CC id AA081350
CC est
CC blastn
CC identity 97
CC region 3. .50
CC id AA046671
CC est
CC Von Heijne matrix
CC score 6.7
CC seq CFSLVLLLTSTWT/TR
CC n=a, g, c or t Location/Qualifiers
FH Key Location/Qualifiers
FT misc_feature 209. .324
FT misc_feature 277. .324
FT sig_peptide 157. .204
FT misc_feature 275. .276
FT misc_feature 325. .326
FT misc_feature 328.
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source 1. .363
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

RESULT 28
MMU3111501
LOCUS
DEFINITION Mus musculus mRNA for lymphatic endothelial hyaluronan receptor (LYVE-1 gene).
ACCESSION AJ3111501
VERSION AJ3111501.1 GI:13162222
KEYWORDS hyaluronan receptor; LYVE-1 gene.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Banerji,S., Ni,J., Wang,S.X., Clasper,S., Su,J., Tammi,R., Jones,M. and Jackson,D.G.
TITLE LYVE-1, a new homologue of the CD44 glycoprotein, is a lymph-specific receptor for hyaluronan
J. Cell Biol. 144 (4), 789-801 (1999)
99156989
10037799
REFERENCE 2
AUTHORS Prevo,R., Banerji,S., Ferguson,D.J., Clasper,S. and Jackson,D.G.
TITLE Mouse LYVE-1 is an endocytic receptor for hyaluronan in lymphatic endothelium
J. Biol. Chem. 276 (22), 19420-19430 (2001)
21276443
11278811
REFERENCE 3 (bases 1 to 1516)
AUTHORS Jackson,D.G.
TITLE Direct Submission
JOURNAL Submitted (16-FEB-2001) Jackson D.G., Institute of Molecular Medicine, MRC Human Immunology Unit, John Radcliffe Hospital, Headington, Oxford, OX3 9DS, UNITED KINGDOM
LOCATION/Qualifiers
1. .1516
/organism="Mus musculus"
/mol_type="mRNA"
/strain="Balb/c"
/db_xref="taxon:10090"
/tissue_type="Digestive tract"
/dev_stage="Adult"
/country="United Kingdom:Oxford"
1. .1516
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241. .1197
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/function="lymphatic endothelial hyaluronan receptor for hyaluronan uptake"
/evidence=experimental
/product="hyaluronan receptor"
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241. .309
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310. .1194
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sig_peptide
mat_peptide

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.01% Indels: 0
DB: 10 Gaps: 0
US-10-079-111-1 (1-322) x MMU3111501 (1-1516)
QY 224 AlaAlaPheLysAsnGluAlaAlaAGlyPheGlyGlyValProThrAlaLeuLeuValLeu 243
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Db 898 GCAGCATTCAGAACGACGAGCTGGGTTTGGAGGTGTCCACCGCCCTGCTGGTGCTG 957
QY 244 AlaLeuLeuPhePheGlyAlaAlaA 252
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Db 958 GCTCTCCTCTTCTTTGGTGTGCCGCT 984
RESULT 29
BC038653
LOCUS Mus musculus extra cellular link domain-containing 1, mRNA (cdna clone MGC:48237 IMAGE:2936961), complete cds.
DEFINITION BC038653
ACCESSION BC038653.1 GI:24047314
VERSION MGC.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2027)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,A., Madan,A., Young,A.C., Shevchenko,Y., Sanchez,A., Whiting,M., Touchman,J.W., Green,E.D., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Grimwood,J., Schmutz,J., Myers,R.M., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Skalska,U., Smailus,D.E., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnurch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
JOURNAL 22388257
MEDLINE 12477932
PUBMED
REFERENCE 2 (bases 1 to 2027)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (15-OCT-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbiology.org>
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 83 Row: m Column: 14

This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

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VSSSAYLASSPDSTTPVSATRAPPLTSMARKTKKICITEVYTEPITMATETEAFVAS
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    /db_xref="CDD:smart00445"

ORIGIN

Alignment Scores:
Pred. No.:      1.9e-20      Length:      2027
Score:          29.00        Matches:      29
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:      9.01%      Indels:          0
DB:              10         Gaps:          0

US-10-079-111-1 (1-322) x BC038653 (1-2027)

QY      224 AlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeuLeuValLeu 243
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Db      849 GCAGCATTCGAAGACGAGCAGCTGGGTTTGAGAGGTGCCACCGCCCTGCTGGTGTGCTG 908
      |||

QY      244 AlaLeuLeuPhePheGlyAlaAlaAala 252
      |||
Db      909 GCTCTCCTCTTCTTCTTGGTGTGCTGCCGCT 935
      |||

RESULT 30
BC038892
LOCUS
DEFINITION
Mus musculus extra cellular link domain-containing 1, mRNA (cDNA
clone MGC:48275 IMAGE:3372151), complete cds.

ACCESSION
BC038892
VERSION
BC038892.1
KEYWORDS
MGC.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2027)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Touchman,J.W., Green,E.D.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 2027)
Strausberg,R.
Direct Submission
Submitted (25-OCT-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-1@mail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 83 Row: 0 Column: 17.

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GAAFKNEAGFGGVP TALLVLALLFFGAAVLAVCYVKRYVKAFFPTTKNQKEMMET
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    /note="LINK; Region: Link (Hyaluronan-binding)"
    /db_xref="CDD:smart00445"
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misc_feature

ORIGIN

Alignment Scores:
Pred. No.: 1.9e-20 Length: 2027

Score:	29.00	Matches:	29
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	9.01%	Indels:	0
DB:	10	Gaps:	0
US-10-079-111-1 (1-322) x BC038892 (1-2027)			
QY	224	AlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeuValLeu	243
Db	849	GCAGCATTCAAGAACGAAGCAGCTGGGTTTGAGGTGTCCCCACCGCCCTGCTGGTGCTG	908
QY	244	AlaLeuLeuPhePheGlyAlaAlaAa	252
Db	909	GCTCTCCTCTTCTTTGGTGTGCCGCT	935
RESULT 31			
AC110451_3/c			
WPCOMMENT			
Sequence split into 4 fragments LOCUS AC110451 Accession AC110451			
Fragment Name	Begin	End	
AC110451_0	1	110000	
AC110451_1	100001	210000	
AC110451_2	200001	310000	
AC110451_3	300001	359529	
Continuation (4 of 4) of AC110451 from base 300001 (AC110451 Rattus norvegicus clone CH2			
Alignment Scores:			
Pred. No.:	5.37e-18	Length:	59529
Score:	28.00	Matches:	28
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	8.70%	Indels:	0
DB:	2	Gaps:	0
US-10-079-111-1 (1-322) x AC110451_3 (1-59529)			
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	49362	AGGTATGTGAAGGCCTTCCTTTTCACAAACAAGATCAACAGAGGAATGATCGAAACC	49303
QY	281	LysValValLysGluGluLysAla	288
Db	49302	AAGGTTGTAAAGGAGGAAAGCT	49279
RESULT 32			
AC130104/c			
LOCUS	AC130104	235382 bp	DNA linear HTG 13-MAY-2003
DEFINITION	Rattus norvegicus clone CH230-226A9, *** SEQUENCING IN PROGRESS		
***, 2 unordered pieces.			
ACCESSION	AC130104		
VERSION	AC130104.3 GI:30578716		
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.		
SOURCE	Rattus norvegicus (Norway rat)		
ORGANISM	Rattus norvegicus		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;			
Rattus.			
REFERENCE	1 (bases 1 to 235382)		
AUTHORS	Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,		

Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Primus,E., Pu,L.-L., Plopper,F., Poindexter,A., Popovic,D., Reeves,K., Regier,M.A., Reigh,R., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Riggs,F., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

Direct Submission

Unpublished

2 (bases 1 to 235382)

Worley,K.C.

Direct Submission

Submitted (08-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 235382)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:23119636.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GJNK
Center clone name: CH230-226A9
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 214760 bases at least Q40

individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Center project name: KBXX
Center clone name: CH230-39G8

----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 217229 bases at least Q40
Consensus quality: 219355 bases at least Q30
Consensus quality: 220806 bases at least Q20
Estimated insert size: 224750; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
 consists of 2 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

* 1 47065: contig of 47065 bp in length
* 47066 47165: gap of unknown length
* 47166 239307: contig of 192142 bp in length.

FEATURES
source

misc_feature
misc_feature

ORIGIN

Alignment Scores:

Pred. No.: 1.99e-17 Length: 239307
Score: 28.00 Matches: 28
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 2 Gaps: 0

US-10-079-111-1 (1-322) x AC129402 (1-239307)

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
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Db 16976 AGGTATGTGAAGGCCCTTCCCTTTACAAACAAGATCAACAGAAAGGAAATGATCGAAACC 17035
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QY 281 LysValValLysGluGluLysAla 288
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Db 17036 AAGGTTGTAAGGAGAGAGAAAGCT 17059
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RESULT 34
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LOCUS
DEFINITION Sus scrofa lymphatic endothelial hyaluronan receptor LYVE-1 mRNA, partial cds.
ACCESSION AY304537
VERSION AY304537.1 GI:32141033

KEYWORDS

SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL

REFERENCE
AUTHORS

TITLE
JOURNAL

FEATURES
source

CDS

ORIGIN

Alignment Scores:

Pred. No.: 1.83e-13 Length: 603
Score: 22.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.83% Indels: 0
DB: 4 Gaps: 0

US-10-079-111-1 (1-322) x AY304537 (1-603)

QY 257 CysTyrValLysArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGlu 276
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Db 538 TGCTACGTCAAAAGGTATGTGAAGCGTTCCTTTTACAAACAAGATCAGCAGAGGAA 597
|||||

QY 277 MetIle 278
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Db 598 ATGATC 603

RESULT 35
AR410765

LOCUS
DEFINITION

ACCESSION
AR410765

VERSION
AR410765.1 GI:40162265

KEYWORDS
SOURCE

ORGANISM
Unclonable.

REFERENCE
AUTHORS

TITLE

JOURNAL
FEATURES

source

Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 603)
Michael, K.W., Xu, S.-H., Voisine, P., Khan, T.A., Feng, J., Li, J.,
Sellke, F.W. and Bianchi, C.
Identification of pig LYVE-1
Unpublished
2 (bases 1 to 603)
Michael, K.W., Xu, S.-H., Voisine, P., Khan, T.A., Feng, J., Li, J.,
Sellke, F.W. and Bianchi, C.
Direct Submission
Submitted (23-MAY-2003) Cardiothoracic Division, Beth Israel
Deaconess Med. Ctr., 330 Brookline Avenue DA-803, Boston, MA 02215,
USA

Location/Qualifiers
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Percent Similarity:		100.00%	Mismatches: 0
Best Local Similarity:		4.97%	Indels: 0
Query Match:		6	Gaps: 0
DB:			
US-10-079-111-1 (1-322) x AR410765 (1-50)			
Qy	59	GluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnVal	74
Db	3	GAGGCCTGTAGGCTGTGGGACTAAGTTTGGCCGCAAGGACCAAGTT	50
RESULT 36			
AX697614			
LOCUS	AX697614	50 bp	DNA linear PAT 02-APR-2003
DEFINITION	Sequence 205 from Patent WO0104311.		
ACCESSION	AX697614		
VERSION	AX697614.1	GI:29498709	
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1		
AUTHORS	Ashkenazi,A.J., Botstein,D., Desnoyers,L., Eaton,D.L., Ferrara,N., Filvaroff,E., Fong,S., Gao,W.Q., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Hillan,K.J., Kljavin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A., Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: WO 0104311-A 205 18-JAN-2001; Genentech Inc. (US)		
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Percent Similarity:		100.00%	Mismatches: 0
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DEFINITION	Secretory and transmembrane polypeptide and nucleic acid encoding the same.		
ACCESSION	BD075536		
VERSION	BD075536.1	GI:22621139	
KEYWORDS	JP 2001516580-A/169.		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1 (bases 1 to 50)		
AUTHORS	Wood,W.I., Gurney,A.L., Goddard,A., Penica,D., Chen,J. and Yuan,J.		

TITLE		Secretory and transmembrane polypeptide and nucleic acid encoding the same	
JOURNAL		Patent: JP 2001516580-A 169 02-OCT-2001; GENENTECH INC	
COMMENT		OS Artificial Sequence PN JP 2001516580-A/169 PD 02-OCT-2001 PF 16-SEP-1998 JP 2000511867 PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR 17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR 17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR 17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR 18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR 17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR 21-OCT-1997 US 60/063486,24-OCT-1997 US 60/062816 PR 24-OCT-1997 US 60/062814,24-OCT-1997 US 60/063127 PR 24-OCT-1997 US 60/063120,24-OCT-1997 US 60/063121 PR 24-OCT-1997 US 60/063045,24-OCT-1997 US 60/063128 PR 27-OCT-1997 US 60/063329,27-OCT-1997 US 60/063327 PR 28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR 28-OCT-1997 US 60/063550,28-OCT-1997 US 60/063542 PR 28-OCT-1997 US 60/063544,28-OCT-1997 US 60/063564 PR 29-OCT-1997 US 60/063734,29-OCT-1997 US 60/063738 PR 29-OCT-1997 US 60/063704,29-OCT-1997 US 60/063435 PR 29-OCT-1997 US 60/064215,29-OCT-1997 US 60/063735 PR 29-OCT-1997 US 60/064103,31-OCT-1997 US 60/063870 PR 03-NOV-1997 US 60/064248,07-NOV-1997 US 60/064809 PR 12-NOV-1997 US 60/065186,17-NOV-1997 US 60/065846 PR 18-NOV-1997 US 60/065693,21-NOV-1997 US 60/066120 PR 21-NOV-1997 US 60/066364,24-NOV-1997 US 60/066772 PR 24-NOV-1997 US 60/066466,24-NOV-1997 US 60/066770 PR 24-NOV-1997 US 60/066511,24-NOV-1997 US 60/066453 PR 25-NOV-1997 US 60/066840 PI WILLIAM I WOOD,AUSTIN L GURNEY,AUDLEY GODDARD,DIANE PENICA, PI JEAN CHEN, PI JEAN YUAN PC C12N15/09,C07K14/47,C07K14/705,C07K16/18,C07K16/28,C07K19/00, PC C12N1/19, PC C12N1/21,C12N5/10,C12P21/02,C12P21/08,C12Q1/02//(C12P21/08, PC C12R1:91), PC C12N15/00,C12N5/00 CC Description of Artificial Sequence: Synthetic FH Key Location/Qualifiers FT source 1..50 FT /organism='Artificial Sequence'.	
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LOCUS	BD172396	50 bp	DNA linear PAT 18-FEB-2003
DEFINITION	Secreted and transmembrane polypeptides and nucleic acids encoding the same.		
ACCESSION	BD172396		
VERSION	BD172396.1	GI:28413696	

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RESULT 40			
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LOCUS	BD173034	50 bp	DNA
DEFINITION	Secreted and transmembrane polypeptides and nucleic acids encoding the same.		
ACCESSION	BD173034		
VERSION	BD173034.1	GI:28414340	
KEYWORDS	JP 2002238587-A/169.		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1 (bases 1 to 50)		
AUTHORS	Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: JP 2002238587-A 169 27-AUG-2002;		
COMMENT	OS Artificial Sequence PN JP 2002238587-A/169 PD 27-AUG-2002 PF 18-DEC-2001 JP 2001385248 PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR 17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR 17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR 17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR 18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR 17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR 21-OCT-1997 US 60/063486,24-OCT-1997 US 60/062816 PR 24-OCT-1997 US 60/062814,24-OCT-1997 US 60/063127 PR 24-OCT-1997 US 60/063120,24-OCT-1997 US 60/063121 PR 24-OCT-1997 US 60/063045,24-OCT-1997 US 60/063128 PR 27-OCT-1997 US 60/063329,27-OCT-1997 US 60/063327 PR 28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR 28-OCT-1997 US 60/063550,28-OCT-1997 US 60/063542 PR 29-OCT-1997 US 60/063734,29-OCT-1997 US 60/063738 PR 29-OCT-1997 US 60/063704,29-OCT-1997 US 60/063435 PR 29-OCT-1997 US 60/064215,29-OCT-1997 US 60/063735 PR 29-OCT-1997 US 60/063732,31-OCT-1997 US 60/064103 PR 31-OCT-1997 US 60/063870,03-NOV-1997 US 60/064248 PR 07-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR 17-NOV-1997 US 60/065846,18-NOV-1997 US 60/065693 PR 21-NOV-1997 US 60/066120,21-NOV-1997 US 60/066364 PR 24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066466 PR 24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR 24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI JIAN ZHENG, PI JEAN YUAN PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC C12N15/02, PC C12P21/02,C12P21/08/(C12P21/02,C12R1:91),(C12P21/02,C12R1:19), PC (C12P21/02,C12R1:645),C12N15/00,C12N5/00,C12N15/00 CC Description of Artificial Sequence: Synthetic FH Key Location/Qualifiers FT source 1. .50 /organism='Artificial Sequence'. Location/Qualifiers 1. .50 /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"		
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KEYWORDS	JP 2002238588-A/169.		
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ORGANISM	artificial sequences.		
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AUTHORS	Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
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artificial sequences.
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Yuan,J.
AUTHORS
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the same
JOURNAL
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24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR
24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09,A61K45/00,A61P1/00,A61P13/12,A61P17/00,A61P17/06, PC

A61P25/00,
PC A61P25/16,A61P25/28,A61P31/12,A61P35/00,C07K14/47,C07K16/18,
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PC A61P43/00,
PC C12P21/08,(C12N1/19,C12R1:645),(C12N1/21,C12R1:19),(C12N5/10,
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PC C12N15/00,C12N5/00,A61K37/02,(C12N5/00,C12R1:91) CC
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source

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Query Match: 4.97% Indels: 0
DB: 6 Gaps: 0

US-10-079-111-1 (1-322) x BD175387 (1-50)

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VERSION
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gene.
SOURCE
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ORGANISM
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Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Schizophyllaceae; Schizophyllum.
REFERENCE
1 (bases 460 to 5883)
AUTHORS
Wendland,J., Vaillancourt,L.J., Hegner,J., Lengeler,K.B.,
Laddison,K.J., Specht,C.A., Raper,C.A. and Kothe,E.
TITLE
The mating-type locus B alpha 1 of Schizophyllum commune contains a
pheromone receptor gene and putative pheromone genes
JOURNAL
EMBO J. 14 (21), 5271-5278 (1995)
MEDLINE
96080162
PUBMED
7489716
REFERENCE
2
AUTHORS
Wendland,J.
TITLE
Direct Submission
JOURNAL
Submitted (02-MAR-1994) J. Wendland, Philipps-Universitaet Marburg,
Karl-von-Frisch Strasse, 35032 Marburg, FRG
REMARK
Revised by author 05-JUL-95 & 20-SEP-95. Revised by [4]
REFERENCE
3 (bases 1 to 5883)
AUTHORS
Wendland,J.
TITLE
Direct Submission
JOURNAL
Submitted (16-APR-1996) J. Wendland, Philipps-Universitaet Marburg,
Karl-von-Frisch Strasse, 35032 Marburg, FRG
COMMENT
On Apr 17, 1996 this sequence version replaced gi:1246904.
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102(b) frag.

B/gvk

GenCore version 5.1.6
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SUMMARIES

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3	2005	98.8	2404	4	US-09-833-381-853	Sequence 853, App
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5	1994	98.3	2372	4	US-09-905-125A-200	Sequence 200, App
6	1994	98.3	2372	4	US-09-902-775A-200	Sequence 200, App
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8	603.6	29.7	1896	4	US-09-724-864-28	Sequence 28, Appl
9	334	16.5	339	2	US-08-892-880-11	Sequence 11, Appl
10	296.8	14.6	492	2	US-08-892-880-12	Sequence 12, Appl
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12	239	11.8	241	4	US-09-620-405B-324	Sequence 324, App
13	239	11.8	241	4	US-09-433-826B-324	Sequence 324, App
14	239	11.8	241	4	US-09-604-287A-324	Sequence 324, App
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22	160	7.9	498	2	US-08-892-880-15	Sequence 15, Appl
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ALIGNMENTS

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; Patent No. 6368794
; GENERAL INFORMATION:
; APPLICANT: Steve Daniel
; APPLICANT: James Gilmore
; APPLICANT: Susan G. Stuart
; APPLICANT: Laura Stuve
; TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: PA-0003 US
; CURRENT APPLICATION NUMBER: US/09/232,160
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 23
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Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2029;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	CCTTGACAAAGTCAGAAGCTTGAAAGCAGGGAAATCCGGATGTCCTCGGTTATGAAGTGGAG	60	
Db	1	CCTTGACAAAGTCAGAAGCTTGAAAGCAGGGAAATCCGGATGTCCTCGGTTATGAAGTGGAG	60	
Qy	61	CAGTGAGTGTGAGCCTCAACATAGTTCAGAACTCTCCATCCGGACTAGTTATTGAGCAT	120	
Db	61	CAGTGAGTGTGAGCCTCAACATAGTTCAGAACTCTCCATCCGGACTAGTTATTGAGCAT	120	
Qy	121	CTGCCTCTCATATCACCAGTGGCCATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCA	180	
Db	121	CTGCCTCTCATATCACCAGTGGCCATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCA	180	
Qy	181	CGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCC	240	
Db	181	CGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCC	240	
Qy	241	TGGTCCAAGGCTCTTTGGGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGG	300	
Db	241	TGGTCCAAGGCTCTTTGGGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGG	300	
Qy	301	GGATCACCTTGTGAGCAAAAGCGCAACCCAGCAGCTGAATTCACAGAAGCTAAGGAGG	360	

Db 301 GGATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGG 360

QY 361 CCTGTAGGCTGCTGGGACTAAAGTTTGGCCGGCAAGGACCAAGTTTGAAACAGCCTTGAAAG 420

Db 361 CCTGTAGGCTGCTGGGACTAAAGTTTGGCCGGCAAGGACCAAGTTTGAAACAGCCTTGAAAG 420

QY 421 CTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCACTCTAGGA 480

Db 421 CTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCACTCTAGGA 480

QY 481 TTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTCTCTGATTTGGAGGTTCCAG 540

Db 481 TTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTCTCTGATTTGGAGGTTCCAG 540

QY 541 TGAGCCGACAGTTTGAGCCCTATTGTTACAACTCATCTGATACTTGGACTAATCTCGTGCA 600

Db 541 TGAGCCGACAGTTTGAGCCCTATTGTTACAACTCATCTGATACTTGGACTAATCTCGTGCA 600

QY 601 TTCCAGAAATTTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACAAACAA 660

Db 601 TTCCAGAAATTTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACAAACAA 660

QY 661 CAGAAATTTATTGTAGTGACAGTACCTACTCGTGGCATCCCTTACTCTACAATACCTG 720

Db 661 CAGAAATTTATTGTAGTGACAGTACCTACTCGTGGCATCCCTTACTCTACAATACCTG 720

QY 721 CCCCTACTACTCTCCTGCTCCAGCTTCCACTTCTATTTCCACGGAGAAAAAATTGA 780

Db 721 CCCCTACTACTCTCCTGCTCCAGCTTCCACTTCTATTTCCACGGAGAAAAAATTGA 780

QY 781 TTTGTGTACAGAAAGTTTATGGAACTAGSACCATGTCTACAGAAACTGAACCATTTG 840

Db 781 TTTGTGTACAGAAAGTTTATGGAACTAGSACCATGTCTACAGAAACTGAACCATTTG 840

QY 841 TTGAAATTAAGCAGCATTCAAGAAATGAAGTGTGGGTTGGAGGTTGCCACGGCTC 900

Db 841 TTGAAATTAAGCAGCATTCAAGAAATGAAGTGTGGGTTGGAGGTTGCCACGGCTC 900

QY 901 TGCTAGTGTCTCTCCTCTTCTTTGGTGTGCTGAGCTGGTCTTGGATTTTGTATGTCA 960

Db 901 TGCTAGTGTCTCTCCTCTTCTTTGGTGTGCTGAGCTGGTCTTGGATTTTGTATGTCA 960

QY 961 AAAGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAAATGATCGAAA 1020

Db 961 AAAGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAAATGATCGAAA 1020

QY 1021 CCAAGTATGTAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAA 1080

Db 1021 CCAAGTATGTAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAA 1080

QY 1081 CTGAPAAAAACCCAGAGAGTCCAAAGAGTCCAAGCAAAACTACCGTGGATGCTTGAAG 1140

Db 1081 CTGAPAAAAACCCAGAGAGTCCAAAGAGTCCAAGCAAAACTACCGTGGATGCTTGAAG 1140

QY 1141 CTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTCATGCTC 1200

Db 1141 CTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTCATGCTC 1200

QY 1201 CTTACCCCTGCCCCAGCTGGGGAAATCAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACC 1260

Db 1201 CTTACCCCTGCCCCAGCTGGGGAAATCAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACC 1260

QY 1261 CTTGGTTCCCTAACTGGAATCAGCTCAGGACTGCCATTTGGACTATGGAGTGCACCAAGAG 1320

Db 1261 CTTGGTTCCCTAACTGGAATCAGCTCAGGACTGCCATTTGGACTATGGAGTGCACCAAGAG 1320

QY 1321 AATGCCCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCTACCTCCAAAGCTTCC 1380

Db 1321 AATGCCCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCTACCTCCAAAGCTTCC 1380

QY 1381 CACGGCCTTCTAGCCTGGCTATGTCTCTAATAATATCCCACTGGGAGAAAGGAGTTTTC 1440

Db 1381 CACGGCCTTCTAGCCTGGCTATGTCTCTAATAATATCCCACTGGGAGAAAGGAGTTTTC 1440

QY 1441 AAAGTGCAAGGACCTAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCCTCCTGGCTGT 1500

Db 1441 AAAGTGCAAGGACCTAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCCTCCTGGCTGT 1500

QY 1501 CTGAGGCTAGGTGGTTGAAAGCCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATT 1560

Db 1501 CTGAGGCTAGGTGGTTGAAAGCCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATT 1560

QY 1561 CCGCAGCTCAGACCCCTTTCTTCAGCTCTGAAAGAGAAACACGTATCCCACTGACATGTC 1620

Db 1561 CCGCAGCTCAGACCCCTTTCTTCAGCTCTGAAAGAGAAACACGTATCCCACTGACATGTC 1620

QY 1621 CTTCTGAGCCCGGTAAGAGCAAAAGAAATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGGA 1680

Db 1621 CTTCTGAGCCCGGTAAGAGCAAAAGAAATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGGA 1680

QY 1681 GATTCTCATAACTTGAGACCTAATCTCTGTAAGCTAAAAATAAGAAATAGAACCAAGGCT 1740

Db 1681 GATTCTCATAACTTGAGACCTAATCTCTGTAAGCTAAAAATAAGAAATAGAACCAAGGCT 1740

QY 1741 GAGGATACGACAGTACACTGTGAGCAGGACTGTAAAAACAGACAGAGGTCAAAAGTGTTTT 1800

Db 1741 GAGGATACGACAGTACACTGTGAGCAGGACTGTAAAAACAGACAGAGGTCAAAAGTGTTTT 1800

QY 1801 CTCTGAACACATTGAGTTGGAATCACTGTTAGAAACACACACACTTACTTTTCTGGTCT 1860

Db 1801 CTCTGAACACATTGAGTTGGAATCACTGTTAGAAACACACACACTTACTTTTCTGGTCT 1860

QY 1861 CTACCACCTGCTGATATTTTCTCTAGGAAATATACTTTTACAAGTACAAAAATAAAAACT 1920

Db 1861 CTACCACCTGCTGATATTTTCTCTAGGAAATATACTTTTACAAGTACAAAAATAAAAACT 1920

QY 1921 CTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGT 1980

Db 1921 CTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGT 1980

QY 1981 AATTTGTTAAAAAGTAATAAAATTCAACAAACATTTAAAAAATAAAAAA 2029

Db 1981 AATTTGTTAAAAAGTAATAAAATTCAACAAACATTTAAAAAATAAAAAA 2029

RESULT 2

US-09-833-381-849
; Sequence 849, Application US/098333381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 849
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-849

Query Match 98.8%; Score 2005; DB 4; Length 2404;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2019; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 2 CTTGACAAAGTCAGAA-GCTTGAAAGCAGGGAATCCGGATGTCTCGGTTATGAAGTGGAG 60

Db 8 CTTGACAAAGTCAGAACGCTTGAAAGCAGGGAATCCGGATGTCTCGGTTATGAAGTGGAG 67

QY 61 CAGTGAGTGTGAGCCTCAACATAGTTCAGAACTCTCCATCCGACTAGTTATTGAGCAT 120

Db 68 CAGTGAGTGTGAGCCTCAACATAGTTCAGAACTCTCCATCCGACTAGTTATTGAGCAT 127

QY	121	CTGCTCTCATATCACCACTGGCCATCTGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCA	180
Db	128	CTGCTCTCATATCACCACTGGCCATCTGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCA	187
QY	181	CGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCC	240
Db	188	CGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCC	247
QY	241	TGGTCCAAAGGCTCTTTGCGTGCAGAAAGACTTTCCATCCAGGTGTATGCAGAAATTATGG	300
Db	248	TGGTCCAAAGGCTCTTTGCGTGCAGAAAGACTTTCCATCCAGGTGTATGCAGAAATTATGG	307
QY	301	GGATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGNAATTTACAGAAAGCTAAGGAGG	360
Db	308	GGATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGNAATTTACAGAAAGCTAAGGAGG	367
QY	361	CCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAG	420
Db	368	CCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAG	427
QY	421	CTAGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGGATTCGTGGTCATCTTAGGA	480
Db	428	CTAGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGGATTCGTGGTCATCTTAGGA	487
QY	481	TTAGCCCAAAACCCCAAGTGTGGGAAAAAATGGGGTGGTGCTGATTTGGAAGGTTCCAG	540
Db	488	TTAGCCCAAAACCCCAAGTGTGGGAAAAAATGGGGTGGTGCTGATTTGGAAGGTTCCAG	547
QY	541	TGAGCCGACAGTTTGAGCCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCA	600
Db	548	TGAGCCGACAGTTTGAGCCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCA	607
QY	601	TTCCAGAAATTATCACCCACCAAGATCCCATATTTCAACACTCATCTGATACTTGGACTA	660
Db	608	TTCCAGAAATTATCACCCACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACA	667
QY	661	CAGAAATTTATTGTCACTGACAGTACCTACTCGGTGGATCCCTTACTCTACAAATACCTG	720
Db	668	CAGAAATTTATTGTCACTGACAGTACCTACTCGGTGGATCCCTTACTCTACAAATACCTG	727
QY	721	CCCCTACTACTCTCCTCGCTCCAGCTTCCACTTCTPATTCACGGAGAAAAAATTGA	780
Db	728	CCCCTACTACTCTCCTCGCTCCAGCTTCCACTTCTPATTCACGGAGAAAAAATTGA	787
QY	781	TTTGTGTACAGAAAGTTTTTATGGAAACTAGCACCACTGTCTACAGAACTGAACCATTTG	840
Db	788	TTTGTGTACAGAAAGTTTTTATGGAAACTAGCACCACTGTCTACAGAACTGAACCATTTG	847
QY	841	TTGAAAAATAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTC	900
Db	848	TTGAAAAATAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTC	907
QY	901	TGCTAGTGCTTGCTCTCTCTTCTTTGGTGTGCAGCTGGTCTTGGATTTTGTATGTCA	960
Db	908	TGCTAGTGCTTGCTCTCTCTTCTTTGGTGTGCAGCTGGTCTTGGATTTTGTATGTCA	967
QY	961	AAAGGTATGTGAAGGCCTTCCCTTTTACAACAAGAAATCAGCAGAAGGAAATGATCGAAA	1020
Db	968	AAAGGTATGTGAAGGCCTTCCCTTTTACAACAAGAAATCAGCAGAAGGAAATGATCGAAA	1027
QY	1021	CCAAAGTAGTAAAGGAGGAGGCAATGATAGCAACCCCTAATGAGGAATCAAAAGAAAA	1080
Db	1028	CCAAAGTAGTAAAGGAGGAGGCAATGATAGCAACCCCTAATGAGGAATCAAAAGAAAA	1087
QY	1081	CTGATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTCCGATCCCTGGAAG	1140
Db	1088	CTGATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTCCGATCCCTGGAAG	1147
QY	1141	CTGAAGTTTAGATGAGACAGAAATGAGGAGACACACTGAGGCTGGTTCTTTTCATGCTC	1200
Db	1148	CTGAAGTTTAGATGAGACAGAAATGAGGAGACACACTGAGGCTGGTTCTTTTCATGCTC	1207

QY	1201	CTTACCCTGCCCCAGCTGGGAAATCAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACC	1260
Db	1208	CTTACCCTGCCCCAGCTGGGAAATCAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACC	1267
QY	1261	CTTGGTTCCTAACTGGAATCAGCTCAGGACTGCCATTTGGACTATGGAGTGCACCAAGAG	1320
Db	1268	CTTGGTTCCTAACTGGAATCAGCTCAGGACTGCCATTTGGACTATGGAGTGCACCAAGAG	1327
QY	1321	AATGCCCTTCTCCTTATTGTAAACCCTGTCTGGATCCTATCCTACCTCCAAAGCTTCC	1380
Db	1328	AATGCCCTTCTCCTTATTGTAAACCCTGTCTGGATCCTATCCTACCTCCAAAGCTTCC	1387
QY	1381	CACGGCCTTCTAGCCTGGCTATGTCCCTAATAATATCCCACTGGGAGAAAGGAGTTTGC	1440
Db	1388	CACGGCCTTCTAGCCTGGCTATGTCCCTAATAATATCCCACTGGGAGAAAGGAGTTTGC	1447
QY	1441	AAAGTGCAAGGACCTTAAACATCTCATCAGTATCCAGTGGTAAAGGGCCTCCTGGCTGT	1500
Db	1448	AAAGTGCAAGGACCTTAAACATCTCATCAGTATCCAGTGGTAAAGGGCCTCCTGGCTGT	1507
QY	1501	CTGAGGCTAGTGGGTTGAAAGCCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATT	1560
Db	1508	CTGAGGCTAGTGGGTTGAAAGCCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATT	1567
QY	1561	CCGCAGCTCAGACCCCTTCTTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTC	1620
Db	1568	CCGCAGCTCAGACCCCTTCTTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTC	1627
QY	1621	CTTCTGAGCCCGGTAAAGACAAAAGAAATGGCAGAAAAAGTTTAGCCCCCTGAAAGCCATGGA	1680
Db	1628	CTTCTGAGCCCGGTAAAGACAAAAGAAATGGCAGAAAAAGTTTAGCCCCCTGAAAGCCATGGA	1687
QY	1681	GATTCTCATAACTTTGAGACCTTAATCTCTGTAAAGCTTAAATAAAGAAATAGAACAAAGCT	1740
Db	1688	GATTCTCATAACTTTGAGACCTTAATCTCTGTAAAGCTTAAATAAAGAAATAGAACAAAGCT	1747
QY	1741	GAGGATACGACAGTACACTGTGACGAGGACTGTAAACACAGACAGGGTCAAAGTGTTTT	1800
Db	1748	GAGGATACGACAGTACACTGTGACGAGGACTGTAAACACAGACAGGGTCAAAGTGTTTT	1807
QY	1801	CTCTGAACACATTGAGTTGGAATCACTGTTTGTAGAACACACACTTACTTTTCTGGTCT	1860
Db	1808	CTCTGAACACATTGAGTTGGAATCACTGTTTGTAGAACACACACTTACTTTTCTGGTCT	1867
QY	1861	CTACCACCTGCTGATAFTTTCTTAGGAAATATACTTTTACAAGTAACAAAAATAAAAACT	1920
Db	1868	CTACCACCTGCTGATAFTTTCTTAGGAAATATACTTTTACAAGTAACAAAAATAAAAACT	1927
QY	1921	CTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGT	1980
Db	1928	CTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGT	1987
QY	1981	AATTTGTTTAAAAAGTAATAAAATTCACAAACATTTAAAAAAA 2025	
Db	1988	AATTTGTTTAAAAAGTAATAAAATTCACAAACATTTGCTGAATA 2032	

RESULT 3
US-09-833-381-853
; Sequence 853, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 853
; LENGTH: 2404

; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-09-833-381-853									
Query Match 98.8%; Score 2005; DB 4; Length 2404;									
Best Local Similarity 99.7%; Pred. No. 0;									
Matches 2019; Conservative 0; Mismatches 5; Indels 1; Gaps 1;									
QY	2	CTTGACAA	GT	CAGAA	-GCTTGAAAGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAG	60			
Db	8	CTTGACAA	GT	CAGAA	CGCTTGAAGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAG	67			
QY	61	CAGTGAGT	GTGAGCCT	CAACATAGTTC	CCAGAACTCTCCATCCGGACTAGTATTGAGCAT	120			
Db	68	CAGTGAGT	GTGAGCCT	CAACATAGTTC	CCAGAACTCTCCATCCGGACTAGTATTGAGCAT	127			
QY	121	CTGCCCTC	TCAATAC	CAGTGGCCATCT	GAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCA	180			
Db	128	CTGCCCTC	TCAATAC	CAGTGGCCATCT	GAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCA	187			
QY	181	CGATGGCC	AGGTGCTT	CAGCCTGGTGT	CTTCTCACTTCCATCTGGACCAAGGCTCC	240			
Db	188	CGATGGCC	AGGTGCTT	CAGCCTGGTGT	CTTCTCACTTCCATCTGGACCAAGGCTCC	247			
QY	241	TGGTCCAA	GGCTCTTT	TGCGTGCAGAA	GAGCTTTCCATCCAGGTGTCATGCAGAAATTATGG	300			
Db	248	TGGTCCAA	GGCTCTTT	TGCGTGCAGAA	GAGCTTTCCATCCAGGTGTCATGCAGAAATTATGG	307			
QY	301	GGATCAC	CCCTTGTG	AGCAAAAAGGCGAAC	CAGCAGCTGAATTTACAGAACTAAGGAGG	360			
Db	308	GGATCAC	CCCTTGTG	AGCAAAAAGGCGAAC	CAGCAGCTGAATTTACAGAACTAAGGAGG	367			
QY	361	CCTGTAG	CTGCTGGGACT	TAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAG	420				
Db	368	CCTGTAG	CTGCTGGGACT	TAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAG	427				
QY	421	CTAGCTTT	TGAAACTT	GCAGCTATGGCTGGGTTGGAGATGGATTCGTTGGTCACTCTTAGGA	480				
Db	428	CTAGCTTT	TGAAACTT	GCAGCTATGGCTGGGTTGGAGATGGATTCGTTGGTCACTCTTAGGA	487				
QY	481	TTAGCCCA	AAACCCCAAGTGTGGGAAA	AAATGGGTTGGGTGCTCGTGAATTTGGAAGGTTCCAG	540				
Db	488	TTAGCCCA	AAACCCCAAGTGTGGGAAA	AAATGGGTTGGGTGCTCGTGAATTTGGAAGGTTCCAG	547				
QY	541	TGAGCCGA	CACAGTTTG	CAGCCTATTGTTACAACTCATCTGATACTTTGGAATACTCGTGCA	600				
Db	548	TGAGCCGA	CACAGTTTG	CAGCCTATTGTTACAACTCATCTGATACTTTGGAATACTCGTGCA	607				
QY	601	TTCCAGAA	ATTATAC	ACCACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACAA	660				
Db	608	TTCCAGAA	ATTATAC	ACCACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACAA	667				
QY	661	CAGAAAT	TATGT	CAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTG	720				
Db	668	CAGAAAT	TATGT	CAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTG	727				
QY	721	CCCCTACT	ACTACT	CCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGA	780				
Db	728	CCCCTACT	ACTACT	CCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGA	787				
QY	781	TTTGTGT	CACAGAAGTTTT	TATGGAACTTAGCACCATGTCTACAGAAACTGAACCATTTG	840				
Db	788	TTTGTGT	CACAGAAGTTTT	TATGGAACTTAGCACCATGTCTACAGAAACTGAACCATTTG	847				
QY	841	TTGAAAA	ATAAAGCAGCAT	TTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTC	900				
Db	848	TTGAAAA	ATAAAGCAGCAT	TTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTC	907				
QY	901	TGCTAGT	CTTGCTCT	CTCTCTTTTGGTGTGCAGCTGGTCTTGGATTTTGTCTATGTCA	960				
Db	908	TGCTAGT	CTTGCTCT	CTCTCTTTTGGTGTGCAGCTGGTCTTGGATTTTGTCTATGTCA	967				
QY	961	AAAGGTAT	GTGAAGGCCTT	CCCTTTTACAAACAAGAAATCAGCAGAAAGGAAATGATCGAAA	1020				

Db	968	AAAGGTAT	GTGAAGGCCTT	CCCTTTTACAAACAAGAAATCAGCAGAAAGGAAATGATCGAAA	1027
QY	1021	CCAAAGT	AGTAAAGGAGGAGAA	GGCCCAATGATAGCAACCCTAATGAGGAATCAAAAGAAAA	1080
Db	1028	CCAAAGT	AGTAAAGGAGGAGAA	GGCCCAATGATAGCAACCCTAATGAGGAATCAAAAGAAAA	1087
QY	1081	CTGATAAA	AAACCCAGAA	GAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAAG	1140
Db	1088	CTGATAAA	AAACCCAGAA	GAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAAG	1147
QY	1141	CTGAAGTT	TAGATGAGACAGAA	ATGAGGAGACACACCTGAGGCTGGTTCTTTTCATGCTC	1200
Db	1148	CTGAAGTT	TAGATGAGACAGAA	ATGAGGAGACACACCTGAGGCTGGTTCTTTTCATGCTC	1207
QY	1201	CTTACCC	TGCCCCAGCT	GGGAAATCAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACC	1260
Db	1208	CTTACCC	TGCCCCAGCT	GGGAAATCAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACC	1267
QY	1261	CTTGGTT	CCTAACTAG	GAATCAGCTCAGGACTGCCATTGGACTATGAGTGCACCAAGAG	1320
Db	1268	CTTGGTT	CCTAACTAG	GAATCAGCTCAGGACTGCCATTGGACTATGAGTGCACCAAGAG	1327
QY	1321	AATGCC	CTTCTCCTTAT	TGTAACCTGTCTGGATCCTATCCTCCTACCTCAAAAGCTTCC	1380
Db	1328	AATGCC	CTTCTCCTTAT	TGTAACCTGTCTGGATCCTATCCTCCTACCTCAAAAGCTTCC	1387
QY	1381	CACGGC	CTTTCTAG	CCTGGCTATGTCTTAATAATATCCCACCTGGGAGAAAGAGTTTTC	1440
Db	1388	CACGGC	CTTTCTAG	CCTGGCTATGTCTTAATAATATCCCACCTGGGAGAAAGAGTTTTC	1447
QY	1441	AAAGT	GCAGGACCT	AAAAACATCTCATCAGTATCCAGTGGTAAAAAGCCTCCTGGCTGT	1500
Db	1448	AAAGT	GCAGGACCT	AAAAACATCTCATCAGTATCCAGTGGTAAAAAGCCTCCTGGCTGT	1507
QY	1501	CTGAGG	CTTAGGTGG	TTGAAAGCCAGGAGTCACTGAGACCAAGGCTTCTCTACTGATT	1560
Db	1508	CTGAGG	CTTAGGTGG	TTGAAAGCCAGGAGTCACTGAGACCAAGGCTTCTCTACTGATT	1567
QY	1561	CCGAG	CTCAGAC	CCCTTTCTTCTAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTC	1620
Db	1568	CCGAG	CTCAGAC	CCCTTTCTTCTAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTC	1627
QY	1621	CTTCTG	AGCCCGTAA	GAGCAAAAGAAATGGCAGAAAAAGTTTAGCCCTGAAAGCCCATGGA	1680
Db	1628	CTTCTG	AGCCCGTAA	GAGCAAAAGAAATGGCAGAAAAAGTTTAGCCCTGAAAGCCCATGGA	1687
QY	1681	GATTCT	CATAAACT	TGAGACCTAATCTCTGTAAAAGCTAAAAATAAGAAATAGAACAAAGCT	1740
Db	1688	GATTCT	CATAAACT	TGAGACCTAATCTCTGTAAAAGCTAAAAATAAGAAATAGAACAAAGCT	1747
QY	1741	GAGGAT	ACGACAGT	ACACTGTGCAGCAGGACTGTAAACACACAGACAGGCTCAAAAGTGT	1800
Db	1748	GAGGAT	ACGACAGT	ACACTGTGCAGCAGGACTGTAAACACACAGACAGGCTCAAAAGTGT	1807
QY	1801	CTCTGA	ACACAT	TGAGTTGGAATCACTGTTTAGAACACACACACTTTTCTTCTGGTCT	1860
Db	1808	CTCTGA	ACACAT	TGAGTTGGAATCACTGTTTAGAACACACACACTTTTCTTCTGGTCT	1867
QY	1861	CTACCA	CTGCTGAT	ATTTTCTCTAGGAAATATATCTTTTACAGTAACAAAAATAAAAACT	1920
Db	1868	CTACCA	CTGCTGAT	ATTTTCTCTAGGAAATATATCTTTTACAGTAACAAAAATAAAAACT	1927
QY	1921	CTTATA	AAATTTCT	ATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGT	1980
Db	1928	CTTATA	AAATTTCT	ATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGT	1987
QY	1981	AAATTT	GTTTAAAAA	AGTAATAAAATTCAAACAAACATTTAAAAAAA	2025
Db	1988	AAATTT	GTTTAAAAA	AGTAATAAAATTCAAACAAACATTTTGTGAATA	2032

US-09-907-794A-200
; Sequence 200, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
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; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
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; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-907-794A-200
Query Match 98.3%; Score 1994; DB 4; Length 2372;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 24 AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 83
Db 1 AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60
Qy 84 GTTCCAGAACTCTCCATCCGACTAGTTATTAGCATCTGCCTCTCATATCACCACTGGC 143
Db 61 GTTCCAGAACTCTCCATCCGACTAGTTATTAGCATCTGCCTCTCATATCACCACTGGC 120
Qy 144 CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 203
Db 121 CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180
Qy 204 GTGTTGCTTCTCACTTCCATCTGGACCAAGGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 263
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Db 241 GAAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAG 300
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Qy 504 AAAAATGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCTAT 563
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Db 541 TGTTACAACTCATCTGATACTTGGACTAATCGTGCACTCTCTAGGATTAGCCCAACCCCAAG 600
Qy 624 GATCCCATATTTCAACACTCAAACTGCAACACACAAACAGAAATTTATTGTGAGTGACGT 683
Db 601 GATCCCATATTTCAACACTCAAACTGCAACACACAAACAGAAATTTATTGTGAGTGACGT 660
Qy 684 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCCCTACTACTACTCCTCCTGCT 743
Db 661 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCCCTACTACTACTCCTCCTGCT 720
Qy 744 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTGTGTACAGAAAGTTTATTG 803
Db 721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTGTGTACAGAAAGTTTATTG 780
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Db 781 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAGCAGCATTCAG 840
Qy 864 AATGAAGCTGCTGGGTTGGAGGTGTCCCCACGGCTCTGCTAGTGTGCTCCTCCTTC 923
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Qy 924 TTTGGTGTGCAGCTGGTCTTGGATTTTGTATGTCAAAAGGTATGTGAAGGCTTCCCT 983
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1081 AAGAGTCCAAAGCAAAAACCTACCGTGCATGCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1140
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1141 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCCCTGCCCAGCTGGGAA 1200
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1201 ATCAAAAGGGCCAAAGAACCAAAAGAGAAAGTCCACCCCTTGGTTCCTAACTGGAATCAGC 1260
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QY 1404 GTCTTAATAATATCCCACTGGGAGAGAAAGGAGTTTGCAAAAGTGCAGGACCTAAAAACATC 1463
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1381 GTCTTAATAATATCCCACTGGGAGAGAAAGGAGTTTGCAAAAGTGCAGGACCTAAAAACATC 1440
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QY 1524 CAAGGAGTCACTGAGACCAAGGCTTTCTACTGATTTCCGCAGCTCAGACCCCTTTCTTCA 1583
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1501 CAAGGAGTCACTGAGACCAAGGCTTTCTACTGATTTCCGCAGCTCAGACCCCTTTCTTCA 1560
QY 1584 GCTCTGAAAGAGAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCCGGTAAGAGCAAA 1643
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1561 GCTCTGAAAGAGAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCCGGTAAGAGCAAA 1620
QY 1644 AGAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1703
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY 1704 TCTCTGTAAGCTAAAAATAAAGAAATAGAAACAAGGCTGAGGATACGAGTACACTGTCA 1763
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1681 TCTCTGTAAGCTAAAAATAAAGAAATAGAAACAAGGCTGAGGATACGAGTACACTGTCA 1740
QY 1764 GCAGGACTGTAAACACAGACAGGGTCAAAAGTGTTTTCTCTGAACACATGTGAGTTGGAAT 1823
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1741 GCAGGACTGTAAACACAGACAGGGTCAAAAGTGTTTTCTCTGAACACATGTGAGTTGGAAT 1800
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1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1860
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1861 AGGAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1920
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Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY 2004 TTCAACAAACATTTAAAAAAA 2025
Db |||||||||||||||||||||||||
1981 TTCAACAAACATTTGCTGAATA 2002

RESULT 5
US-09-905-125A-200
; Sequence 200, Application US/09905125A

; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
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; PRIOR APPLICATION NUMBER: PCT/US99/20594
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; PRIOR FILING DATE: 1999-12-02
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; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-905-125A-200

Query Match									
Best Local Similarity 98.3%; Score 1994; DB 4; Length 2372;									
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;									
QY	24	AGCAGGAAATCCGGATGTC	CGGTTATGAAGTGGAGCAGT	GAGTGTGAGCCTCAACATA	83				
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QY	324	GCGAACCCAGCAGCTGA	ATTTCACAGAAAGCTA	AGGAGCCTGTAGGCTG	383				
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QY	504	AAAAATGGGGTGGGTG	CTCCTGATTTGGAAGG	TTCCAGTGAGCCGACAG	563				
Db	481	AAAAATGGGGTGGGTG	CTCCTGATTTGGAAGG	TTCCAGTGAGCCGACAG	540				
QY	564	TGTTACAACTCATCTG	ACTTGGACTAACTCGT	GCATTCAGAAATTATC	623				
Db	541	TGTTACAACTCATCTG	ACTTGGACTAACTCGT	GCATTCAGAAATTATC	600				
QY	624	GATCCCATATTTCAAC	ACTCAAACTGCAACACA	CAAAACAGAAATTTAT	683				
Db	601	GATCCCATATTTCAAC	ACTCAAACTGCAACACA	CAAAACAGAAATTTAT	660				
QY	684	ACCTACTCGTGGCATC	CCCTTACTCTACAATA	CTGCCCCCTACTACT	743				
Db	661	ACCTACTCGTGGCATC	CCCTTACTCTACAATA	CTGCCCCCTACTACT	720				
QY	744	CCAGCTTCCACTTCTA	TTCCACGGAGAAAAA	ATTGATTTGTGCACAGA	803				
Db	721	CCAGCTTCCACTTCTA	TTCCACGGAGAAAAA	ATTGATTTGTGCACAGA	780				
QY	804	GAAACTAGCACCATG	TCACAGAACTGAACCA	TTTGTGAAAAATAAAG	863				
Db	781	GAAACTAGCACCATG	TCACAGAACTGAACCA	TTTGTGAAAAATAAAG	840				
QY	864	AATGAAGCTGCTGGG	TTGGAGGTGTCCCC	ACGGCTCTGCTAGTGC	923				
Db	841	AATGAAGCTGCTGGG	TTGGAGGTGTCCCC	ACGGCTCTGCTAGTGC	900				
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Db	961	TTTACAAAACAAGAA	TACAGCAAGGAAATG	ATCGAAACCAAAAGT	1020				
QY	1044	GCCAATGATAGCAAC	CCCTAATGAGGAAT	CAAAGAAAACTGATA	1103				

Db	1021	 GCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACTGATAAAAACCCAGAAGAGTCC	1080
QY	1104	 AAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCTGAAAGTTTAGATGAGACAGAAA	1163
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QY	1164	 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCCTGCCCCAGCTGGGAA	1223
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QY	1284	 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC	1343
Db	1261	 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC	1320
QY	1344	 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCTTTCTAGCCTGGCTAT	1403
Db	1321	 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCTTTCTAGCCTGGCTAT	1380
QY	1404	 GTCCTAAATAATATCCCACTGGGAGAAAGAGATTTTGCAAGTGCAAGGACCTTAAACATC	1463
Db	1381	 GTCCTAAATAATATCCCACTGGGAGAAAGAGATTTTGCAAGTGCAAGGACCTTAAACATC	1440
QY	1464	 TCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGGTTGAAAAGC	1523
Db	1441	 TCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGGTTGAAAAGC	1500
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Db	1621	 AGAATGGCAGAAAAAGTTTAGCCCTGAAAAGCCATGGAGATTCTCATAACTTGAGACCTAA	1680
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QY	1824	 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCCTGCTGATATTTCTCT	1883
Db	1801	 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCCTGCTGATATTTCTCT	1860
QY	1884	 AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT	1943
Db	1861	 AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT	1920
QY	1944	 GAGTTACAGAAATGATTACTTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA	2003
Db	1921	 GAGTTACAGAAATGATTACTTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA	1980
QY	2004	 TTCAACAAACATTTTAAAAAAA 2025	
Db	1981	 TTCAACAAACATTTTGTGAATA 2002	

RESULT 6
US-09-902-775A-200
; Sequence 200, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-775A-200
Query Match 98.3%; Score 1994; DB 4; Length 2372;
Best Local Similarity 99.8%; Pred. No. 0;

		Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;			
QY	24	AGCAGGGAATCCGGATGTCTCGGTATGAAGTGGAGCAGTGAGTGGCCCTCAACATA	83		
Db	1	AGCAGGGAATCCGGATGTCTCGGTATGAAGTGGAGCAGTGAGTGGCCCTCAACATA	60		
QY	84	GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC	143		
Db	61	GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC	120		
QY	144	CATCTGAGTGTTCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG	203		
Db	121	CATCTGAGTGTTCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG	180		
QY	204	GTGTTGCTTCTCACTTCATCTGGACACGAGGCTCCTGGTCCAAAGCTCTTTCGCTGCA	263		
Db	181	GTGTTGCTTCTCACTTCATCTGGACACGAGGCTCCTGGTCCAAAGCTCTTTCGCTGCA	240		
QY	264	GAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGGATCACCTTGTGAGCAAAAAG	323		
Db	241	GAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGGATCACCTTGTGAGCAAAAAG	300		
QY	324	GCGAACCCAGCAGCTGAATTTTCACAGAAGCTAAGGAGGCCTGTAGGTGCTGGGACTAAGT	383		
Db	301	GCGAACCCAGCAGCTGAATTTTCACAGAAGCTAAGGAGGCCTGTAGGTGCTGGGACTAAGT	360		
QY	384	TTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT	443		
Db	361	TTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT	420		
QY	444	GGCTGGGTGGAGATGGATTTCGTGTCATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGG	503		
Db	421	GGCTGGGTGGAGATGGATTTCGTGTCATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGG	480		
QY	504	AAAAATGGGGTGGGTGCTCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT	563		
Db	481	AAAAATGGGGTGGGTGCTCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT	540		
QY	564	TGTTACAACCTCATCTGATCTTGGACTAACTCGTGCAATTCAGAAATATCACCACCAA	623		
Db	541	TGTTACAACCTCATCTGATCTTGGACTAACTCGTGCAATTCAGAAATATCACCACCAA	600		
QY	624	GATCCCATATTCAACACTCAAACTGCAACACAAACACAGAATTTATTGTCAGTGACAGT	683		
Db	601	GATCCCATATTCAACACTCAAACTGCAACACAAACACAGAATTTATTGTCAGTGACAGT	660		
QY	684	ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTTACTACTCTCCTCTGCT	743		
Db	661	ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTTACTACTCTCCTCTGCT	720		
QY	744	CCAGTTCCTCACTTCTATTCCACGGAGAAAAAATTTGATTGTGTACAGAAATTTTATG	803		
Db	721	CCAGTTCCTCACTTCTATTCCACGGAGAAAAAATTTGATTGTGTACAGAAATTTTATG	780		
QY	804	GAACTAGCACCATGTCTACAGAACTGAACCATTTGTTGAAAAATAAAGCAGCATTCAAG	863		
Db	781	GAACTAGCACCATGTCTACAGAACTGAACCATTTGTTGAAAAATAAAGCAGCATTCAAG	840		
QY	864	AATGAAGCTGTGGTTTGGAGGTGTCCCACGGCTCTGTAGTGTCTCTCTCTTTC	923		
Db	841	AATGAAGCTGTGGTTTGGAGGTGTCCCACGGCTCTGTAGTGTCTCTCTCTTTC	900		
QY	924	TTTGGTGTGCAGCTGGTCTTTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCTTCCCT	983		
Db	901	TTTGGTGTGCAGCTGGTCTTTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCTTCCCT	960		
QY	984	TTTCAAAACAAGAAATCAGCAGAGGAAATGATCGAAACCAAAGTAGTAAGGAGGAGAAG	1043		
Db	961	TTTCAAAACAAGAAATCAGCAGAGGAAATGATCGAAACCAAAGTAGTAAGGAGGAGAAG	1020		
QY	1044	GCCATGATAGCAACCTTAATGAGGAATCAAAGAAAACTGTATAAAACCCAGAGAGTCC	1103		
Db	1021	GCCATGATAGCAACCTTAATGAGGAATCAAAGAAAACTGTATAAAACCCAGAGAGTCC	1080		

QY 1104 AAGAGTCCAAAGCAAACTACCGTGCATGCCTGGAAGCTGAAGTTAGATGAGACAGAAA 1163
Db |||||||
QY 1081 AAGAGTCCAAAGCAAACTACCGTGCATGCCTGGAAGCTGAAGTTAGATGAGACAGAAA 1140
Db |||||||
QY 1164 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCCTGCCCCAGCTGGGAA 1223
Db |||||||
QY 1141 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCCTGCCCCAGCTGGGAA 1200
QY 1224 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCTTGGTTCTCTAACTGGAATCAGC 1283
Db |||||||
QY 1201 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCTTGGTTCTCTAACTGGAATCAGC 1260
QY 1284 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1343
Db |||||||
QY 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1320
QY 1344 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCTTCTAGCCTGGCTAT 1403
Db |||||||
QY 1321 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCTTCTAGCCTGGCTAT 1380
QY 1404 GTCCTAAATAATATCCCACTGGGAGAAAGGAGTTTGTCAAAGTGCAGGACCTAAACATC 1463
Db |||||||
QY 1381 GTCCTAAATAATATCCCACTGGGAGAAAGGAGTTTGTCAAAGTGCAGGACCTAAACATC 1440
QY 1464 TCATCAGTATCCAGTGGTAAAGGCTCCTGGCTGCTCAGGCTAGGTGGTTGAAAGC 1523
Db |||||||
QY 1441 TCATCAGTATCCAGTGGTAAAGGCTCCTGGCTGCTCAGGCTAGGTGGTTGAAAGC 1500
QY 1524 CAAGGAGTCACTGAGACCAAGGCTTCTACTGATTCGGAGCTCAGACCCCTTCTTCA 1583
Db |||||||
QY 1501 CAAGGAGTCACTGAGACCAAGGCTTCTACTGATTCGGAGCTCAGACCCCTTCTTCA 1560
QY 1584 GCTCTGAAAGAGAAACACGATCCACCTGCATGTCTCTGAGCCCGTAAAGCAAA 1643
Db |||||||
QY 1561 GCTCTGAAAGAGAAACACGATCCCACTGCATGTCTCTGAGCCCGTAAAGCAAA 1620
QY 1644 AGAATGGCAGAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1703
Db |||||||
QY 1621 AGAATGGCAGAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680
QY 1704 TCTCTGTAAAGCTAAATAAAGAAATAGAACAGGCTGAGGATACGACGTACACTGTCA 1763
Db |||||||
QY 1681 TCTCTGTAAAGCTAAATAAAGAAATAGAACAGGCTGAGGATACGACGTACACTGTCA 1740
QY 1764 GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTCTCTGAACACATTTGAGTTGGAAT 1823
Db |||||||
QY 1741 GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTCTCTGAACACATTTGAGTTGGAAT 1800
QY 1824 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACCTGCTGATATTTCTCT 1883
Db |||||||
QY 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACCTGCTGATATTTCTCT 1860
QY 1884 AGGAAATATACTTTACAGTAACAAATAAAACCTCTTATAAATTTCTATTTTATCT 1943
Db |||||||
QY 1861 AGGAAATATACTTTACAGTAACAAATAAAACCTCTTATAAATTTCTATTTTATCT 1920
QY 1944 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAGTAATAAAA 2003
Db |||||||
QY 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAGTAATAAAA 1980
QY 2004 TTCAACAAACATTTTAAACAAAA 2025
Db |||||||
QY 1981 TTCAACAAACATTTTGTGTAATA 2002

RESULT 7

US-08-892-880-1
; Sequence 1, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.

; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2313 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..1056
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 154..1056
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 91..153
; US-08-892-880-1

Query Match 94.4%; Score 1915.2; DB 2; Length 2313;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1920; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 98 CATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGTGTTT 157
Db |||||||
QY 158 CCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCAC 217
Db |||||||
QY 66 CCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCAC 125
QY 218 TTCCATCTGGACCAAGGCTCCTGGTCCAGGCTCTTTGCGTGCAGAAAGAGCTTTCCAT 277
Db |||||||
QY 126 TTCCATCTGGACCAAGGCTCCTGGTCCAGGCTCTTTGCGTGCAGAAAGAGCTTTCCAT 185
QY 278 CCAGGTGTCTATGCAGAAATTATGGGGATCACCTTGTGAGCAAAAAGCGAACCCAGCAGCT 337
Db |||||||
QY 186 CCAGGTGTCTATGCAGAAATTATGGGGATCACCTTGTGAGCAAAAAGCGAACCCAGCAGCT 245
QY 338 GAATTTCACAGAGCTAAGGAGGCTGTAGGCTGTGGACTAAGTTTGGCCGGAAGGA 397
Db |||||||
QY 246 GAATTTCACAGAGCTAAGGAGGCTGTAGGCTGTGGACTAAGTTTGGCCGGAAGGA 305
QY 398 CCAAGTTGAAACAGCCTTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGA 457
Db |||||||

Db 306 CCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGCAACTTGCAGCTATGGCTGGGTGGCGA 365

Qy 458 TGGATTCTGGTTCATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGGAAAAAATGGGGTGGG 517

Db 366 TGGATTCTGGTTCATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGGAAAAAATGGGGTGGG 425

Qy 518 TGTCCTGATTGGAAAGGTTCCAGTGAGCGGACAGTTTGCAGCCTATGTGTTACAACTCATC 577

Db 426 TGTCCTGATTGGAAAGGTTCCAGTGAGCGGACAGTTTGCAGCCTATGTGTTACAACTCATC 485

Qy 578 TGATACTTGGACTAACTCGTGCAATCCAGAAATATCACCAACCAAGATCCCATATTCAA 637

Db 486 TGATACTTGGACTAACTCGTGCAATCCAGAAATATCACCAACCAAGATCCCATATTCAA 545

Qy 638 CACTCAAACTGCAACACAAACAAACAGAAATTTATGTGAGTGACAGTACTCGGTGGC 697

Db 546 CACTCAAACTGCAACACAAACAAACAGAAATTTATGTGAGTGACAGTACTCGGTGGC 605

Qy 698 ATCCCCCTTACTTACAAATACCTGCCCTTACTACTCTCCTCTGCTCCAGCTTCCACTTC 757

Db 606 ATCCCCCTTACTTACAAATACCTGCCCTTACTACTCTCCTCTGCTCCAGCTTCCACTTC 665

Qy 758 TATTCCACGGAGAAAAAATTGATTGTGTACAGAAAGTTTTTATGGAACACTAGCACCAT 817

Db 666 TATTCCACGGAGAAAAAATTGATTGTGTACAGAAAGTTTTTATGGAACACTAGCACCAT 725

Qy 818 GTCTACAGAACTGAACCACTTTGTTGAAATAAAGCAGCATTCAGAAATGAAGCTGCTGG 877

Db 726 GTCTACAGAACTGAACCACTTTGTTGAAATAAAGCAGCATTCAGAAATGAAGCTGCTGG 785

Qy 878 GTTTGGAGGTGTCCTCCACGGCTCTGCTAGTGCTTGCTCTCCTCTCTTTGGTGTGCAGC 937

Db 786 GTTTGGAGGTGTCCTCCACGGCTCTGCTAGTGCTTGCTCTCCTCTCTTTGGTGTGCAGC 845

Qy 938 TGGTCTTGATTGTTGCTATGTCAAAGGATGTGAAGGCCTTCCCTTTTACAAACAAGAA 997

Db 846 TGGTCTTGATTGTTGCTATGTCAAAGGATGTGAAGGCCTTCCCTTTTACAAACAAGAA 905

Qy 998 TCAGCAGAAGGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAA 1057

Db 906 TCAGCAGAAGGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAA 965

Qy 1058 CCCTAATGAGGAATCAAAGAAACTGTATAAAACCCAGAAAGTCCAAGAGTCCAAGCAA 1117

Db 966 CCCTAATGAGGAATCAAAGAAACTGTATAAAACCCAGAAAGTCCAAGAGTCCAAGCAA 1025

Qy 1118 AACTACCGTGCATGCTGGAAGCTGGAAGTGAAGTTAGATGAGACAGAAATGAGGAGACACAC 1177

Db 1026 AACTACCGTGCATGCTGGAAGCTGGAAGTGAAGTTAGATGAGACAGAAATGAGGAGACACAC 1085

Qy 1178 TGAGGCTGTTTCTTTTCATGCTCCTTACCCTGCCCCAGCTGGGAAATCAAAAGGGCCAA 1237

Db 1086 TGAGGCTGTTTCTTTTCATGCTCCTTACCCTGCCCCAGCTGGGAAATCAAAAGGGCCAA 1145

Qy 1238 AGAACCAAGAGAAAGTCCACCTTGTTCTCTAACTGGAATCAGCTCAGGACTGCCATT 1297

Db 1146 AGAACCAAGAGAAAGTCCACCTTGTTCTCTAACTGGAATCAGCTCAGGACTGCCATT 1205

Qy 1298 GGACTATGGAGTGCAACCAAGAGAAATGCCCTTCTCCTTATTGTAACCCCTGTGGATCCT 1357

Db 1206 GGACTATGGAGTGCAACCAAGAGAAATGCCCTTCTCCTTATTGTAACCCCTGTGGATCCT 1265

Qy 1358 ATCCTCCTACCTCCAAAGCTTCCCACGGCCTTTCTAGCCTGGCTATGTCTCTAATAATATC 1417

Db 1266 ATCCTCCTACCTCCAAAGCTTCCCACGGCCTTTCTAGCCTGGCTATGTCTCTAATAATATC 1325

Qy 1418 CCACTGGGAGAAAGGAGTTTGTCAAAGTGCAAGGACCTAAACATCTCATCAGTATCCAG 1477

Db 1326 CCACTGGGAGAAAGGAGTTTGTCAAAGTGCAAGGACCTAAACATCTCATCAGTATCCAG 1385

Qy 1478 TGGTAAAAAGGCCTCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGCCAAAGGAGTCACTGA 1537

Db 1386 TGGTAAAAAGGCCTCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGCCAAAGGAGTCACTGA 1445

Qy 1538 GACCAAGGCTTTCTCTACTGATTCCGAGCTCAGACCCCTTTCTTCAGCTCTGAAAGAGAA 1597

Db 1446 GACCAAGGCTTTCTCTACTGATTCCGAGCTCAGACCCCTTTCTTCAGCTCTGAAAGAGAA 1505

Qy 1598 ACACGTATCCCACCTGACATGTCTTCTGAGCCCGGTAAAGAGCAAAAGAAATGGCAGAAA 1657

Db 1506 ACACGTATCCCACCTGACATGTCTTCTGAGCCCGGTAAAGAGCAAAAGAAATGGCAGAAA 1565

Qy 1658 GTTTAGCCCTGAAAGCCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAGCTA 1717

Db 1566 GTTTAGCCCTGAAAGCCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAGCTA 1625

Qy 1718 AAATAAGAAATAGAAACAAGGCTGAGATACGACAGTACACTGTGAGAGGGACTGTAAA 1777

Db 1626 AAATAAGAAATAGAAACAAGGCTGAGATACGACAGTACACTGTGAGAGGGACTGTAAA 1685

Qy 1778 CACAGACAGGTCAAAAGTGTCTTCTGAAACACATTGAGTTGGAACTACTGTTTAGAACA 1837

Db 1686 CACAGACAGGTCAAAAGTGTCTTCTGAAACACATTGAGTTGGAACTACTGTTTAGAACA 1745

Qy 1838 CACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTAGGAAATATACTTT 1897

Db 1746 CACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTAGGAAATATACTTT 1805

Qy 1898 TACAAGTAAACAAAAATAAAACCTTATAAAAAATTTCTATTTTATCTGAGTTACAGAAATG 1957

Db 1806 TACAAGTAAACAAAAATAAAACCTTATAAAAAATTTCTATTTTATCTGAGTTACAGAAATG 1865

Qy 1958 ATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCACAAACATTT 2017

Db 1866 ATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCACAAACATTT 1925

Qy 2018 AAAAAAA 2025

Db 1926 GCTGAATA 1933

RESULT 8

US-09-724-864-28

; Sequence 28, Application US/09724864

; Patent No. 6380362

; GENERAL INFORMATION:

; APPLICANT: Watson, James D

; APPLICANT: Murison, James G.

; TITLE OF INVENTION: Polynucleotides, polypeptides expressed

; TITLE OF INVENTION: by the polynucleotides and methods for their use.

; FILE REFERENCE: 11000.1050U1

; CURRENT APPLICATION NUMBER: US/09/724,864

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678

; PRIOR FILING DATE: 1999-12-23

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 28

; LENGTH: 1896

; TYPE: DNA

; ORGANISM: Mouse

US-09-724-864-28

Query Match 29.7%; Score 603.6; DB 4; Length 1896;

Best Local Similarity 76.2%; Pred. No. 2.8e-167;

Matches 786; Conservative 0; Mismatches 234; Indels 12; Gaps 3;

Qy 163 GCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCA 222

Db 42 GCCCCGGAGGGATCTGCACAATGCTCCAGCACACTAGCCTGGTGTACTCTCGCCTCTA 101

Qy 223 TCTGGACCACGAGGCTCCTGGTCCAAGGCTTTTCCGTGCAGAAGAGCTTTCCATCCAGG 282

Db 102 TTTGGACCACCTAGGCACCCAGTCCAAGGTGCCACCTCGTGAAGACCTTTCCAT--TT 158

Qy 283 TGTCATGCAGAATTATGGGGATCACCCCTTGTAGCAAAAAGGCGAACCCAGCAGCTGAATT 342

Db	159	CTACATGCAGAAATCATGGCGTGTGCCCTTGTGGGCAGAAA	CAAAAACCCACAGATGAATT	218
QY	343	TCACAGAACTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGACCAAG	402	
Db	219	TCACAGAAGCCAACGAGGCCTGTAAGATGCTGGGACTGACTCTGGCCAGCAGGACCAGG	278	
QY	403	TTGAAACAGCCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGAT	462	
Db	279	TAGAGTCAGCGCAGAAATCTGGCTTTGAGACTTGCAGCTATGGATGGTGGAGAACAGT	338	
QY	463	TCGTGCTCATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCC	522	
Db	339	TCCTGTTCATCCCTCGGATTTTCTCAAACCCCAAGTGTGGGAAAGATGGCAAAGTGTCC	398	
QY	523	TGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATA	582	
Db	399	TGATTTGGAATGCTCCCTCCAGCCAAAAAGTTCAAAGCCTATTGCCAACAACTCATCCGACA	458	
QY	583	CTTGGACTAACTCGTGCAATCCAGAAATTATCACCACCAAGATCCCATATTCAACACTC	642	
Db	459	CCTGGGTTAACTCCTGCAATCCAGAAATCGTTACCACATTTTACCCCGTGTGGACACTC	518	
QY	643	AAACTGCAACACAAAACAACAGAAATTATTGTCAAGTACAGTACCTACTCTCGTGGCATCCC	702	
Db	519	A-----AACACCCGCAACAGAGTTTCTGTGACGACGAGCGGCTACCTTGGCTTCATCCC	572	
QY	703	CTTACTCTACAATACTGCCCCCTACTACTACTCTCCTGCTCAGCTTCCACTTCTATTCT	762	
Db	573	CTGACTCCACAACACCTG---TTTCTGCCACCAACCCGGGCTCCACCTTTGACCTCCATGG	629	
QY	763	CACGGAGAAAAAAATTGATTTGTGTACAGAAAGTTTATGGAAACTAGCACCATGTCTA	822	
Db	630	CACGGAAGACAAAAAAGATTGTATCACGGAAGTTTATACAGAACCTATCACCATGGCTA	689	
QY	823	CAGAAACTGAACCATTTGTGTAATAAAGCAGCATTCAGAATGAAGCTGTGGGTTTG	882	
Db	690	CAGAAACAGAAGCATTTGTGCAAGTGAGCAGCATTCAGAAACGAAAGCAGCTGGGTTTG	749	
QY	883	GAGGTGTCCCCACGGCTCTGCTAGTGTCTGCTCTCCTCTTCTTTGGTGTGCAGCTGGTC	942	
Db	750	GAGGTGTCCCCACCGCCCTGCTGGTGTCTGCTCTCCTCTTCTTTGGTGTGCCGCTGTC	809	
QY	943	TTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGATCAGC	1002	
Db	810	TGGCTGTTTGCTACGTGAAGAAGGTATGTGAAGGCCTTCCCTTTCACAAACCAAGATCAAC	869	
QY	1003	AGAAGGAAATGATCGAAACCAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCTA	1062	
Db	870	AGAAGGAAATGATCGAAACCAAGTTGTAAGGAAGAGAGGCTGATGACGTCAACGCTA	929	
QY	1063	ATGAGGAATCAAAGAAAACTGATAAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAACTA	1122	
Db	930	ATGAAGAATCAAAGAAAAACCATTAATAAACCCAGAGGAGGCAAGAGTCCAACCAAACTA	989	
QY	1123	CCGTGCGATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGG	1182	
Db	990	CGGTGCGATGCTTAGAAGCTGAAGTTTAGATGCAAGAGAGTGGAGAAGGTGCACACGAGG	1049	
QY	1183	CTGGTTTCTTTC	1194	
Db	1050	CAAGTTTTCATGC	1061	

RESULT 9
US-08-892-880-11/c
; Sequence 11, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN

```

; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HERewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

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Query Match 16.5%; Score 334; DB 2; Length 339;
Best Local Similarity 98.5%; Pred. No. 2.3e-88;
Matches 334; Conservative 0; Mismatches 5; Indels

QY	1489	CCTCCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTT	1548
Db	339	CCTCCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGCNAAGGAGTCACTGAGACCAAGGCTT	280
QY	1549	TCTCTACTGATTCGGCAGCTCAGACCCCTTTCTTCAGTCTCTGAAAGAGAAACACGTATCCC	1608
Db	279	NCTCTACTGATTCGGCAGCTCAGACCCCTTNCCTTCAGTCTCTGAAAGAGAAACACGTATCCC	220
QY	1609	ACCTGACATGTCTTCTTGAGCCCGGTAAGAGCAAAAGAAATGGCAGAAAAGTTTAGCCCCCT	1668
Db	219	ACCTGACATGTCTTCTTGAGCCCGGTAAGAGCAAAAGAAATGGCAGAAAAGTTTAGCCCCCT	160
QY	1669	GAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAGCTAAAATAAGAAA	1728
Db	159	GAAAGCCATGGAGANTCTCATAACTTGAGACCTAATCTCTGTAAGCTNAAATAAGAAA	100
QY	1729	TAGAACAAAGCTGAGGATACGACAGTACACTGTGACAGGAGCTGTAAACACAGACAGGG	1788
Db	99	TAGAACAAAGCTGAGGATACGACAGTACACTGTGACAGGAGCTGTAAACACAGACAGGG	40
QY	1789	TCAAAGTGTCTTCTTGAAACACATTGAGTTGGAATCACT	1827
Db	39	TCAAAGTGTCTTCTTGAAACACATTGAGTTGGAATCACT	1

RESULT 10
US-08-892-880-12
; Sequence 12, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.

; TITLE OF INVENTION: CD44-LIKE PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 492 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-892-880-12

Query Match 14.6%; Score 296.8; DB 2; Length 492;
Best Local Similarity 98.3%; Pred. No. 2.6e-77;
Matches 298; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 98 CATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCGATGGCCATCTGAGGTGTT 157
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Db 14 CATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCGATGGCCATCTGAGGTGTT 73

QY 158 CCCTGGCTCTGAAGGGTAGGCACGATGCCAGGTGCTTCAGCCTGGTGTCTTCTCAC 217
|
Db 74 CCCTGGCTCTGAAGGGTAGGCACGATGCCAGGTGCTTCAGCCTGGTGTCTTNTCAC 133

QY 218 TTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAGAGCTTTCCAT 277
|
Db 134 TTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAGAGCTTTCCAT 193

QY 278 CCAGGTGTCATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAGCGCAACCAGCAGCT 337
|
Db 194 CCAGGTGTCATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAGCGCAACCAGCAGCT 253

QY 338 GAATTTACAGAAGCTAAGGAGGCTGTAGGCTGTGGACTAAGTTTGGCCGGCAAGGA 397
|
Db 254 GAATTTACAGAAGCTAAGGAGGCTGTAGGTTGCTNGGACTAAGTTTGGCCGGCAAGGC 313

QY 398 CCA 400
|
Db 314 CCA 316

RESULT 11
US-09-389-681-324/c
; Sequence 324, Application us/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yuqui, Jiang
; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C3
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 324
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-389-681-324

Query Match 11.8%; Score 239; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.7e-60;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1518 GAAAGCCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTT 1577
|
Db 241 GAAAGCCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTT 182

QY 1578 TCTTCAGCTCTGAAAGAGAAACACGTATCCACCTGACATGTCTTCTTGAGCCCCGTAAG 1637
|
Db 181 TCTTCAGCTCTGAAAGAGAAACACGTATCCACCTGACATGTCTTCTTGAGCCCCGTAAG 122

QY 1638 AGCAAAAGAATGGCAGAAAAGTTTAGCCCCCTGAAAAGCCATGGAGATTCTCATAACTTGAG 1697
|
Db 121 AGCAAAAGAATGGCAGAAAAGTTTAGCCCCCTGAAAAGCCATGGAGATTCTCATAACTTGAG 62

QY 1698 ACCTAATCTCTGTAAGCTAAATAAAGAAATAGAACAAAGGCTGAGGATACGACAGTAC 1756
|
Db 61 ACCTAATCTCTGTAAGCTAAATAAAGAAATAGAACAAAGGCTGAGGATACGACAGTAC 3

RESULT 12

US-09-620-405B-324/c
; Sequence 324, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:

; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 324
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-620-405B-324

Query Match 11.8%; Score 239; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.7e-60;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1518 GAAAGCCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTT 1577
|
Db 241 GAAAGCCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTT 182

QY 1578 TCTTCAGCTCTGAAAGAGAAACACGTATCCACCTGACATGTCTTCTTGAGCCCCGTAAG 1637
|
Db 181 TCTTCAGCTCTGAAAGAGAAACACGTATCCACCTGACATGTCTTCTTGAGCCCCGTAAG 122

QY 1638 AGCAAAAGAATGGCAGAAAAGTTTAGCCCCCTGAAAAGCCATGGAGATTCTCATAACTTGAG 1697
|

```
Db      121 AGCAAAAGAATGGCAGAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG 62
QY      1698 ACCTAATCTCTGTAAAGCTTAAAGCTAAAGAAATAGAAACAAAGGCTGAGGATACGACAGTAC 1756
Db      61  ACCTAATCTCTGTAAAGCTTAAAGCTTAAAGAAATAGAAACAAAGGCTGAGGATACGACAGTAC 3
```

```
RESULT 13
US-09-433-826B-324/c
; Sequence 324, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 324
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-433-826B-324
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Query Match      11.8%; Score 239; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.7e-60;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1518 GAAAGCCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTT 1577
Db      241  GAAAGCCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTT 182

QY      1578 TCTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCTTCTGAGCCCGGTAAG 1637
Db      181  TCTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCTTCTGAGCCCGGTAAG 122

QY      1638 AGCAAAAGAATGGCAGAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG 1697
Db      121  AGCAAAAGAATGGCAGAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG 62

QY      1698 ACCTAATCTCTGTAAAGCTTAAAGCTTAAAGAAATAGAAACAAAGGCTGAGGATACGACAGTAC 1756
Db      61  ACCTAATCTCTGTAAAGCTTAAAGCTTAAAGAAATAGAAACAAAGGCTGAGGATACGACAGTAC 3
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RESULT 14
US-09-604-287A-324/c
; Sequence 324, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 324
; LENGTH: 241
; TYPE: DNA
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; ORGANISM: Homo sapiens
US-09-604-287A-324

Query Match      11.8%; Score 239; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.7e-60;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1518 GAAAGCCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTT 1577
Db      241  GAAAGCCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTT 182

QY      1578 TCTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCTTCTGAGCCCGGTAAG 1637
Db      181  TCTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCTTCTGAGCCCGGTAAG 122

QY      1638 AGCAAAAGAATGGCAGAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG 1697
Db      121  AGCAAAAGAATGGCAGAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG 62

QY      1698 ACCTAATCTCTGTAAAGCTTAAAGCTTAAAGAAATAGAAACAAAGGCTGAGGATACGACAGTAC 1756
Db      61  ACCTAATCTCTGTAAAGCTTAAAGCTTAAAGAAATAGAAACAAAGGCTGAGGATACGACAGTAC 3
```

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RESULT 15
US-09-834-759-324/c
; Sequence 324, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 324
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-759-324
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Query Match      11.8%; Score 239; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.7e-60;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1518 GAAAGCCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTT 1577
Db      241  GAAAGCCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTT 182

QY      1578 TCTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCTTCTGAGCCCGGTAAG 1637
Db      181  TCTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCTTCTGAGCCCGGTAAG 122

QY      1638 AGCAAAAGAATGGCAGAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG 1697
Db      121  AGCAAAAGAATGGCAGAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG 62

QY      1698 ACCTAATCTCTGTAAAGCTTAAAGCTTAAAGAAATAGAAACAAAGGCTGAGGATACGACAGTAC 1756
Db      61  ACCTAATCTCTGTAAAGCTTAAAGCTTAAAGAAATAGAAACAAAGGCTGAGGATACGACAGTAC 3
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fetch
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:      September 15, 2004, 16:29:45 ; Search time 493 Seconds
              (without alignments)
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Title:      US-10-079-111-1
Perfect score: 322
Sequence:    1 MARCFSLVLLTTSIWTRLL.....NPEESKSPSKTVRCLEAEV 322

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Searched:    3373863 seqs, 2124099041 residues
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Total number of hits satisfying chosen parameters: 174
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=100 -DOALIGN=200 -THR_SCORE=quality -THR_MIN=12 -ALIGN=50 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10079111@cgn 1 1 470 @runat_13092004_102223_13977 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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3:  geneseqn2000s.*
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6:  geneseqn2002s.*
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8:  geneseqn2003bs.*
9:  geneseqn2003cs.*
10: geneseqn2004s.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					Description	
Result No.	Score	Match	Length	ID		
1	322	100.0	1755	5	AAF93818	Aaf93818 Human cDN
2	322	100.0	2027	10	ADE71449	Ade71449 Human cDN
3	322	100.0	2029	3	AAZ98172	Aaz98172 Human sig
4	322	100.0	2029	10	ADE71445	Ade71445 Human cDN
5	322	100.0	2372	2	AAX52250	Aax52250 Protein P
6	322	100.0	2372	3	ADC78520	Adc78520 Human PRO
7	322	100.0	2372	4	AAF72408	Aaf72408 Human PRO
8	322	100.0	2372	4	AAF92060	Aaf92060 Human PRO

9	322	100.0	2372	6	ABS74380	Abs74380 Human cDN
10	322	100.0	2372	6	ABL88087	Ab188087 Human PRO
11	322	100.0	2372	6	ABL95576	Ab195576 Human ang
12	322	100.0	2372	7	ACA59060	Aca59060 Human PRO
13	322	100.0	2372	7	ACA58457	Aca58457 cDNA enco
14	322	100.0	2372	7	ACA60164	Aca60164 Human cDN
15	322	100.0	2372	7	ACD07564	Acd07564 Novel hum
16	322	100.0	2372	7	ACA91166	Aca91166 Novel hum
17	322	100.0	2372	7	ACD81543	Acd81543 Human cDN
18	322	100.0	2372	7	ACA60365	Aca60365 Novel hum
19	322	100.0	2372	7	ABX771612	Abx771612 Human cDN
20	322	100.0	2372	7	ACH06944	Ach06944 Human sec
21	322	100.0	2372	7	ACA58812	Aca58812 cDNA enco
22	322	100.0	2372	7	ACA63988	Aca63988 cDNA enco
23	322	100.0	2372	7	ACA91252	Aca91252 cDNA enco
24	322	100.0	2372	7	ACD45151	Acd45151 Human sec
25	322	100.0	2372	7	ABX96181	Abx96181 Human sec
26	322	100.0	2372	7	ACA05502	Aca05502 cDNA enco
27	322	100.0	2372	7	ACA93699	Aca93699 Human cDN
28	322	100.0	2372	7	ACD20169	Acd20169 Human sec
29	322	100.0	2372	7	ACA67273	Aca67273 cDNA enco
30	322	100.0	2372	7	ACH66246	Ach66246 Novel hum
31	322	100.0	2372	7	ACD02300	Acd02300 Novel hum
32	322	100.0	2372	7	ACA89291	Aca89291 Novel hum
33	322	100.0	2372	7	ACA68928	Aca68928 Novel hum
34	322	100.0	2372	7	ACA54972	Aca54972 Novel hum
35	322	100.0	2372	7	ACA98450	Aca98450 Human PRO
36	322	100.0	2372	8	ACA63375	Aca63375 cDNA enco
37	322	100.0	2372	8	ACD19807	Acd19807 Human sec
38	322	100.0	2372	8	ADB29405	Adb29405 Human sec
39	322	100.0	2372	8	ADB17062	Adb17062 Human cDN
40	322	100.0	2372	8	ACH03578	Ach03578 Human sec
41	322	100.0	2372	8	ADA18261	Ada18261 Human sec
42	322	100.0	2372	8	ACD66954	Acd66954 Human cDN
43	322	100.0	2372	8	ADA19867	Ada19867 Novel hum
44	322	100.0	2372	8	ADB17250	Adb17250 Human cDN
45	322	100.0	2372	8	ACD83115	Acd83115 Human PRO
46	322	100.0	2372	8	ADA16236	Ada16236 Human sec
47	322	100.0	2372	8	ADA20039	Ada20039 Novel hum
48	322	100.0	2372	8	ACD82092	Acd82092 Human sec
49	322	100.0	2372	8	ADA42381	Ada42381 Human sec
50	322	100.0	2372	8	ACD23293	Acd23293 Human PRO
51	322	100.0	2372	8	ADA00336	Ada00336 Human sec
52	322	100.0	2372	8	ADA16660	Ada16660 Human sec
53	322	100.0	2372	8	ADA13089	Ada13089 Human sec
54	322	100.0	2372	8	ADA41957	Ada41957 Human sec
55	322	100.0	2372	8	ADA17304	Ada17304 Human sec
56	322	100.0	2372	8	ADA42807	Ada42807 Human sec
57	322	100.0	2372	8	ACD23655	Acd23655 Human PRO
58	322	100.0	2372	8	ADB85578	Adb85578 Novel hum
59	322	100.0	2372	8	ADB77726	Adb77726 Human sec
60	322	100.0	2372	9	ADB74862	Adb74862 Human sec
61	322	100.0	2372	9	ADB68257	Adb68257 Human PRO
62	322	100.0	2372	9	ADB68064	Adb68064 Human PRO
63	322	100.0	2372	9	ADB90881	Adb90881 Novel hum
64	322	100.0	2372	9	ADC28508	Adc28508 Human sec
65	322	100.0	2372	9	ADC39708	Adc39708 Human sec
66	322	100.0	2372	9	ADC40222	Adc40222 Human sec
67	322	100.0	2372	9	ADC19046	Adc19046 Human sec
68	322	100.0	2372	9	ADC34346	Adc34346 Human sec
69	322	100.0	2372	9	ADC29401	Adc29401 Human sec
70	322	100.0	2372	9	ADC28932	Adc28932 Human sec
71	322	100.0	2372	9	ADC40817	Adc40817 Human sec
72	322	100.0	2372	9	ADC19474	Adc19474 Human sec
73	322	100.0	2372	9	ADC06961	Adc06961 Human PRO
74	322	100.0	2372	9	ADC17140	Adc17140 cDNA sequ
75	322	100.0	2372	9	ADC33922	Adc33922 Human sec
76	322	100.0	2372	9	ADC12992	Adc12992 Human sec
77	322	100.0	2372	9	ADC14838	Adc14838 Novel hum
78	322	100.0	2372	9	ADC52333	Adc52333 Novel hum
79	322	100.0	2372	9	ADC12444	Adc12444 Human sec
80	322	100.0	2372	9	ADD10320	Add10320 Human sec
81	322	100.0	2372	9	ADD11280	Add11280 Human sec

82	322	100.0	2372	9	ADD04005	Add04005 Human sec
83	322	100.0	2372	9	ADD03581	Add03581 Human sec
84	322	100.0	2372	9	ADD37073	Add37073 Human sec
85	322	100.0	2372	9	ADD36009	Add36009 Novel hum
86	322	100.0	2372	9	ADE34833	Ade34833 Human sec
87	322	100.0	2372	10	ADC52143	Adc52143 Novel hum
88	322	100.0	2372	10	ADE79278	Ade79278 Human sec
89	322	100.0	2372	10	ADE79702	Ade79702 Human sec
90	322	100.0	2372	10	ADE73378	Ade73378 Human sec
91	322	100.0	2372	10	ADE41281	Ade41281 Human sec
92	322	100.0	2372	10	ADE73913	Ade73913 Human sec
93	314	97.5	2324	4	ABA09223	Aba09223 Human PRO
94	287	89.1	1680	9	ADD04999	Add04999 Human sec
95	258	80.1	1127	7	ACA10111	Aca10111 Human NOV
96	239	74.2	2313	2	AAV22687	Aav22687 DNA encod
97	239	74.2	2369	6	ABL90698	Ab190698 Human pol
98	235	73.0	2967	3	AAC59803	Aac59803 Human sec
99	125	38.8	411	8	ACH20895	Ach20895 Human adu
100	125	38.8	596	6	ABT09892	Abt09892 Human bre

ALIGNMENTS

RESULT 1
AAF93818
ID AAF93818 standard; cDNA; 1755 BP.
XX
AC AAF93818;
XX
DT 23-MAY-2001 (first entry)
XX
DE Human cDNA encoding a membrane or secretory protein clone PSEC0135.
XX
KW Human; secretory protein; membrane protein; vaccine; gene therapy;
KW rheumatoid arthritis; diabetes; ss.
XX Homo sapiens.
OS
PN EP1067182-A2.
XX
PD 10-JAN-2001.
XX
PF 07-JUL-2000; 2000EP-00114090.
XX
PR 08-JUL-1999; 99JP-00194179.
PR 11-JAN-2000; 2000JP-00118775.
PR 02-MAY-2000; 2000JP-00183766.
XX
PA (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
PI
XX WPI; 2001-093989/11.
DR P-PSDB; AAB88391.
XX
XX Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT gene therapy or as candidate target molecules in drug development.
XX
PS Claim 1; SEQ ID NO 149; 609pp + Sequence Listing; English.
XX
XX This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC which encode human secretory or membrane proteins represented by AAB88317
CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
CC invention. The invention also includes methods for the production of
CC antibodies directed against the proteins, and cDNA sequences, which can
CC be used in vaccines. The polynucleotide sequences can be used in gene
CC therapy. The polynucleotide sequences and the proteins they encode may be
CC used in the prevention, treatment and diagnosis of diseases associated
CC with inappropriate secretory protein/membrane protein expression. The
CC nucleic acids and complementary sequences may also be used as DNA probes
CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
CC and quantitate the presence of similar nucleic acid sequences in samples.

CC They may also be used to study the expression and function of secretory
CC proteins/membrane polypeptides and their role in metabolism. The
CC polypeptides may be used as antigens in the production of antibodies
CC against them and in assays to identify modulators (agonists and
CC antagonists) of expression and activity. The antibodies and antagonists
CC may also be used as therapeutic agents to down regulate expression and
CC activity. The antibodies may also be used as diagnostic agents for
CC detecting the presence of the polypeptides in samples (e.g. by enzyme
CC linked immunosorbant assay (ELISA)). Examples of diseases which may be
CC treated include rheumatoid arthritis and diabetes
XX
SQ Sequence 1755 BP; 502 A; 422 C; 406 G; 425 T; 0 U; 0 Other;
Alignment Scores: 1.12e-304 Length: 1755
Pred. No.: 322.00 Matches: 322
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB:
US-10-079-111-1 (1-322) x AAF93818 (1-1755)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
DB 201 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCATTCCATCTGGACCACGAGGCTCCTG 260
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
DB 261 GTCCAAGGCTCTTTCGCTGCAGAAAGAGCTTCCATCCAGGTGTCTCAGAAATTATGGGG 320
QY 41 IleThrLeuValSerLysAlaAsnGlnLeuAsnPheThrGluAlaLysGluAla 60
DB 321 ATCACCCCTTGAGCAAAAGCGAACCCAGCAGCTGAATTTACAGAGAGCTAAGGAGGCC 380
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
DB 381 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAGTTGAAACAGCCTTGAAAGCT 440
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
DB 441 AGCTTTGAAACTTGCAGCTATGGCTGGTGGGTTGGAGATGGATTCTGTGGTCTCTTAGGATT 500
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
DB 501 AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCTGTATTGGAGGTTCCAGTG 560
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
DB 561 AGCCGACAGTTTGCAGCTATTGTTACAACTATCTGATCTGATCTGGACTAATCGTGCATT 620
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
DB 621 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACACAACAACA 680
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
DB 681 GAATTTATTGTCAGTGACAGTACCTACTCTGGTGGATCCCTTACTCTACATAATACCTGCC 740
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
DB 741 CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 800
QY 201 CysValThrGluValPheMetGluThrSerThrSerThrMetSerThrGluThrGluProPheVal 220
DB 801 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 860
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
DB 861 GAAAAATAAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 920
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260

Db 921 CTAGTGCTTGCTCTCCCTCTCTTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAA 980
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db 981 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGATCAGCAGAAGGAATGATCGAAACC 1040
QY 281 LysValVallysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1041 AAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT 1100
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1101 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCT 1160
QY 321 GluVal 322
Db 1161 GAAGTT 1166

RESULT 2
ADE71449

ID ADE71449 standard; cDNA; 2027 BP.

AC ADE71449;

DT 29-JAN-2004 (first entry)

DE Human cDNA encoding PDEBC #2.

XX breast cancer; PDEBC; metastatic; human; ss; gene.

KW Homo sapiens.

OS US2003124543-A1.

PN 03-JUL-2003.

PF 20-FEB-2002; 2002US-00079111.

XX 15-JAN-1999; 99US-00232160.

PA (STUA/) STUART S G.
PA (STRE/) STREETER D G.

XX Stuart SG, Streeter DG;

XX WPI; 2004-009141/01.
DR P-PSDB; ADE71444.

PT A new cDNA encoding a protein differentially expressed in breast cancer
PT designated PCEBC is useful to stage, treat, and monitor progression or
PT treatment of breast cancer, particularly an invasive, metastatic stage of
PT the disease.

XX Claim 2; Fig 1; 31pp; English.

PS The invention relates to an isolated cDNA encoding a protein that is
XX differentially expressed in breast cancer, designated PDEBC. The
CC invention is useful to diagnose breast cancer. The invention is also
CC useful to stage, treat, and monitor progression or treatment of breast
CC cancer, particularly an invasive, metastatic stage of the disease. The
CC present sequence represents cDNA encoding human PDEBC Incyte 3044710CB1.
CC Note: There are two sequences that have been assigned SEQ ID 2 in the
CC specification, the present sequence represents the sequence given in
CC figure 1.

XX Sequence 2027 BP; 612 A; 461 C; 445 G; 509 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.28e-304 Length: 2027
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 10 Gaps: 0
US-10-079-1111-1 (1-322) x ADE71449 (1-2027)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 181 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCTG 240
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 241 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCTATGCAGAAATATATGGG 300
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 301 ATCACCCCTTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTTCACAGAAGCTAAGGAGGCC 360
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 361 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCT 420
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 421 AGCTTTGAAACTTGCAGCTATGGCTGGTGGATGGATTCGTGGTCACTCTCTAGGATT 480
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 481 AGCCCAAAACCCCAAGTGTGGGAAAAAATGGGTGGTGTCTGTATTGGAAGGTTCCAGTG 540
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 541 AGCCGACAGTTTGACGCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATT 600
QY 141 ProGluIleIleThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 601 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACACTGCAACACAAACA 660
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 661 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC 720
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 721 CCTACTACTCTCTCTCTCTCCAGCTTCCAGCTTCTATTCCACGGAGAAAAAATTGATT 780
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 781 TGTGTACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 840
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 841 GAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 900
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 901 CTAGTGCTTGCTCTCTCTCTTTTGGTGTGCAGCTGGTCTTTGGATTGTGTCAAA 960
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db 961 AGGTATGTGAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAATGATCGAAACC 1020
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysThr 300
Db 1021 AAAGTAGTAAAGGAGGAGAGGCGCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT 1080
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1081 GATAAAAACCCAGAAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCT 1140
QY 321 GluVal 322
Db 1141 GAAGTT 1146

AAZ98172		ID AAZ98172 standard; cDNA; 2029 BP.	
XX	AC	AAZ98172;	
XX	DT	11-MAY-2000 (first entry)	
XX	DE	Human signal peptide containing protein HSPP-64 cDNA SEQ ID NO:198.	
XX	KW	Human; signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; parkinson's disease; Huntington's diseases; ovulatory defect; muscular dystrophy; ss.	
XX	OS	Homo sapiens.	
XX	PN	WO200000610-A2.	
XX	PD	06-JAN-2000.	
XX	PF	25-JUN-1999; 99WO-US014484.	
XX	PR	26-JUN-1998; 98US-0090762P.	
XX	PR	31-JUL-1998; 98US-0094983P.	
XX	PR	01-OCT-1998; 98US-0102686P.	
XX	PR	11-DEC-1998; 98US-0112129P.	
XX	PA	(INCY-) INCYTE PHARM INC.	
XX	PI	Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR; Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL; Bandman O;	
XX	DR	WPI; 2000-160673/14.	
XX	DR	P-PSDB; AAY87287.	
XX	PT	New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease.	
XX	PS	Claim 9; Page 288-289; 327pp; English.	
XX	CC	AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic, neuroprotective, cardiovascular and antiasthmatic activities, and can be used in gene therapy. HSPPs can be used to treat or prevent disorders associated with decreased activity or function of HSPP. Antagonists of HSPP are used to treat or prevent disorders associated with increased activity or function of HSPP. Such diseases include cell proliferation (including cancer), inflammation, cardiovascular, neurological, reproductive or developmental disorders, (e.g. arteriosclerosis, cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia, asthma, Crohn's disease, microbial or other infections, congestive or ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP nucleic acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for diagnosis and monitoring), in gene therapy, as antisense, triplex-forming or ribozyme therapeutics, for detecting related sequences or genetic variations, and for chromosomal mapping. HSPP are also used to raise specific antibodies (Ab) and to screen for agonists and antagonists (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP-related diseases (in usual immunoassays), as therapeutic antagonists, in competitive drug screens, and for purification of HSPP from natural sources	
XX	SQ	Sequence 2029 BP; 612 A; 463 C; 445 G; 509 T; 0 U; 0 Other;	

Alignment Scores:		1.28e-304	Length:	2029
Pred. No.:	Score:	322.00	Matches:	322
Percent Similarity:	Best Local Similarity:	100.00%	Conservative:	0
Query Match:	Indels:	100.00%	Mismatches:	0
DB:	Gaps:	3		0
US-10-079-111-1 (1-322) x AAZ98172 (1-2029)				
Qy	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu	20	
Db	183	ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCAGGCTCCTG	242	
Qy	21	ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly	40	
Db	243	GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG	302	
Qy	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60	
Db	303	ATCACCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTACAGAAAGTAAGGAGGCC	362	
Qy	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80	
Db	363	TGTAGGCTGCTGGACTAAGTTTGGCCGGCAAGGACCAAGTGAAGACAGCCTTGAAAGCT	422	
Qy	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100	
Db	423	AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTGCTGTCATCTCTAGGATT	482	
Qy	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120	
Db	483	AGCCCAAAACCCCAAGTGTGGGAAAAAATGGGGTGGTCTCTGATTGGAAAGTTCCAGTG	542	
Qy	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140	
Db	543	AGCCGACAGTTTGCAGCCTATTGTTACAACACTCATCTGATACTTGGACTAACTCGTGCAAT	602	
Qy	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160	
Db	603	CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA	662	
Qy	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180	
Db	663	GAATTTATGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	722	
Qy	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200	
Db	723	CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	782	
Qy	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220	
Db	783	TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATTGTCTACAGAAACTGAACCATTTGTT	842	
Qy	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240	
Db	843	GAATAATAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG	902	
Qy	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260	
Db	903	CTAGTGCTTGCTCTCTCTTCTTGGTGTGCTGCAGTGGTCTTGGATTTTGTCTATGTCAA	962	
Qy	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280	
Db	963	AGGTATGTGAAGGCCTTCCCTTTTACAAAACAAGAAATCAGCAGAAAGAAATGATCGAAACC	1022	
Qy	281	LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300	
Db	1023	AAAGTACTAAAGGAGGAGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT	1082	
Qy	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320	

Db 1083 GATAAAACCAGAGAGTCCAGAGTCCAAAGCAAACTACCGTGGATGCCTGGAAGCT 1142

Qy 321 GluVal 322
| | | | |

Db 1143 GAAGTT 1148

RESULT 4
ADE71445
ID ADE71445 standard; cDNA; 2029 BP.
XX
AC ADE71445;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human cDNA encoding PDEBC Incyte 3044710CB1.
XX
KW breast cancer; PDEBC; metastatic; human; ss; gene.

OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 183..1151
FT /*tag= a
FT /product= "PDEBC"
XX

PN US2003124543-A1.
XX
PD 03-JUL-2003.
XX
PF 20-FEB-2002; 2002US-00079111.
XX
PR 15-JAN-1999; 99US-00232160.
XX

PA (STUA/) STUART S G.
PA (STRE/) STREETER D G.
XX
PI Stuart SG, Streeter DG;
XX
DR WPI; 2004-009141/01.
DR P-PSDB; ADE71444.
XX

PT A new cDNA encoding a protein differentially expressed in breast cancer
PT designated PCEBC is useful to stage, treat, and monitor progression or
PT treatment of breast cancer, particularly an invasive, metastatic stage of
PT the disease.

Claim 2; SEQ ID NO 2; 31pp; English.

The invention relates to an isolated cDNA encoding a protein that is
differentially expressed in breast cancer, designated PDEBC. The
invention is useful to diagnose breast cancer. The invention is also
useful to stage, treat, and monitor progression or treatment of breast
cancer, particularly an invasive, metastatic stage of the disease. The
present sequence represents cDNA encoding human PDEBC Incyte 3044710CB1.
Note: There are two sequences that have been assigned SEQ ID 2 in the
specification, the present sequence represents the sequence given in the
sequence listing.

Sequence 2029 BP; 612 A; 463 C; 445 G; 509 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.28e-304 Length: 2029
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x ADE71445 (1-2029)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
| | | | |

Db 183 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 242

Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
| | | | |

Db 243 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGG 302

Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
| | | | |

Db 303 ATCACCCCTTGTGAGCAAAAAGCGAACCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 362

Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
| | | | |

Db 363 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAAACAGCCTTGAAAGCT 422

Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
| | | | |

Db 423 AGCTTTGAAAACCTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCACTCTCTAGGATT 482

Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
| | | | |

Db 483 AGCCCAAAACCCCAAGTGTGGGAAAAAATGGGGTGGGTGCTCCTGATTTGGAAGGTTCCAGTG 542

Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerSerAspThrTrpThrAsnSerCysIle 140
| | | | |

Db 543 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATT 602

Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
| | | | |

Db 603 CCAGAAATTATCACCCACCAAGATCCCATATTTCAACACTCAAACTGCAACACAACA 662

Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
| | | | |

Db 663 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 722

Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
| | | | |

Db 723 CCTACTACTCTCCTCCTGCTCCAGCTTCCACITTCCTATTTCCACGGAGAAAAAATTGATT 782

Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
| | | | |

Db 783 TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 842

Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
| | | | |

Db 843 GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTGGAGGTGTCCCCACGGCTCTG 902

Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
| | | | |

Db 903 CTAGTGTCTGCTCTCTCTCTTTTGGTGTCTGAGTGGTCTTTGGATTTTGTATGTCAAA 962

Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
| | | | |

Db 963 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC 1022

Qy 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
| | | | |

Db 1023 AAAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT 1082

Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
| | | | |

Db 1083 GATAAAACCCAGAGAGTCCAAGAGTCCACAGCAAAACTACCGTGGATGCGCTGGAAGCT 1142

Qy 321 GluVal 322
| | | | |

Db 1143 GAAGTT 1148

RESULT 5
AAx52250
ID AAX52250 standard; DNA; 2372 BP.
XX
AC AAX52250;
XX
DT 25-JUN-1999 (first entry)
XX

DE Protein PRO263 cDNA clone DNA34431-1171.
XX
KW Secreted protein; transmembrane protein; human; enterocolitis;
KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
KW congenital microvillus atrophy; skin disease; cell growth;
KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;
KW dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;
KW wound healing; tissue repair; ss.

XX Homo sapiens.

PN WO9914328-A2.

XX 25-MAR-1999.

PF 16-SEP-1998; 98WO-US019330.

XX 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059115P.

PR 17-SEP-1997; 97US-0059117P.

PR 17-SEP-1997; 97US-0059119P.

PR 17-SEP-1997; 97US-0059121P.

PR 17-SEP-1997; 97US-0059122P.

PR 17-SEP-1997; 97US-0059184P.

PR 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 15-OCT-1997; 97US-0062125P.

PR 17-OCT-1997; 97US-0062285P.

PR 17-OCT-1997; 97US-0062287P.

PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0062814P.

PR 24-OCT-1997; 97US-0062816P.

PR 24-OCT-1997; 97US-0063045P.

PR 24-OCT-1997; 97US-0063120P.

PR 24-OCT-1997; 97US-0063121P.

PR 24-OCT-1997; 97US-0063127P.

PR 24-OCT-1997; 97US-0063128P.

PR 27-OCT-1997; 97US-0063327P.

PR 27-OCT-1997; 97US-0063329P.

PR 28-OCT-1997; 97US-0063541P.

PR 28-OCT-1997; 97US-0063542P.

PR 28-OCT-1997; 97US-0063544P.

PR 28-OCT-1997; 97US-0063549P.

PR 28-OCT-1997; 97US-0063550P.

PR 28-OCT-1997; 97US-0063564P.

PR 29-OCT-1997; 97US-0063435P.

PR 29-OCT-1997; 97US-0063704P.

PR 29-OCT-1997; 97US-0063732P.

PR 29-OCT-1997; 97US-0063734P.

PR 29-OCT-1997; 97US-0063735P.

PR 29-OCT-1997; 97US-0063738P.

PR 29-OCT-1997; 97US-0064215P.

PR 31-OCT-1997; 97US-0063870P.

PR 31-OCT-1997; 97US-0064103P.

PR 03-NOV-1997; 97US-0064248P.

PR 07-NOV-1997; 97US-0064809P.

PR 12-NOV-1997; 97US-0065186P.

PR 17-NOV-1997; 97US-0065846P.

PR 18-NOV-1997; 97US-0065693P.

PR 21-NOV-1997; 97US-0066120P.

PR 21-NOV-1997; 97US-0066364P.

PR 24-NOV-1997; 97US-0066453P.

PR 24-NOV-1997; 97US-0066466P.

PR 24-NOV-1997; 97US-0066511P.

PR 24-NOV-1997; 97US-0066770P.

PR 24-NOV-1997; 97US-0066772P.

PR 25-NOV-1997; 97US-0066840P.

XX (GETH) GENENTECH INC.

PA Wood WI, Gurney AL, Goddard A, Pennica D, Chen J, Yuan J;

XX

DR WPI; 1999-229533/19.
DR P-PSDB; AAY13379.
XX
PT New isolated human genes and polypeptides used in, e.g. treatment of
PT gastrointestinal ulceration.
XX
PS Claim 2; Fig 73; 320pp; English.
XX
CC AAX52213-74 encode secreted and transmembrane human proteins, and are
CC obtained from cDNA libraries, prepared from fetal lung, fetal kidney,
CC fetal brain, fetal liver and fetal retina. The encoded polypeptides have
CC specific uses based on their homology to known polypeptides, e.g. PRO211
CC and PRO217 can be used for disorders associated with the preservation and
CC maintenance of gastrointestinal mucosa and the repair of acute and
CC chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome,
CC gastrointestinal ulceration and congenital microvillus atrophy), skin
CC diseases associated with abnormal keratinocyte differentiation (e.g.
CC psoriasis, epithelial cancers such as lung squamous cell carcinoma of the
CC vulva and gliomas), potent effects on cell growth and development,
CC diseases related to growth or survival of nerve cells including
CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies or cancer.
CC PRO265 can be used as for fibromodulin, e.g. for reducing dermal
CC scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may
CC be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can
CC be used as an anti-thrombotic agent; PRO287 polypeptides and portions may
CC have therapeutic applications in wound healing and tissue repair; PRO317
CC can be used for treating problems of the kidney, uterus, endometrium,
CC blood vessels, or related tissue, e.g. in the heart of genital tract
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-079-111-1 (1-322) x AAX52250 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCTGGTGTTCCTCACTTCCATCTGGACCACGAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTCGTGTCAGAGAGCTTTCATCCAGGTGTCAGAAATTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTTCACAGAAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTTCGTGGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAACCCCAAGTGTGGGAAAATGGGGTGGGTCTCCTGATTTGGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACACTCATCTGATACCTTGGACTAACTCGTGCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCACCACCAAGATCCCATATTTCAACACTCAAACCTGCAACACAAACA 639

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
|||
Db 760 TGTGTACAGAGTTTATTGGAACCTAGCACCATGTCTACAGAACTGAACCATTTGTT 819

QY 221 GluAsnLysAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
|||
Db 820 GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGTTTGGAGGTGCCCCACGGCTCTG 879

QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
|||
Db 880 CTAGTGCTTGCTCTCCTCTTCTTTGGTGTGCAGCTGGTCTTGGAATTTGCTATGTCAA 939

QY 261 ArgTyrValLysAlaPhePropheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
|||
Db 940 AGGTATGTGAAGCCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAATGATCGAAACC 999

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAAGAAACT 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
|||
Db 1060 GATAAAACCAGAGAGTCCAAAGAGTCCAAAGCAAAACTACCGTGCATGCTTGGAGCT 1119

QY 321 GluVal 322
|||||
Db 1120 GAAGTT 1125

RESULT 7
AAF72408
ID AAF72408 standard; cDNA; 2372 BP.
XX
AC AAF72408;

DT 24-APR-2001 (first entry)

DE Human PRO263 cDNA.

XX Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW antiarthritic; antinfertility; antidiabetic; antiviral; diabetes;
KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW ischaemia; inflammation; ss.

XX Homo sapiens.

XX WO200104311-A1.

XX 18-JAN-2001.

PF 22-FEB-2000; 2000WO-US004414.

PR 07-JUL-1999; 99US-0143048P.

PR 26-JUL-1999; 99US-0145698P.

PR 28-JUL-1999; 99US-0146222P.

PR 08-SEP-1999; 99WO-US020594.

PR 13-SEP-1999; 99WO-US020944.

PR 15-SEP-1999; 99WO-US021090.

PR 15-SEP-1999; 99WO-US021547.

PR 05-OCT-1999; 99WO-US023089.

PR 29-NOV-1999; 99WO-US028214.

PR 30-NOV-1999; 99WO-US028313.

PR 02-DEC-1999; 99WO-US028564.

PR 02-DEC-1999; 99WO-US028565.

PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.

PR 20-DEC-1999; 99WO-US030999.

PR 05-JAN-2000; 2000WO-US000219.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;

PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2001-081051/09.
DR P-PSDB; AAB80247.
XX
PT Sixty one nucleic acids encoding PRO polypeptides which are useful in the
PT treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
PT cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
PT disease).
XX Claim 2; Fig 73; 393pp; English.
XX The present sequence is one of sixty one nucleic acids encoding novel
CC secreted and transmembrane PRO polypeptides. The PRO polypeptides are
CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
CC squamous cell carcinoma), gastrointestinal disorders (e.g.
CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,
CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.
CC endometrial bleeding, angiogenesis, ischaemias such as coronary ischaemia,
CC atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid
CC arthritis, multiple sclerosis), infertility, AIDS and diabetes and
CC retinal disorders such as retinitis pigmentosum. The PRO nucleic acids
CC have applications in molecular biology, including use as hybridization
CC probes, and in chromosome and gene mapping
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-079-111-1 (1-322) x AAF72408 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
|||
Db 160 ATGCCCAGGTGCTTCAGCCTGGTGTGCTTCTCATTCCATCTGGACCACGAGGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
|||
Db 220 GTCCAAGGCTCTTTGCGTGCAGAGAGGCTTTCATCCAGGTGTCATGCAGAAATTATGGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
|||
Db 280 ATCACCCCTGTGAGCAAAAAGCGAACCCAGGACCAAGTTGAAACAGCCTTGAAAGCT 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
|||
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
|||
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTTCGTGTCATCTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
|||
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAATGGGGTGGGTGCTCTGATTGGAAAGTTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
|||
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACACTCATCTGATACITGGACTAACTCGTGCA 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
|||
Db 580 CCAGAAATTATCACCCAAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

Db 640 GAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

Db 700 CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

Db 760 TGTGTACAGAAAGTTTTTATGAAAACTAGCACCATGTCTACAGAACTGAACCAATTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240

Db 820 GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260

Db 880 CTAGTGCTTGCTCTCCTCTCTTTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAAA 939

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280

Db 940 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAAATGATCGAAACC 999

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300

Db 1000 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACT 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320

Db 1060 GATAAAAAACCCAGAGAGTCCAGAGTCCCAAGCAAAACTACCGTCCGATGCCTGGAGCT 1119

QY 321 GluVal 322

Db 1120 GAAGTT 1125

RESULT 8

AAF92060

ID AAF92060 standard; cDNA; 2372 BP.

XX AC AAF92060;

XX DT 15-MAY-2001 (first entry)

XX DE Human PRO263 cDNA.

XX KW Human; PRO protein; mapping; ss.

XX OS Homo sapiens.

XX PN WO200116318-A2.

XX PD 08-MAR-2001.

XX PF 24-AUG-2000; 2000WO-US023328.

XX PR 01-SEP-1999; 99WO-US020111.

XX PR 15-SEP-1999; 99WO-US021090.

XX PR 07-DEC-1999; 99US-0169495P.

XX PR 09-DEC-1999; 99US-0170262P.

XX PR 11-JAN-2000; 2000US-0175481P.

XX PR 18-FEB-2000; 2000WO-US004341.

XX PR 18-FEB-2000; 2000WO-US004342.

XX PR 22-FEB-2000; 2000WO-US004414.

XX PR 01-MAR-2000; 2000WO-US005601.

XX PR 03-MAR-2000; 2000US-0187202P.

XX PR 21-MAR-2000; 2000US-0191007P.

XX PR 30-MAR-2000; 2000WO-US008439.

XX PR 25-APR-2000; 2000US-0199397P.

XX PR 22-MAY-2000; 2000WO-US014042.

XX PR 05-JUN-2000; 2000US-0209832P.

XX PA (GETH) GENENTECH INC.

XX

PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;

XX

DR WPI; 2001-183260/18.

XX P-PSDB; AAB87528.

PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular

PT biology, including use as hybridization probes, and in chromosome and

XX gene mapping.

PS Claim 2; Fig 5; 278pp; English.

XX

CC The present sequence is the coding sequence for a human PRO polypeptide

CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO

CC antagonists or anti-PRO antibodies are useful for preparation of a

CC medicament useful in the treatment of a condition which is responsive to

CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO

CC protein may also be employed as molecular weight markers for protein

CC electrophoresis. The PRO coding sequence has applications in molecular

CC biology, including use as hybridisation probes, and in chromosome and

CC gene mapping

XX

SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.49e-304 Length: 2372

Score: 322.00 Matches: 322

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 4 Gaps: 0

US-10-079-111-1 (1-322) x AAF92060 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20

Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTGTTCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

Db 220 GTCCAAGGCTCTTTGGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60

Db 280 ATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

Db 340 TGTAGGCTGTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100

Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCTGGTCACTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

Db 460 AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTGTGAAGGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerSerAspThrTrpThrAsnSerCysIle 140

Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACCTTGGACTAACTCGTGCAAT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

Db 580 CCAGAAAATTATCACCAACCAAGATCCCATATTCAAACTCAAACTGCAACACAAACAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

Db 640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

Db 700 CCTACTACTCTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
760 TGTGTCACAGAAGTTTATTATGGAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
820 GAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGTTTGGAGGTGTCCCCACGGCTCTG 879

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLysGlyPheCysTyrValLys 260
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
880 CTAGTGCTTGCTCTCCTCTCTTTTGGTGCTGCAGCTGGTCTTGGATTGTGCTATGTCAA 939

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
940 AGGTATGTGAAGCCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAATGATCGAAACC 999

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1000 AAAGTAGTAAAGGAGGAGGAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAACT 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1060 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAAGCAAAACTACCGTGCATGCCTGGAAGCT 1119

QY 321 GluVal 322
Db |||||||
1120 GAAGTT 1125

RESULT 9
ABS74380
ID ABS74380 standard; cdna; 2372 BP.
XX
AC ABS74380;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human cdna encoding secreted/transmembrane protein PRO263.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;
KW antiarthritic; osteopathic; sports-related joint problem;
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN US2002119130-A1.
XX
PD 29-AUG-2002.
XX
PF 06-DEC-2001; 2001US-00006867.
XX
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0064215P.
PR 22-APR-1998; 98US-0082797P.
PR 29-APR-1998; 98US-0083495P.
PR 15-MAY-1998; 98US-0085579P.
PR 02-JUN-1998; 98US-0087759P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 11-JUN-1998; 98US-0088863P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089653P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 24-JUN-1998; 98US-0090444P.
PR 25-JUN-1998; 98US-0090688P.

PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 02-JUL-1998; 98US-0091628P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097979P.
PR 01-SEP-1998; 98US-0098749P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100930P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101475P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101916P.
PR 30-SEP-1998; 98US-0102570P.
PR 06-OCT-1998; 98US-0103449P.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021194.
PR 22-DEC-1999; 99WO-US030720.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032378.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.

(GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

WPI; 2002-731348/79.
P-PSDB; ABG95853.

New isolated secreted and transmembrane PRO polypeptide useful for
modulating biological activity of a cell, or for treating sports-related
joint problems, osteoarthritis or rheumatoid arthritis.

Claim 2; Fig 5; 399pp; English.

The invention relates to an isolated secreted and transmembrane PRO
polypeptide having 80 % sequence identity to a sequence appearing as
ABG95851-ABG95934 or their associated signal peptide, or a sequence of an

CC extracellular domain of the proteins with their associated signal peptide
CC or lacking its associated signal peptide. Also included are the nucleic
CC acids encoding the proteins, vectors, host cells, fusion proteins and
CC antibodies which specifically bind to the proteins. The proteins are
CC useful for detecting a polypeptide designated as A, B, C or D in a sample
CC suspected of containing an A, B, C or D polypeptide, by contacting the
CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
CC conjugate in the sample, where the formation of the conjugate is
CC indicative of the presence of an A, B, C or D polypeptide in the sample,
CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
CC H or I polypeptide is labeled with a detectable label or is attached to a
CC solid support. The proteins are useful for linking a bioactive molecule
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC or I, or antibodies against them are useful for modulating a biological
CC activity of a cell expressing a polypeptide designated as A, B, C or D or
CC E, F, G, H, or I. The cell is killed. The proteins are useful for
CC identifying agonists or antagonists, for the preparation of a medicament
CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic useful reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence encodes a novel secreted or transmembrane protein of the
CC invention

XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-079-111-1 (1-322) x ABS74380 (1-2372)

QY	1	MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu	20
Db	160	ATGCCAGGTGCTTCAGCCCTGGTGTGCTTCTCACTTCCATCTGGACCAGGGCTCCTG	219
QY	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	220	GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTCTCATGCAGAAATTATGGG	279
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	280	ATCACCCCTGTGAGCAAAAAGCGAACCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC	339
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGGCTGCTGGACTAAGTTTGGCCGCAAGGACCAAGTGAACAGCCTTGAAGCT	399
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	400	AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTGGTGCATCTCTAGGATT	459
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120

Db	460	AGCCCAAAACCCCAAGTGTGGAAAAAATGGGGTGGGTGCTCTGATTTGGAAGGTTCCAGTG	519
QY	121	SerArgGlnPheAlaIaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	520	AGCCGACAGTTTGCAGCCTATTGTTACAACACTCATCTGATACTTGGACTAACTCGTGCA	579
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA	639
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTTATTGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	699
QY	181	ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	700	CCTACTACTCTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	759
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATCTGTACAGAAACTGAACCATTTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCCCCACGGCTCTG	879
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCystYrValLys	260
Db	880	CTAGTGTCTTGTCTCTCTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGTATGTCAAA	939
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC	999
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1000	AAAGTAGTAAAGGAGGAGGAGGCCAATGATAGCAACCTTAATGAGGAATCAAAGAAACT	1059
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAACCCAGAGAGTCCAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAGACT	1119
QY	321	GluVal 322	
Db	1120	GAAAGTT 1125	
RESULT 10			
ABL88087	ID	ABL88087 standard; cDNA; 2372 BP.	
XX	AC	ABL88087;	
XX	XX	16-MAY-2002 (first entry)	
XX	DE	Human PRO263 cDNA sequence SEQ ID NO:31.	
XX	KW	Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;	
XX	KW	vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;	
XX	KW	gene therapy; cardiovascular disorder; endothelial disorder; cancer;	
XX	KW	angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;	
XX	KW	age-related macular degeneration; arterial restenosis; angina;	
XX	KW	rheumatoid arthritis; myocardial infarction; thrombophlebitis;	
XX	KW	lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;	
XX	OS	wound healing; chromosome mapping; gene mapping; gene; ss.	
XX	XX	Homo sapiens.	
XX	PN	WO200200690-A2.	
XX	XX	03-JAN-2002.	
XX	PF	20-JUN-2001; 2001WO-US019692.	

PR 23-JUN-2000; 2000US-0213637P.
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.

(GETH) GENENTECH INC.

Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

WPI; 2002-090516/12.
P-PSDB; ABB84832.

One hundred and eighty seven nucleic acids encoding PRO polypeptides,
useful in diagnosis and treatment of cardiovascular (e.g. myocardial
infarction), endothelial or angiogenic disorders in a mammal.

Claim 2; Fig 31; 565pp; English.

ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
ABB85003. The PRO proteins and polynucleotides have cardiac, cytostatic,
antiangiogenic, hypotensive, vulnery and antiarteriosclerotic
activities, and can be used in gene therapy. The PRO polynucleotides,
proteins, agonists and antagonists are useful for treating or diagnosing
a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
angiogenesis (such as breast carcinoma and liver carcinoma) and wound
healing. The PRO polynucleotides have applications in molecular biology,
including use as hybridisation probes, and in chromosome and gene
mapping. ABL88259 to ABL88267 represent primers and probes used in the
exemplification of the present invention

Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
US-10-079-111-1 (1-322) x ABL88087 (1-2372)			
QY	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTlpThrThrArgLeuLeu	20
Db	160	ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCATTCCATCTGGACCACGAGGCTCCTG	219
QY	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	220	GTCCAAGGCTCTTTGCGTGCAGAAAGCTTTCCATCCAGGTGTCTGCAGAAATTATGGG	279
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	280	ATCACCCCTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTTCACAGAAGCTAAGGAGCC	339
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGGCTGCTGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT	399
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgile	100
Db	400	AGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGGATTTCGTGGTCACTCTTAGGATT	459
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTlpLysValProVal	120
Db	460	AGCCCAAAACCCCAAGTGTGGAAAAAATGGGTGGTGTCTTGATTGGAAGGTTCCAGTG	519
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTlpThrAsnSerCysile	140
Db	520	AGCCGACAGTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCAAT	579
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATTATCACCCAAAGATCCCATATTTCAACACTCAAACCTGCAACACAAACA	639
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTTATGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC	699
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuile	200
Db	700	CCTACTACTACTCCTCTCTCCAGTTCCTTCTATTCACGGAGAAAAAATTGATT	759
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal	220
Db	760	TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATTGTCTACAGAAACTGAACCATTTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGTTTGGAGGTGTCCCCACGGCTCTG	879
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGTGTGCTCTCCTCTTCTTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAA	939
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCCCTTCCCTTTTACAAAACAAGAAATCAGCAGAGGAAATGATCGAA	999
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluSerLysLysThr	300
Db	1000	AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCTTAATGAGGAATCAAGAAACT	1059
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAAACCCAGAAAGATCCAGAGTCCAAGCAAACTACCGTGGATGCCTGGAAGCT	1119
QY	321	GluVal 322	
Db	1120	GAAAGTT 1125	

DR WPI; 2003-328338/31.
DR P-PSDB; ABU71625.
XX
PT Isolated nucleic acid useful for e.g., treating pathological disorders
PT encodes a secreted or transmembrane protein.
XX
PS Claim 2; Fig 73; 473pp; English.
XX
CC The invention relates to human PRO polypeptides (secreted or
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC PRO polypeptides and polynucleotides can be used in treating pathological
CC disorders and tumours, in therapeutic treatment of cardiac insufficiency
CC disorders and in therapeutic treatment of disorders involving protein
CC secretion by the pancreas, including diabetes. They can also be used in
CC treating disorders associated with the preservation and maintenance of
CC gastrointestinal mucosa and the repair of acute and chronic mucosal
CC lesions, and skin diseases associated with abnormal keratinocyte
CC differentiation (e.g., psoriasis, epithelial cancers such as lung
CC squamous cell carcinoma, epidermoid carcinoma of the vulva and gliomas).
CC The sequences can be used as molecular markers for protein
CC electrophoresis purposes and can be utilised in protein-protein binding
CC assays, biochemical screening assays, immunoassays and cell-based assays.
CC This sequence represents a human PRO polynucleotide of the invention
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:
Pred. NO.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACA59060 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCTGGTGGTTGCTTCTCACATTCATCTGGACCACGAGGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279

QY 41 IleThrLeuValSerLysLysAlaAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTGGCCGGCAAGGACCAAGTTGAACAGCCTTGAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGGATTCTGGTTCATCTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAAATGGGTGGGTGTCCTGAATTGGAAAGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTTAACCTCGTGCAAT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTATTGTCAGTGACAGTACTACTCGTGGCATCCCTTACTCTACAATACCTGCC 699

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

Db 700 CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATGTATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db 760 TGTGTCACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 820 GAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCACGGCTCTG 879

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCTCTTCTTTTGGTGTCTGCAGCTGGTCTTGGATTTTGTATGTCAA 939

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC 999

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCTTAATGAGGAATCAAGAAAACT 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAAACTACCGTGCATGCGCTGGAAGCT 1119

QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 13
ACA58457
ID ACA58457 standard; cDNA; 2372 BP.
XX
AC ACA58457;
DT 10-JUN-2003 (first entry)
XX
DE cDNA encoding human PRO polypeptide #36.
KW Human; secreted and transmembrane protein; PRO polypeptide; cancer;
KW Alzheimer's disease; ischaemia; cytostatic; nootropic; vasotropic;
KW neuroprotective; gene; ss.
XX Homo sapiens.
XX US2002192659-A1.
PN
XX
PD 19-DEC-2002.
XX
PF 10-JUL-2001; 2001US-00902853.
XX
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.

PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
PA (GETH) GENENTECH INC.
XX

PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-361832/34.
DR P-PSDB; ABU71480.

XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or
PT PRO1868, useful in molecular biology, chromosome and gene mapping, in

PT
XX

generating antisense RNA and DNA, and in gene therapy.
Claim 2; Fig 73; 474pp; English.

CC The present invention relates to the isolation of novel human secreted
CC and transmembrane proteins (PRO polypeptides), and the polynucleotide
CC sequences encoding them. The polynucleotide sequences are useful in
CC molecular biology, as hybridisation probes, in chromosome and gene
CC mapping, in generating antisense RNA and DNA, and in gene therapy. The
CC polynucleotide sequences may also be used in preparing PRO polypeptides
CC by recombinant techniques, and in generating either transgenic animals or
CC knock-out animals which, in turn, are useful in the development and
CC screening of therapeutically useful reagents. The PRO polypeptides or
CC their antibodies are useful in preparing a medicament for treating a
CC condition responsive to the polypeptide or antibody, such as cancer,
CC Alzheimer's disease or ischaemia, and in various diagnostic assays. The
CC present sequence encodes a human PRO polypeptide of the invention

SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACA58457 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTCCATCTGGACCACGAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAGGCTCTTTGCGTGCAGAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTTCAGAAAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGGTCTATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTGGAAAGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCAAT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCCACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTCAGTGACAGTACCTACTCTCGTGGCATCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeulle 200
Db 700 CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db 760 TGTGTACACAGAAAGTTTTTATGAAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

CC PRO protein extracellular domain. Also included are a vector comprising
CC the PRO nucleic acid, a host cell comprising the vector, producing a PRO
CC polypeptide (by culturing the host cell for the expression of the PRO
CC polypeptide, and recovering the PRO polypeptide from the cell culture),
CC an isolated PRO polypeptide (having at least 80% sequence identity to: (a)
CC a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino
CC acid sequence encoded by a nucleic acid molecule deposited with an ATCC
CC number (detailed in the specification); or (c) an extracellular domain of
CC a PRO polypeptide or to a PRO polypeptide lacking its associated signal
CC peptide), a chimaeric molecule comprising a PRO polypeptide of fused to a
CC heterologous amino acid sequence, an anti-PRO antibody, detecting a
CC PRO245 or PRO1868 in a sample suspected of containing the polypeptide,
CC linking a bioactive molecule to a cell expressing a PRO245 or PRO1868 and
CC modulating at least one biological activity of a cell expressing a PRO245
CC or PRO1868. Nucleic acids which encode PRO can be used to generate either
CC transgenic animals or knock-out animals which may be used in the
CC development and screening of therapeutically useful reagents. The nucleic
CC acids may also be used in gene therapy, in chromosome identification, as
CC chromosome markers, or in generating probes. The PRO polypeptides are
CC useful as molecular markers for protein electrophoresis, and the isolated
CC nucleic acids may be used for recombinantly expressing those markers. The
CC PRO polypeptides and nucleic acids may also be used in tissue typing.
CC Anti-PRO antibodies are useful in diagnostic assays for PRO, and in
CC affinity purification of PRO from recombinant cell culture or natural
CC sources. The present sequence encodes a PRO protein
XX

SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACA60164 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCATCTGGACACAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAGAGCTTCCATCCAGGTGTCATGCAGAATTATGGGG 279
QY 41 ileThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAGCGAACCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCTCTGATTGGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTGGACTAACTCGTGCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCCACCAAGATCCCATATTCAACACTCAAACTGCAACACAACAACA 639
QY 161 GluPheIleValSerAspSerThrThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db 760 TGTGTACAGAAAGTTTATTGGAACCTAGCACCATTGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTCTGCTCTCTCTTTTGGTGTGCTGCAGCTGGTCTTGGATTCTGCTATGTCAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGGAGGCCAATGATAGCAACCTTAATGAGGAATCAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCAGAGAGTCCAAGAGTCCAAGAGTCCAAGCAAACTACCGTGGATGCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125
RESULT 15
ACD07564
ID ACD07564 standard; cDNA; 2372 BP.
XX
AC ACD07564;
XX
DT 07-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO263 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; pharmaceutical;
KW diagnostic; biosensor; bioreactor; Parkinson's disease;
KW Alzheimer's disease; inflammation; nephritis; wound healing;
KW nerve repair; collateral blood vessel formation; cancer;
KW colorectal cancer; haemorrhage; rheumatoid arthritis; diabetes;
KW cirrhosis; fibrosis; restenosis; dermal fibrotic condition; keloid;
KW scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis;
KW infertility; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002197671-A1.
XX
PD 26-DEC-2002.
XX
PF 17-JUL-2001; 2001US-00907824.
XX
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.

XX (GETH) GENENTECH INC.

PA Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;

PI Williams PM, Wood WI;
XX WPI; 2003-370793/35.
DR P-PSDB; ABO01809.
XX
PT New genes and secreted and transmembrane polypeptides (e.g. PRO245 or
PT PRO335), useful for treating or diagnosing e.g. Alzheimer's disease,
PT cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia
PT or strokes.
XX
PS Claim 2; Fig 73; 482pp; English.
XX
CC The invention describes a new isolated nucleic acid molecule comprising
CC the full length coding sequence of the DNA deposited with the American
CC Type Culture Collection (e.g. ATCC Deposit No. 209258) ,or a sequence
CC with at least 80% identity to a DNA encoding a PRO polypeptide comprising
CC any of 61 sequences having 164-1119 amino acids fully defined in the
CC specification. The PRO polypeptides or polynucleotides are useful as
CC pharmaceuticals, diagnostics, biosensors or bioreactors. These are
CC particularly useful for detecting or treating e.g. Parkinson's disease,
CC Alzheimer's disease, inflammations, nephritis, wound healing, nerve
CC repair, collateral blood vessel formation, cancers (e.g. colorectal
CC cancer), haemorrhage (or reduce risk for haemorrhage), rheumatoid
CC arthritis, diabetes, cirrhosis of the liver, fibrosis of the lungs,
CC restenosis, dermal fibrotic conditions (e.g. keloids or scarring),
CC ischaemia, strokes, hypertension, heart attacks, atherosclerosis, or
CC infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep,
CC pigs, goats, or rabbits) The PRO polypeptides are useful as targets for
CC therapeutic intervention in these diseases, and diagnostic determination
CC of the presence of these diseases. The PRO polypeptides are also useful
CC as molecular weight markers, or for chromosome identification. The PRO
CC genes are useful as hybridisation probes, or for screening libraries of
CC human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
CC therapy, particularly for replacing a defective gene. This sequence
CC encodes a novel human secreted and transmembrane PRO polypeptide
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACD07564 (1-2372)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCCAGGTGCTTCAGCCTGGTGTGTCTTCTCATTCCATCTGGACCACGAGGCTCCTG 219
Qy 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAGCGAACCCAGCAGCTGAATTCACAGAAGCTAAGGAGGCC 339
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 399
Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGATGGATGGATGGTGCATCTCTAGGATT 459
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCCTGATTGGAAGGTTCCAGTG 519
Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTGACGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAGAGTTTATGGAAGCTAGCACCATGTCTACAGAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTCAAGATGAAGCTGTGGGTTTGGAGGTGTCCCGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCTCTCTTTGGTGTGCTGAGCTGGTCTTGGATTTTGGCTATGTCAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAlaAsnAspSerAsnProAsnGluGluSerLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTCCGATGCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 16
ACA91166
ID ACA91166 standard; cdna; 2372 BP.
XX
AC ACA91166;
XX
DT 11-JUL-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO263 cdna.
XX
KW Human; secreted and transmembrane protein; PRO; antibody therapy;
KW pharmaceutical; diagnostic; biosensor; bioreactor; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003018173-A1.
XX
PD 23-JAN-2003.
XX
PF 01-MAY-2002; 2002US-00063515.
XX
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-401702/38.
DR P-PSDB; ABU90878.

XX
PT
PT
PT
PT
XX
PS
XX
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
XX
SQ

New antibody useful for identifying PRO polypeptides, for affinity purification of PRO polypeptides, and for preparing a medicament for diagnosing or treating conditions responsive to the antibody or PRO polypeptide.
Disclosure; Fig 5; 345pp; English.
The invention describes an antibody that specifically binds to a PRO polypeptide having a fully defined amino acid sequence given in the specification. The antibody is useful in identifying PRO polypeptides, useful for various industrial applications, including pharmaceuticals, diagnostics, biosensors and bioreactors. The antibody is also used for affinity purification of PRO polypeptides from recombinant cell culture or natural sources. The antibody, PRO polypeptide, or its agonists or antagonists, may be used for preparing a medicament for diagnosing or treating a condition responsive to the antibody, PRO polypeptide, or its agonists or antagonists. This sequence encodes a novel human secreted and transmembrane PRO polypeptide
Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACA91166 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTTCCTTCTCATTCCATCTGGACACGAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAGAGCTTTCATCCAGGTGTCTGCAGAAATTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTTCAGAAAGCTAAGGAGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgile 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCCAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCCTGATTGGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTACAACTCATCTGATACTTGGACTAACTCGTGCAATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTGACGTACCTACTCTCGTGGCATCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

Db 760 TGTGTACAGAAAGTTTTTATGGAACCTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGAGGTGTCCCCACGGCTCTG 879
Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTCTGCTCTCTCTTTGTTGGTGTGCAGCTGGTCTTGGAATTTTGCTATGTCAAA 939
Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAATGATCGAAACC 999
Qy 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAGGAGGAGGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT 1059
Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrValArgCysLeuGluAla 320
Db 1060 GATAAAAACCCAGAGAGTCCAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAAGCT 1119
Qy 321 GluVal 322
Db 1120 GAAGTT 1125
RESULT 17
ACD81543
ID ACD81543 standard; cDNA; 2372 BP.
XX
AC ACD81543;
XX
DT 18-SEP-2003 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO263.
KW Human; ss; gene; secreted/transmembrane protein; PRO; tumour; cancer;
KW cytostatic.
XX
OS Homo sapiens.
XX
PN US2003009013-A1.
XX
PD 09-JAN-2003.
XX
PF 01-MAY-2002; 2002US-00063519.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
XX (GETH) GENENTECH INC.
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-447384/42.
DR P-PSDB; ABO33937.
XX
PT New isolated antibody specifically binding a PRO polypeptide, useful for
PT the preparation of a medicament for treating disorders with the aberrant
PT expression or activity of the PRO polypeptide, such as tumor conditions
PT and cancer.
XX
PS Disclosure; Fig 5; 223pp; English.
XX
CC The invention relates to an antibody that binds to a secreted or
CC transmembrane protein designated PRO1446 appearing as ABO33941. The
CC protein is one of 84 PRO polypeptides which (along with their encoding
CC nucleic acids) are disclosed in the specification. The methods and
CC compositions of the present invention are useful for the preparation of a
CC medicament for the treatment of disorders associated with the aberrant
CC expression or activity of the PRO polypeptide, such as tumour conditions
CC and cancer. They can also be used to generate transgenic or knockout
CC animals useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides and encoding nucleic acids can be used as
CC molecular weight markers for protein electrophoresis, chromosome
CC identification and tissue typing. The antibodies may be used in various
CC diagnostic, competitive binding and/or immunoprecipitation assays. The
CC present sequence encodes a PRO polypeptide
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACD81543 (1-2372)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCATCTGGACCACGAGGCTCCTG 219
Qy 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGG 279
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTTGTGAGCAAAAGCGAACCCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 339
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTGGCCCGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 399
Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGATGGATTTCGTGGTCACTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
|||||

Db 460 AGCCCAAACCCCAAGTGTGGAAAAATGGGTGGTGTCTGATTTTGGAAGGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
|||||

Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCAAT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
|||||

Db 580 CCAGAAATTATCACCAAAAGATCCCATATTCAACACTCAAACCTGCAACAAACAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
|||||

Db 640 GAAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
|||||

Db 700 CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
|||||

Db 760 TGTGTACAGAAAGTTTATTGGAACCTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
|||||

Db 820 GAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTGTCACCGGCTCTG 879

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
|||||

Db 880 CTAGTGCTTGCTCTCTCTCTTCTTTGGTGCTGAGCTGGTCTTGGATTTTGCTATGTCAA 939

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
|||||

Db 940 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAAAGGAATGATCGAAACC 999

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
|||||

Db 1000 AAAGTAGTAAAGAGAGGAGAGGCCAATGATACCAACCCCTAATGAGGAATCAAAGAAACT 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
|||||

Db 1060 GATAAAACCCAGAGAGTCCAGAGTCCCAAGAGTCCCAAGCAAAACTACCGTGGATGCCTGGAAGCT 1119

QY 321 GluVal 322

Db 1120 GAAGTT 1125

RESULT 18
ACA60365
ID ACA60365 standard; cDNA; 2372 BP.
XX
AC ACA60365;
XX
DT 11-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO263 cDNA.
XX
KW Human; secreted and transmembrane polypeptide; gene;
KW ss. chromosome mapping; gene mapping; transgenic animal; knockout animal;
KW therapeutic agent screening; chromosome identification; tissue typing;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN US2003018183-A1.
XX
PD 23-JAN-2003.
XX
PF 01-MAY-2002; 2002US-00063512.
XX

PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-330984/31.
DR P-PSDB; ABU71954.
XX
PT New secreted and transmembrane PRO polypeptides and nucleic acid
PT molecules encoding the polypeptides, useful in gene therapy or preparing
PT a medicament for treating a condition that is responsive to the PRO
PT polypeptide or antibody.
XX
PS Disclosure; Fig 5; 409pp; English.
XX
CC The invention describes novel isolated PRO polypeptides. The PRO
CC polypeptides or anti-PRO antibodies are useful in preparing a medicament
CC for treating a condition that is responsive to the PRO polypeptide or
CC antibody. The PRO nucleotide sequences may be used as hybridisation
CC probes in chromosome and gene mapping, or in generating antisense RNA and
CC DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in
CC assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knockout animals, which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification, and tissue typing. The
CC PRO polypeptides and nucleic acid molecules are also useful in gene
CC therapy, and as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. This sequence encodes a novel human secreted
CC and transmembrane PRO polypeptide
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACA60365 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
|||||
Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTGTTGTTCTCTCACTTCCATCTGGACACGAGGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
|||||
Db 220 GTCCAAGGCTCTTTCGTGCAGAAAGAGCTTTCATCCAGGTGTCTATGCAGAAATTATGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuLeuAsnPheThrGluAlaLysGluAla 60
|||||
Db 280 ATCACCCCTGTGAGCAAAAGCGCAACCCAGCAGCTGAATTTTCACAGAAAGCTAAGGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
|||||
Db 340 TGTAGGCTGTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
|||||
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGTCATCTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
|||||
Db 460 AGCCCAAACCCCAAGTGTGGAAAAATGGGTGGTGTCTGATTTTGGAAGGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
|||||
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCAAT 579

QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160	PR	17-SEP-1997;	97US-0059121P.
Db	580	CCAGAAATTATCACCCACCAAGATCCCATATTCAACACTCAAACCTGCAACACACAACA	639	PR	17-SEP-1997;	97US-0059122P.
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180	PR	17-SEP-1997;	97US-0059184P.
Db	640	GAATTATTGTGAGTACAGTACCTACTCGTGGCATCCCTTACTCTACAATACCTGCC	699	PR	18-SEP-1997;	97US-0059263P.
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200	PR	18-SEP-1997;	97US-0059266P.
Db	700	CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	759	PR	15-OCT-1997;	97US-0062125P.
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220	PR	17-OCT-1997;	97US-0062285P.
Db	760	TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	819	PR	17-OCT-1997;	97US-0062287P.
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240	PR	21-OCT-1997;	97US-0063486P.
Db	820	GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG	879	PR	24-OCT-1997;	97US-0063486P.
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260	PR	24-OCT-1997;	97US-0063121P.
Db	880	CTAGTGTGCTCTCCTCTTCTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAAA	939	PR	24-OCT-1997;	97US-0063127P.
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280	PR	24-OCT-1997;	97US-0063128P.
Db	940	AGGTATGTGAAGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGAAATGATCGAAACC	999	PR	27-OCT-1997;	97US-0063327P.
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300	PR	27-OCT-1997;	97US-0063329P.
Db	1000	AAAGTAGTAAGGAGGAGGAGGCCCAATGATAGCAACCTATGAGGAATCAAAGAAACT	1059	PR	28-OCT-1997;	97US-0063541P.
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320	PR	28-OCT-1997;	97US-0063542P.
Db	1060	GATAAAACCCAGAGAGTCCAAGAGTCCAAGCTCCAAGCAAAACTACCGTCCGATGCCTGGAAGCT	1119	PR	28-OCT-1997;	97US-0063544P.
QY	321	GluVal 322		PR	28-OCT-1997;	97US-0063549P.
Db	1120	GAAGTT 1125		PR	28-OCT-1997;	97US-0063550P.
RESULT 19						97US-0063564P.
ABX71612						97US-0063735P.
ID	ABX71612 standard; cDNA; 2372 BP.					97US-0063738P.
XX						97US-0064215P.
AC	ABX71612;					97US-0063870P.
XX						97US-0064103P.
DT	10-MAR-2003 (first entry)					97US-0064248P.
XX						97US-0064809P.
DE	Human cDNA encoding secreted/transmembrane protein PRO263.					97US-0065186P.
XX						97US-0065846P.
KW	Human; PRO; secreted protein; transmembrane protein; enterocolitis;					97US-0065693P.
KW	gastrointestinal ulceration; skin disease; ss; gene;					97US-0066120P.
KW	abnormal keratinocyte differentiation; psoriasis; epithelial cancer;					97US-0066364P.
KW	squamous cell carcinoma; Alzheimer's disease; Parkinson's disease;					97US-0066453P.
KW	amyotrophic lateral sclerosis; inflammatory disease;					97US-0066511P.
KW	rheumatoid arthritis; asthma; multiple sclerosis; organ failure;					97US-0066770P.
KW	atherosclerosis; cardiac injury; infertility; birth defect;					97US-0066772P.
KW	premature aging; AIDS; acquired immunodeficiency syndrome; cancer;					97US-0066770P.
XX	diabetic complication; wound repair.					97US-0066772P.
OS	Homo sapiens.					97US-0066772P.
XX						97US-0066772P.
PN	US2002132240-A1.					97US-0066772P.
XX						97US-0066772P.
PD	19-SEP-2002.					97US-0066772P.
XX						97US-0066772P.
PF	18-JUL-2001; 2001US-00909320.					97US-0066772P.
XX						97US-0066772P.
PR	17-SEP-1997; 97US-0059113P.					97US-0066772P.
PR	17-SEP-1997; 97US-0059115P.					97US-0066772P.
PR	17-SEP-1997; 97US-0059117P.					97US-0066772P.
PR	17-SEP-1997; 97US-0059119P.					97US-0066772P.

PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-147434/14.
DR P-PSDB; ABU54382.
XX
PT New PRO polypeptides and nucleic acid molecules, useful in diagnosing or
PT treating inflammatory diseases, organ failure, atherosclerosis, cardiac
PT injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's
PT disease.
XX
PS Claim 2; Fig 73; 473pp; English.
XX
CC The invention relates to an isolated PRO polypeptide having at least 80%
CC amino acid sequence identity to: (a) any one of 61 fully defined amino
CC acid sequences given in the specification (appearing as ABU54347-
CC ABU54407); (b) an amino acid sequence encoded by the nucleotide sequence
CC deposited under American Type Culture Collection (accession numbers
CC listed in the specification); (c) any one of the PRO sequences which
CC lacks its associated signal peptide; (d) an extracellular domain of the
CC PRO polypeptide with its associated signal peptide; or (e) an
CC extracellular domain of the PRO polypeptide which lacks its associated
CC signal peptide. Also include are the nucleic acids encoding the PRO
CC polypeptides, vectors, host cells and anti-PRO antibodies. The PRO
CC polypeptides and nucleic acids are useful in diagnosing or treating
CC enterocolitis, gastrointestinal ulceration, skin diseases associated with
CC abnormal keratinocyte differentiation, e.g. psoriasis or epithelial
CC cancers such as squamous cell carcinoma, Alzheimer's disease, Parkinson's
CC disease, amyotrophic lateral sclerosis, inflammatory diseases, e.g.
CC rheumatoid arthritis, asthma or multiple sclerosis, organ failure,
CC atherosclerosis, cardiac injury, infertility, birth defects, premature
CC aging, AIDS, cancer, diabetic complications, or mutations in general. The
CC polypeptides are also useful for wound repair and associated therapies
CC concerned with re-growth of tissue. The nucleotide sequences may be used
CC as hybridisation probes in chromosome and gene mapping, or in generating
CC antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO
CC polypeptides, in assays to identify other proteins or molecules involved
CC in binding reaction, to generate transgenic animals or knockout animals,
CC which in turn are useful in the development and screening of
CC therapeutically useful reagents, for chromosome identification, and
CC tissue typing. The PRO polypeptides and nucleic acid molecules are also
CC useful in gene therapy, and as molecular weight markers for protein
CC electrophoresis purposes. The anti-PRO antibodies may be used in
CC diagnostic assays for PRO, or for the affinity purification of PRO from
CC recombinant cell culture or natural sources. The present sequence encodes
CC a PRO polypeptide
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0
US-10-079-111-1 (1-322) x ABX71612 (1-2372)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluSerIleGlnValSerCysArgIleMetGly 40

Db 220 GTCCAAGGCTCTTTTGGCTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTTCACAGAAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGGTGGAGATGGATTCTGTGTCATCTTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCCTGATTTGGAAGGTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAAGATCCCATATTCAACTCAAACTGCAACACAAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTGAGTGACAGTACCTACTCTCGTGGCATCCCTTACTCTACAATAACCTGCC 699
QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db 760 TGTGTACACAGAAGTTTATGGAAACTAGACCATGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCAACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTCTCTCTCTCTCTTTTGGTGTCTGCAGTGGTCTTGGATTTTGTCTATGTCAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAAACAAGAATCAGCAGAAGGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGGCGCAATGATAGCAACCTTAATGAGGAATCAAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAACCCAGAGAGTCCAGAGTCCAAAGCAAACTACCCGTGGATGCCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125
RESULT 20
ACH06944
ID ACH06944 standard; cDNA; 2372 BP.
XX
AC ACH06944;
XX
DT 08-OCT-2003 (first entry)
XX
DE Human secreted/transmembrane polypeptide PRO263 cDNA.
XX
KW Human; gene; ss; abnormal bleeding; gynaecological disease; asthma;

KW hysterectomy; angiogenesis; coronary ischaemic condition; skin disease;
KW gastrointestinal mucosa disorder; acute mucosal lesion; neuropathy; ALS;
KW chronic mucosal lesion; abnormal keratinocyte differentiation; psoriasis;
KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
KW uncontrolled cell growth; cancer; blood coagulation cascade; thrombosis;
KW haemorrhage; endometrial bleeding; angiogenesis; wound healing; tumour;
KW tissue repair; rheumatoid arthritis; multiple sclerosis; tissue typing.
XX
OS Homo sapiens.
XX
PN US2003044839-A1.
XX
PD 06-MAR-2003.
XX
PF 10-JUL-2001; 2001US-00902903.
XX
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
PA (GETH) GENENTECH INC.

Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
Williams PM, Wood WI;

WPI; 2003-492258/46.
P-PSDB; ABO47397.

Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating abnormal bleeding involved in gynecological diseases, skin diseases and neurodegenerative diseases.

Claim 3; Fig 73; 478pp; English.

The invention relates to an isolated PRO polypeptide. PRO317 is useful in diagnosing or treating abnormal bleeding involved in gynecological diseases e.g. to avoid or lessen the need for hysterectomy. PRO317 may also be useful as an agent that affects angiogenesis and PRO317 is useful in anti-tumour indications or in treating coronary ischaemic conditions. PRO211 and PRO217 polypeptides are useful for treating disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis). PRO187 polypeptide is useful for treating Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis (ALS), neuropathies and disease related to uncontrolled cell growth, e.g. cancer. PRO219 polypeptide plays a regulatory role in the blood coagulation cascade. PRO246 polypeptides which serves as tumour specific antigens may be exploited as therapeutic targets for anti-tumour drugs. PRO269 polypeptide is useful as an antithrombotic agent with reduced risk for haemorrhage as compared with heparin. PRO317 polypeptide is useful in treating endometrial bleeding angiogenesis. PRO287 polypeptides and portion have therapeutic applications in wound healing and tissue repair. PRO234 polypeptides are useful for treating asthma, rheumatoid arthritis, psoriasis and multiple sclerosis. The polypeptide and its nucleic acid

PA (GETH) GENENTECH INC.
XX Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX WPI; 2003-330485/31.
DR P-PSDB; ABU71508.
XX New isolated antibody specifically binding a PRO polypeptide, useful for
PT the preparation of a medicament for treating disorders with the aberrant
PT expression or activity of the PRO polypeptide, such as tumor conditions
PT and cancer.
XX Example 4; Page 69-70; 406pp; English.
XX The invention relates to an antibody that binds to a polypeptide with a
CC fully defined sequence given in the specification. The methods and
CC compositions (containing antibodies that specifically bind a PRO
CC polypeptide) of the present invention are useful for the preparation of a
CC medicament for the treatment of disorders associated with the aberrant
CC expression or activity of the PRO polypeptide, such as tumour conditions
CC and cancer. They can also be used to generate transgenic or knockout
CC animals useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides and encoding nucleic acids can be used as
CC molecular weight markers for protein electrophoresis, chromosome
CC identification and tissue typing. The PRO polypeptides are useful to
CC induce angiogenesis e.g wound healing; in the treatment of sports-related
CC joint problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The
CC antibodies may be used in various diagnostic, competitive binding and/or
CC immunoprecipitation assays. The present sequence represents a cDNA
CC encoding a PRO polypeptide of the invention
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACA58812 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db ATGGCCAGGTGCTTCAGCCTGGTGTCTCCTCCTCCATCCAGGCTGGACCCAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db GTCCAGGCTCTTTGCGTGCAGAGAGCTTCCATCCAGGTGTATGCAGAAATTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db ATCACCCCTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTTCACAGAAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db TGTAGGCTGCTGGGACTAAGTTTGGCGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
Db AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db AGCCCAAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCTGTATTTGGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db AGCCGACAGTTTGAGCCCTATTGTTACAACACTCATCTGATACTTGGACTAACTCGTGCATT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACATACCTGCC 699
QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db CCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db TGTGTACAGAGAGTTTATGGAACCTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db GAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db CTAGTGCTTGCTCTCTCTCTTTTGGTGCTGCAGCTGGTCTTTGGATTTTGTATGTCAAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGATCAGCAGAAGGAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db AAAGTAGTAAAGGAGGAGGAGGCCAATGATAGCAACCTTAATGAGGAATCAAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db GATAAAAACCCAGAGAGTCCAGAGTCCAAGAGTCCAAGCAAAACTACCGTCCGATGCTGGAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125
RESULT 22
ACA63988
ID ACA63988 standard; cDNA; 2372 BP.
XX AC ACA63988;
XX 16-JUN-2003 (first entry)
XX cDNA encoding human PRO polypeptide #3.
DE Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; gene; ss.
XX Homo sapiens.
OS US2002182638-A1.
PN 05-DEC-2002.
XX 02-MAY-2002; 2002US-00063547.
PD 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.


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PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005601.
PR 21-MAR-2000; 2000WO-US005841.
PR 22-MAY-2000; 2000WO-US007532.
PR 02-JUN-2000; 2000WO-US014042.
PR 22-AUG-2000; 2000WO-US015264.
PR 24-AUG-2000; 2000US-00644848.
PR 18-SEP-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH ) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CX, Wood WI;
XX
DR WPI; 2003-328612/04.
DR P-PSDB; ABU72289.
XX
PT An isolated secreted transmembrane polypeptide designated PRO, useful as
PT a therapeutic agent.
XX
PS Disclosure; Fig 5; 236pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the treatment of a condition responsive to anti-PRO antibody.
CC Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting
CC its expression in specific cells, tissues or serum, and for affinity
CC purification of PRO from recombinant cell culture or natural sources.
CC ACA63986-ACA64069 represent cDNA sequences encoding the human PRO
CC polypeptides of the invention
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0
US-10-079-111-1 (1-322) x ACA63988 (1-2372)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCCTGGTGTGTTCTTCACTTCATCTGGACCACGAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGGTGTCAGAAAGAGCTTTCCATCCAGGTGTATGCAGAATTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTTGTGAGCAAAAAGCGCAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGCC 339
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QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyYaspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTTCGTGGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAAATGGGGTGGTCTCTGATTTGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACATCATCTGATACTTGGACTTAACCTCGTGCA 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTCAGTGACAGTACCTACTCGTGGCATCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db 760 TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATATAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCGCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTGCTCTCCTCTCTTTGGTGCTGCAGCTGGTCTTGGATTGTCTATGTCAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAAATGATCGAAACC 999
QY 281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGGCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAACTACCGTGCATGCCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125
RESULT 23
ACA91252
ID ACA91252 standard; cDNA; 2372 BP.
XX
AC ACA91252;
XX
DT 14-JUL-2003 (first entry)
XX
DE cDNA encoding human PRO polypeptide #3.
XX
KW Human; PRO polypeptide; secreted protein; transmembrane protein; rectal;
KW lung; stomach; oesophageal; skin; tumour; cancer; cytostatic;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
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Claim 2; Fig 73; 477pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or polynucleotides are also useful as pharmaceuticals, diagnostics, biosensors or bioreactors, for detecting or treating e.g. hyperplasia, endometriosis, cancers (e.g. those involving solid tumours), ischaemia, coronary arterial disease, polycystic kidney disease, chronic or acute renal failure, or inflammatory responses (e.g. asthma, rheumatoid arthritis, psoriasis or multiple sclerosis) in mammals. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequences presented in ABX96017-ABX96378 are the genes encoding, the primers amplifying and the probes detecting the PRO polynucleotides of the invention.

SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.49e-304	Length:	2372
Score:	322.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	7	Gaps:	0

US-10-079-111-1 (1-322) x ABX96181 (1-2372)

QY	1	Met	Ala	Arg	Cys	Phe	Ser	Leu	Val	Leu	Leu	Leu	Thr	Ser	Ile	Trp	Thr	Thr	Arg	Leu	Leu	20
DB	160	ATG	GCC	AGG	TGCTT	CAG	CTGGT	TGCTT	CTC	ACTT	CCATCT	CGG	ACCAC	GAG	GCCT	CTG						219
QY	21	Val	Gln	Gly	Ser	Leu	Arg	Ala	Glu	Glu	Ser	Ile	Gln	Val	Ser	Cys	Arg	Ile	Met	Gly	40	
DB	220	GTCC	AAG	GCCTCTT	TTC	CGTGC	AGAC	AGCTT	TCC	ATCC	AGGTG	TCATG	CAG	AATAT	TATG	GGG					279	
QY	41	Ile	Thr	Leu	Val	Ser	Lys	Lys	Ala	Asn	Gln	Gln	Leu	Asn	Phe	Thr	Glu	Ala	Lys	Glu	Ala	60
DB	280	ATC	ACCC	TTGTG	AGCA	AAAG	CGAA	CGAAC	CAG	CAGCT	TGA	ATTTC	CAG	AAGCT	TAA	GAG	GCC				339	
QY	61	Cys	Arg	Leu	Leu	Gly	Leu	Ser	Leu	Ala	Gly	Lys	Asp	Gln	Val	Glu	Thr	Ala	Leu	Lys	Ala	80
DB	340	TGT	AGG	CTGCT	GGACT	TAAG	TTTGG	CCGG	CAAG	GACCA	AGTTG	AAAC	CAG	CTTGA	AAAG	CTT	GAAA	AGCT			399	
QY	81	Ser	Phe	Glu	Thr	Cys	Ser	Tyr	Gly	Trp	Val	Gly	Asp	Gly	Phe	Val	Val	Ile	Ser	Arg	Ile	100
DB	400	AGCT	TTGAA	ACTTGC	AGCTAT	GGCT	GGGTGG	AGAT	TGG	ATTC	GGTGC	ATCT	CTAG	GATT	CTCT	AGG	ATT				459	
QY	101	Ser	Pro	Asn	Pro	Lys	Cys	Gly	Lys	Asn	Gly	Val	Gly	Val	Leu	Ile	Trp	Lys	Val	Pro	Val	120
DB	460	AGC	CAA	AAC	CCCAAG	TGTGG	AAAAA	ATGG	GGTGG	TGCT	CTGATT	TGA	AAG	GTTC	CA	GTG					519	
QY	121	Ser	Arg	Gln	Phe	Ala	Ala	Tyr	Cys	Tyr	Asn	Ser	Ser	Asp	Thr	Trp	Thr	Asn	Ser	Cys	Ile	140
DB	520	AGC	CGA	CAG	TTTGC	AGC	TATG	TTACA	ACTCAT	CTG	ATAC	TCTTG	GA	CTAA	CTCG	TGC	ATT				579	
QY	141	Pro	Glu	Ile	Ile	Thr	Thr	Lys	Asp	Pro	Ile	Phe	Asn	Thr	Gln	Thr	Ala	Thr	Gln	Thr	Thr	160
DB	580	CCAG	AAAT	TAT	CAC	CAAC	CAAG	ATCC	CA	TAT	TCA	CAC	ACTCA	AACTG	CA	ACACA	CA	CA	CA	CA	CA	639
QY	161	Glu	Phe	Ile	Val	Ser	Asp	Ser	Thr	Tyr	Ser	Val	Ala	Ser	Pro	Tyr	Ser	Thr	Ile	Pro	Ala	180
DB	640	GAA	TTT	ATT	TGT	CAG	TGAC	AGT	ACCT	ACT	CGG	TGG	CATCCC	CTT	ACT	CT	CTA	CA	AT	AC	CT	699
QY	181	Pro	Thr	Thr	Thr	Pro	Pro	Ala	Pro	Ala	Ser	Thr	Ser	Ile	Pro	Arg	Arg	Lys	Lys	Leu	Ile	200
DB	700	CCT	ACT	ACT	ACT	CTCT	CTGCT	CC	AGCTT	CC	ACTT	CT	TAT	CC	ACG	GAG	AAAA	AAAT	TG	ATT		759
QY	201	Cys	Val	Thr	Glu	Val	Phe	Met	Glu	Thr	Ser	Thr	Met	Ser	Thr	Glu	Thr	Glu	Pro	Phe	Val	220
DB	760	TGT	GT	TC	AC	GAA	AGTTT	TAT	TG	GA	AACT	AG	CAC	CAT	GT	CT	AC	GAA	AACT	GA	AC	819

PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.

XX (GETH) GENENTECH INC.

PA Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
XX Filaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;

PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2003-331485/31.
DR P-PSDB; ABU67380.
XX
PT Sixty one isolated nucleic acids encoding a PRO polypeptide, e.g. PRO245
PT or PRO1868, useful in chromosome and gene mapping, in generating
PT antisense RNA and DNA, and in treating cancer and Alzheimer's disease.
XX
PS Example 33; Fig 73; 481pp; English.
XX
CC The invention relates to sixty one nucleic acids encoding PRO
CC polypeptides (secreted and transmembrane). The polynucleotide is useful
CC in molecular biology, including uses as hybridisation probes, in
CC chromosome and gene mapping, in generating antisense RNA and DNA, and in
CC gene therapy. The polynucleotide may also be used in preparing PRO
CC polypeptides by recombinant techniques, and in generating either
CC transgenic animals or knock-out animals which, in turn, are useful in the
CC development and screening of therapeutically useful reagents. The PRO
CC polypeptide or the antibody is used in preparing a medicament for
CC treating a condition responsive to the polypeptide or antibody, such as
CC mucosal lesions e.g. ulcers and enterocolitis, skin disease e.g.
CC psoriasis, cancer e.g. lung cancer and colon cancer, nerve cell disease
CC e.g. Alzheimer's disease and Parkinson's disease, Usher syndrome,
CC atrophial areata, angiogenesis, inflammatory disease e.g asthma and
CC rheumatoid arthritis, ischaemia, and in various diagnostic assays. The
CC present sequence represents an cDNA which encodes a PRO polypeptide
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACA05502 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCCAGGTGCTTCAGCCCTGGTGTGTCTTCTCATTCCATCTGGACCACGAGGTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAGGCTCTTTGCGTGCAGAGAGAGCTTTCATCCAGGTGTATGCAGATTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAGGCGAACCAGCAGCTGAATTCACAGAAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGCTGTGGGACTAAGTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGTGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCCAAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCTCTGATTGGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTATACAACTCATCTGATACCTTGGACTAAGTTCGTGCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCACCAAGATCCCATATATTCAACACTCAAACTGCAACACAAACAACA 639

Db	160	ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCATTCCATCTGACCAACGAGGCTCCTG	219
Qy	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	220	GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGG	279
Qy	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	280	ATCACCCCTTGTGAGCAAAAGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC	339
Qy	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAACACAGCCTTGAAAGCT	399
Qy	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	400	AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCTGTGTCATCTCTAGGATT	459
Qy	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	460	AGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTGGAAGGTTCCAGTG	519
Qy	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	520	AGCCGACAGTTTGCAGCCTATTGTACAACTCATCTGATACTTGGACTAACTCGTGCAATT	579
Qy	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATTATCACCCCAAGATCCCATATTCAACACTCAAACACTGCAACACAAACA	639
Qy	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTATTGTGAGTACAGTACAGTACCTACTCGGTGGCATCCCCCTACTCTACAATACCTGCC	699
Qy	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeulle	200
Db	700	CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATTGATT	759
Qy	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTCAAGAAAGTTTATGGAACACTAGCACCATTGTCTACAGAAACTGAACCAATTGTT	819
Qy	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG	879
Qy	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGTGCTCTCCTCTTCTTTTGGTGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAA	939
Qy	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCCCTTCCCCTTTTACAAACAAGAAATCAGCAGAGGAAATGATCGAAACC	999
Qy	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1000	AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT	1059
Qy	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAACCCAGAAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCTGGAAGCT	1119
Qy	321	GluVal	322
Db	1120	GAAGTT	1125
RESULT	28		
ACD20169			
ID	ACD20169	standard; cDNA; 2372 BP.	
XX			
AC	ACD20169;		
XX			

DT	25-AUG-2003	(first entry)	
XX			
DE		Human secreted / transmembrane polypeptide PRO263 cDNA.	
XX			
KW		Human; ss; gene; gene therapy; tumour; tissue typing; obesity; diabetes;	
KW		hypoinsulinaemia; hyperinsulinaemia; vascular permeability;	
KW		cardiac insufficiency disorder; immune response; regeneration; cartilage;	
KW		auditory hair cell; hearing loss; bone disorder; sports injury;	
KW		arthritis.	
XX			
OS		Homo sapiens.	
XX			
PN		US2003036060-A1.	
XX			
PD		20-FEB-2003.	
XX			
PF			
XX			
PR		12-JUL-2001; 2001US-00904859.	
PR			
PR		17-SEP-1997; 97US-0059113P.	
PR		17-SEP-1997; 97US-0059115P.	
PR		17-SEP-1997; 97US-0059117P.	
PR		17-SEP-1997; 97US-0059119P.	
PR		17-SEP-1997; 97US-0059121P.	
PR		17-SEP-1997; 97US-0059122P.	
PR		17-SEP-1997; 97US-0059184P.	
PR		18-SEP-1997; 97US-0059263P.	
PR		18-SEP-1997; 97US-0059266P.	
PR		15-OCT-1997; 97US-0062125P.	
PR		17-OCT-1997; 97US-0062285P.	
PR		17-OCT-1997; 97US-0062287P.	
PR		21-OCT-1997; 97US-0063486P.	
PR		24-OCT-1997; 97US-0062814P.	
PR		24-OCT-1997; 97US-0062816P.	
PR		24-OCT-1997; 97US-0063045P.	
PR		24-OCT-1997; 97US-0063120P.	
PR		24-OCT-1997; 97US-0063121P.	
PR		24-OCT-1997; 97US-0063127P.	
PR		24-OCT-1997; 97US-0063128P.	
PR		27-OCT-1997; 97US-0063327P.	
PR		27-OCT-1997; 97US-0063329P.	
PR		28-OCT-1997; 97US-0063541P.	
PR		28-OCT-1997; 97US-0063542P.	
PR		28-OCT-1997; 97US-0063544P.	
PR		28-OCT-1997; 97US-0063549P.	
PR		28-OCT-1997; 97US-0063550P.	
PR		28-OCT-1997; 97US-0063564P.	
PR		29-OCT-1997; 97US-0063435P.	
PR		29-OCT-1997; 97US-0063704P.	
PR		29-OCT-1997; 97US-0063732P.	
PR		29-OCT-1997; 97US-0063734P.	
PR		29-OCT-1997; 97US-0063735P.	
PR		29-OCT-1997; 97US-0063738P.	
PR		29-OCT-1997; 97US-0064215P.	
PR		31-OCT-1997; 97US-0063870P.	
PR		31-OCT-1997; 97US-0064103P.	
PR		03-NOV-1997; 97US-0064248P.	
PR		07-NOV-1997; 97US-0064809P.	
PR		12-NOV-1997; 97US-0065186P.	
PR		17-NOV-1997; 97US-0065846P.	
PR		18-NOV-1997; 97US-0065693P.	
PR		21-NOV-1997; 97US-0066120P.	
PR		21-NOV-1997; 97US-0066364P.	
PR		24-NOV-1997; 97US-0066453P.	
PR		24-NOV-1997; 97US-0066466P.	
PR		24-NOV-1997; 97US-0066511P.	
PR		24-NOV-1997; 97US-0066770P.	
PR		24-NOV-1997; 97US-0066772P.	
PR		25-NOV-1997; 97US-0066840P.	
PR		12-DEC-1997; 97US-0069425P.	
PR		04-JUN-1998; 98US-0088026P.	
PR		10-SEP-1998; 98US-0099803P.	
PR		10-SEP-1998; 98WO-US018824.	
PR		14-SEP-1998; 98US-0100262P.	

PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.

(GETH) GENENTECH INC.

PA Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
XX Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX

DR WPI; 2003-417923/39.
DR P-PSDB; ABO14900.

XX
PT Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.

XX Claim 2; Fig 73; 469pp; English.

XX The invention relates to an isolated, secreted and transmembrane
CC polypeptide, termed PRO polypeptide. The polypeptide is useful for
CC identifying agonists or antagonists of the polypeptide, for preparing
CC variants of the polypeptide, as molecular weight markers for protein
CC electrophoresis purpose and the nucleic acid is useful for recombinantly
CC expressing those markers. The polypeptide is also useful as therapeutic
CC agent. PRO is useful in assays to identify other proteins or molecules
CC involved in binding interaction. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, in generation of
CC antisense RNA and DNA, in the preparation of PRO polypeptide, for
CC generating transgenic animals or knockout animals which in turn are
CC useful in the development and screening of therapeutically useful
CC reagents, to construct hybridisation probes for mapping the gene which
CC encodes the PRO and for the genetic analysis of individuals with genetic
CC disorders, in gene therapy, for chromosome identification, as chromosome
CC marker, and for generating probes for polymerase chain reaction (PCR),
CC Northern analysis, Southern analysis and Western analysis. PRO antibody
CC is useful in diagnostic assays for PRO, e.g. detecting its expression in
CC specific cells, tissues or serum and for affinity purification of PRO

CC from recombinant cell culture or natural sources. The polypeptide or its
CC antibody is useful for the preparation of medicament for treating
CC conditions which is responsive to the PRO polypeptide or anti-PRO
CC antibody e.g. tumour. The polypeptide and the nucleic acid is useful for
CC tissue typing. The polypeptide is useful for treating obesity, diabetes
CC or hypo- or hyper-insulinaemia and cardiac insufficiency disorders, for
CC inhibiting tumour growth, enhances vascular permeability and immune
CC response, for inducing regeneration of auditory hair cells and for
CC treating hearing loss in mammals and for treating bone and/or cartilage
CC disorders such as sports injuries and arthritis. The present sequence
CC represents cDNA encoding a human secreted and transmembrane PRO
CC polypeptide

XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACD20169 (1-2372)

QY 1 MetAlaAArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20

Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTGTTCTTCATCTCCATCTGGACCCACGAGGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

Db 220 GTCCAAGGCTCTTTCGTGCAGAAAGAGCTTTCATCCAGGTGTCATGCAGAAATATGGGG 279

QY 41 IleThrLeuValSerLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60

Db 280 ATCACCCCTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

Db 340 TGTAGGCTGCTGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100

Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGTGGAGATGGATTTCGTGGTCACTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

Db 460 AGCCCAACCCCAAGTGTGGGAAAATGGGGTGGGTGTCCTGATTTGGAAAGGTTCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

Db 520 AGCCGACAGTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

Db 640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

Db 760 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATTGTCTACAGAAACTGAACCATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240

Db 820 GAAATAAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879

Db 640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAAATACCTGCC 699

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220

Db 760 TGTGTACAGAAAGTTTTATGGAAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240

Db 820 GAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrVallys 260

Db 880 CTAGTGCTTGCTCTCCTCTCTTTTGGTGTGCTGAGCTGGTCTTGGATTTTGGTATGTCAAA 939

QY 261 ArgTyrVallysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280

Db 940 AGGTATGTGAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAATGATCGAAACC 999

QY 281 LysValVallysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300

Db 1000 AAAGTAGTAAAGAGGAGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAAGAAACT 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320

Db 1060 GATAAAACCAGAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAAGCT 1119

QY 321 GluVal 322

Db 1120 GAAGTT 1125

RESULT 30

ACH66246

ID ACH66246 standard; cDNA; 2372 BP.

XX AC ACH66246;

XX DT 14-OCT-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO263 cDNA.

XX KW Human; secreted and transmembrane protein; PRO; gene; ss.

XX OS Homo sapiens.

XX PN US2003027986-A1.

XX PD 06-FEB-2003.

XX PF 02-MAY-2002; 2002US-00063549.

XX PR 30-DEC-1998; 98KR-00062142.

PR 08-MAR-1999; 99WO-US005028.

PR 14-MAY-1999; 99US-00311832.

PR 14-MAY-1999; 99WO-US010733.

PR 25-AUG-1999; 99US-00380137.

PR 25-AUG-1999; 99US-00380138.

PR 25-AUG-1999; 99US-00380139.

PR 25-AUG-1999; 99US-00380142.

PR 15-SEP-1999; 99US-00397342.

PR 18-OCT-1999; 99US-00403297.

PR 12-NOV-1999; 99US-00423844.

PR 30-DEC-1999; 99WO-US031274.

PR 18-FEB-2000; 2000WO-US004341.

PR 01-MAR-2000; 2000WO-US005601.

PR 02-MAR-2000; 2000WO-US005841.

PR 21-MAR-2000; 2000WO-US007532.

PR 22-MAY-2000; 2000WO-US014042.

PR 02-JUN-2000; 2000WO-US015264.

PR 22-AUG-2000; 2000US-00644848.

PR 24-AUG-2000; 2000WO-US023328.

PR 18-SEP-2000; 2000US-00664610.

PR 18-SEP-2000; 2000US-00665350.

PR 08-NOV-2000; 2000US-00709238.

PR 10-NOV-2000; 2000WO-US030873.

PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.

PR 20-DEC-2000; 2000WO-US034956.

PR 28-FEB-2001; 2001WO-US006520.

PR 22-MAR-2001; 2001US-00816744.

PR 10-MAY-2001; 2001US-00854208.

PR 10-MAY-2001; 2001US-00854280.

PR 30-MAY-2001; 2001US-00870574.

PR 01-JUN-2001; 2001WO-US017800.

PR 05-JUN-2001; 2001US-00874503.

PR 29-JUN-2001; 2001US-00869599.

PR 18-JUL-2001; 2001US-00908827.

PR 06-DEC-2001; 2001US-00006867.

XX (GETH) GENENTECH INC.

PA Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;

XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

DR WPI; 2003-456358/43.

DR P-PSDB; ABO53263.

XX PRO polypeptide, useful for preparing a medicament for treating a condition associated with PRO polypeptide.

XX Disclosure; Fig 5; 222pp; English.

CC The invention describes an isolated polypeptide having at least 80, 85, 90, 95 or 99% identity with: (a) a sequence having 46-335 amino acids, or its extracellular domain; (b) a sequence having 46-335 amino acids, CC lacking its associated signal peptide; or (c) an amino acid sequence CC encoded by the full-length coding sequence of the cDNA (ATCC accession CC number 209956). The PRO (secreted and transmembrane) polypeptide is CC useful for preparing a medicament for treating a condition associated CC with PRO polypeptide. This sequence encodes a novel human secreted and CC transmembrane PRO polypeptide

XX SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.49e-304 Length: 2372

Score: 322.00 Matches: 322

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACH66246 (1-2372)

QY 1 MetaAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20

Db 160 ATGCCAGGTGCTTCAGCCTGGTGTGTTCTCATTCCATCTGGACCACGAGGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

Db 220 GTCCAAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnLysLeuAsnPheThrGluAlaLysGluAla 60

Db 280 ATCACCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTCACAGAAGTAAGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

Db 340 TGTAGGCTGCTGGGACTAAGTTGGCCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

Db	400	AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGGTCATCTCTAGGATT	459
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	460	AGCCAAACCCCAAGTGTGGGAAAAATGGGTGGGTCTCTGATTGGGAAGGTTCAGTG	519
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	520	AGCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGGACTAACTCGTGCATT	579
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACA	639
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC	699
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	700	CCTACTACTACTCCTCTCTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	759
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu	240
Db	820	GAAATAAAGCAGCATTCAGAATGAAGCTGTGGGTGGAGGTGTCCCCACGGCTCTG	879
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGCTTGCTCTCCTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGTATGTCAAA	939
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAATGATCGAAACC	999
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluSerLysLysThr	300
Db	1000	AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCTTAATGAGGAATCAAAGAAAACT	1059
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAAAGCT	1119
QY	321	GluVal 322	
Db	1120	GAAGTT 1125	
RESULT 31			
ACD02300			
ID	ACD02300	standard; cDNA; 2372 BP.	
XX	XX		
AC	ACD02300;		
XX	XX		
XX	30-JUL-2003	(first entry)	
XX	XX		
DE	XX	Novel human secreted and transmembrane protein PRO263 cDNA.	
XX	XX		
KW	XX	Human; secreted and transmembrane protein; PRO; cytostatic; gene therapy;	
KW	XX	cancer; chromosome mapping; gene mapping; diagnostic; biosensor;	
KW	XX	bioreactor; gene; ss.	
XX	XX		
OS	XX	Homo sapiens.	
XX	XX		
PN	XX	US2002183493-A1.	
XX	XX		
PD	XX	05-DEC-2002.	
XX	XX		
PF	XX	02-MAY-2002; 2002US-00063530.	
XX	XX	30-DEC-1998; 98KR-00062142.	
PR	XX		

PT useful in gene therapy, for chromosome identification or for tissue
PT typing.

XX PS Disclosure; Fig 5; 235pp; English.

XX CC The invention describes an isolated polypeptide comprising 80 % amino
CC acid sequence identity with: (a) a sequence comprising 556 amino acids,
CC given in the specification, or its extracellular domain, with or without
CC its associated signal peptide; or (b) a sequence of a polypeptide encoded
CC by a full-length coding sequence of the cDNA deposited under American
CC Type Culture Collection (ATCC) accession number 209902. The new PRO
CC polypeptide or the nucleic acid encoding the PRO polypeptide is useful in
CC gene therapy, for chromosome identification or for tissue typing. This
CC sequence encodes a novel human secreted and transmembrane PRO polypeptide
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACA89291 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCAC TTCATCCATCTGGACCACGAGGCTCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAACCCCAAGTGTGGGAAAAATGGGTGGTGTCCTGATTGGAAAGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACA ACTCATCTGATACTTGGACTAACTCGTGCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTATTGTGAGTACAGTACCTACTCTCGTGGCATCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240

Db 820 GAAAAATAAGCAGCATTCAGAATGAAGCTGCTGGTTTGGAGGTGTCCCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrVallys 260
Db 880 CTAGTGCTTGCTCTCTCTCTTTTGGTGTGCAGCTGGTCTTGGATTTTGTATGTCAAA 939
QY 261 ArgTyrVallysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAATCAGCAGAAGAAATGATCGAAACC 999
QY 281 LysValVallysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCTTAATGAGGAATCAAAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125
RESULT 33
ACA68928
ID ACA68928 standard; cDNA; 2372 BP.
XX
AC ACA68928;
DT 26-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO263 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic;
KW immunotherapy; cancer; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002183494-A1.
XX
PD 05-DEC-2002.
XX
PF 02-MAY-2002; 2002US-00063551.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.

PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00909827.
PR 06-DEC-2001; 2001US-00006867.
XX (GETH) GENENTECH INC.
XX
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
XX WPI; 2003-340981/32.
DR P-PSDB; ABU82477.
XX
PT New antibody that specifically binds to a PRO polypeptide, useful in
PT preparing a medicament for treating a condition, e.g. cancer, responsive
PT to the antibody, and in diagnostic and purification assays for the PRO
PT polypeptide.
XX
PS Disclosure; Fig 5; 235pp; English.
XX
CC The invention describes an antibody that binds to a novel human secreted
CC and transmembrane PRO polypeptide. The antibody is useful in preparing a
CC medicament for treating a condition e.g. cancer. The antibody may also be
CC used in diagnostic assays for PRO polypeptide in specific cells, tissue
CC or serum, and in affinity purification of the polypeptide. This sequence
CC encodes a novel human secreted and transmembrane PRO polypeptide
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACA68928 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCAGGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGGGTGCAGAGAGCTTCCATCCAGGTGTCATGAGAATTATGGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTTGAGCAAAAAGGCGAACCCAGCAGCTGAATTCACAGAACTAAGGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCACTCTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCCAAACCCAAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTTCGAAGGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTriphThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACACTCATCTGATACTTGGACTAACTCGTGCATT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACACAACAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699

QY 181 ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAAAGTTTATTGGAACACTAGACCATGTCTACAGAAACTGACCATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTCTTGCCTCTCTCTTTTGGTGCTGCAGCTGGTCTTTGGATTTCGTATGTCAAA 939

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCTTCCCTTTTACAAAACAAGAATCAGCAGAAGGAATGATCGAAACC 999

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGGCGCAATGATAGTACCAACCTTAATGAGGAATCAAAAGAAACT 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTCCGATGCCTGGAAGCT 1119

QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 34
ACA54972
ID ACA54972 standard; cDNA; 2372 BP.
XX
AC ACA54972;
XX
DT 05-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO263 cDNA.
XX
KW Human; secreted and transmembrane protein; gene therapy; psoriasis;
KW enterocolitis; gastrointestinal ulceration; skin disease;
KW keratinocyte differentiation; epithelial cancer; Alzheimer's disease;
KW squamous cell carcinoma; Parkinson's disease; inflammatory disease;
KW amyotrophic lateral sclerosis; rheumatoid arthritis; asthma;
KW multiple sclerosis; organ failure; atherosclerosis; cardiac injury;
KW infertility; birth defect; premature aging; AIDS; cancer;
XX diabetic complication; wound repair; tissue re-growth; gene; ss.
OS Homo sapiens.
XX
PN US2003017463-A1.
XX
XX
PD 23-JAN-2003.
XX
XX 11-JUL-2001; 2001US-00903640.
PF
XX 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.

PR	15-OCT-1997;	97US-00621125P.	PR	24-FEB-2000; 2000WO-US005004.	
PR	17-OCT-1997;	97US-0062285P.	PR	02-MAR-2000; 2000WO-US005841.	
PR	17-OCT-1997;	97US-0062287P.	PR	20-MAR-2000; 2000WO-US007377.	
PR	21-OCT-1997;	97US-0063486P.	PR	30-MAR-2000; 2000WO-US008439.	
PR	24-OCT-1997;	97US-0062814P.	PR	22-MAY-2000; 2000WO-US014042.	
PR	24-OCT-1997;	97US-0062816P.	PR	02-JUN-2000; 2000WO-US015264.	
PR	24-OCT-1997;	97US-0063045P.	PR	28-JUL-2000; 2000WO-US020710.	
PR	24-OCT-1997;	97US-0063120P.	PR	24-AUG-2000; 2000WO-US023328.	
PR	24-OCT-1997;	97US-0063121P.	PR	18-SEP-2000; 2000US-00665350.	
PR	24-OCT-1997;	97US-0063127P.	XX		
PR	24-OCT-1997;	97US-0063128P.	PA	(GETH) GENENTECH INC.	
PR	27-OCT-1997;	97US-0063327P.	XX		
PR	27-OCT-1997;	97US-0063329P.	PI	Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;	
PR	28-OCT-1997;	97US-0063541P.	PI	Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;	
PR	28-OCT-1997;	97US-0063542P.	PI	Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;	
PR	28-OCT-1997;	97US-0063544P.	PI	Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;	
PR	28-OCT-1997;	97US-0063549P.	PI	Williams PM, Wood WI;	
PR	28-OCT-1997;	97US-0063550P.	XX		
PR	28-OCT-1997;	97US-0063564P.	DR	WPI; 2003-341586/32.	
PR	29-OCT-1997;	97US-0063435P.	DR	P-PSDB; ABU69657.	
PR	29-OCT-1997;	97US-0063704P.	XX		
PR	29-OCT-1997;	97US-0063732P.	PT	New PRO polypeptides and nucleic acid molecules, useful in diagnosing or	
PR	29-OCT-1997;	97US-0063734P.	PT	treating inflammatory diseases, organ failure, atherosclerosis, cardiac	
PR	29-OCT-1997;	97US-0063735P.	PT	injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's	
PR	29-OCT-1997;	97US-0063738P.	PT	disease.	
PR	29-OCT-1997;	97US-0064215P.	XX		
PR	31-OCT-1997;	97US-0063870P.	PS	Claim 2; Fig 73; 473pp; English.	
PR	31-OCT-1997;	97US-0064103P.	XX		
PR	03-NOV-1997;	97US-0064248P.	CC	The invention describes sixty one nucleic acids encoding PRO polypeptides	
PR	07-NOV-1997;	97US-0064809P.	CC	(secreted and transmembrane). The PRO polypeptides and nucleic acids are	
PR	12-NOV-1997;	97US-0065186P.	CC	useful in diagnosing or treating enterocolitis, gastrointestinal	
PR	17-NOV-1997;	97US-0065846P.	CC	ulceration, skin diseases associated with abnormal keratinocyte	
PR	18-NOV-1997;	97US-0065693P.	CC	differentiation, e.g. psoriasis or epithelial cancers such as squamous	
PR	21-NOV-1997;	97US-0066120P.	CC	cell carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic	
PR	21-NOV-1997;	97US-0066364P.	CC	lateral sclerosis, inflammatory diseases, e.g. rheumatoid arthritis,	
PR	24-NOV-1997;	97US-0066453P.	CC	asthma or multiple sclerosis, organ failure, atherosclerosis, cardiac	
PR	24-NOV-1997;	97US-0066466P.	CC	injury, infertility, birth defects, premature aging, AIDS, cancer,	
PR	24-NOV-1997;	97US-0066511P.	CC	diabetic complications, or mutations in general. The polypeptides are	
PR	24-NOV-1997;	97US-0066770P.	CC	also useful for wound repair and associated therapies concerned with re-	
PR	24-NOV-1997;	97US-0066772P.	CC	growth of tissue. The PRO polypeptides and nucleic acid molecules are	
PR	25-NOV-1997;	97US-0066840P.	CC	also useful in gene therapy, and as molecular weight markers for protein	
PR	12-DEC-1997;	97US-0069425P.	CC	electrophoresis purposes. The anti-PRO antibodies may be used in	
PR	04-JUN-1998;	98US-0088026P.	CC	diagnostic assays for PRO, or for the affinity purification of PRO from	
PR	10-SEP-1998;	98US-0099803P.	CC	recombinant cell culture or natural sources. This sequence encodes a	
PR	10-SEP-1998;	98WO-US018824.	CC	novel human PRO polypeptide	
PR	14-SEP-1998;	98US-0100262P.	XX		
PR	14-SEP-1998;	98WO-US019177.	SQ	Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;	
PR	16-SEP-1998;	98WO-US019330.			
PR	17-SEP-1998;	98US-0100858P.			
PR	17-SEP-1998;	98WO-US019437.			
PR	13-OCT-1998;	98US-0104080P.	Alignment Scores:		
PR	20-NOV-1998;	98US-0109304P.	Pred. No.:	1.49e-304	Length: 2372
PR	01-DEC-1998;	98WO-US025108.	Score:	322.00	Matches: 322
PR	22-DEC-1998;	98US-0113296P.	Percent Similarity:	100.00%	Conservative: 0
PR	07-JUL-1999;	99US-0143048P.	Best Local Similarity:	100.00%	Mismatches: 0
PR	26-JUL-1999;	99US-0145698P.	Query Match:	100.00%	Indels: 0
PR	28-JUL-1999;	99US-0146222P.	DB:	7	Gaps: 0
PR	08-SEP-1999;	99WO-US020594.			
PR	13-SEP-1999;	99WO-US020944.	US-10-079-111-1 (1-322) x ACA54972 (1-2372)		
PR	15-SEP-1999;	99WO-US021090.	Qy	1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20	
PR	15-SEP-1999;	99WO-US021547.	Db	160 ATGCCCAGGTGCTTCAGCCCTGGTGTGTTCTTCACTTCATCTGGACCACGAGGTCCTG 219	
PR	05-OCT-1999;	99WO-US023089.	Qy	21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40	
PR	29-NOV-1999;	99WO-US028214.	Db	220 GTCCAAGGCTCTTTGCGTGCGAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATATGGG 279	
PR	30-NOV-1999;	99WO-US028313.	Qy	41 IleThrLeuValSerLysLysAlaAAsnGlnGlnLeuAenPheThrGluAlaLysGluAla 60	
PR	01-DEC-1999;	99WO-US028301.	Db	280 ATCACCCCTTGTGAGCAAAAGCGGAACCAACGACGAGCTGAATTTACAGAAGCTAAGGAGCC 339	
PR	02-DEC-1999;	99WO-US028564.	Qy	61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80	
PR	16-DEC-1999;	99WO-US030095.	Db	340 TGTAGGCTGCTGGGACTTAAGTTTGGCCGGCAAGGACCAAGTTGAACAGCCTTGAAGCT 399	
PR	20-DEC-1999;	99WO-US030911.			
PR	20-DEC-1999;	99WO-US030999.			
PR	05-JAN-2000;	2000WO-US000219.			
PR	11-FEB-2000;	2000WO-US003565.			
PR	22-FEB-2000;	2000WO-US004414.			

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACITTCGAGCTATGGCTGGTTGGAGATGGATTCTGTGTCATCTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAACCCCAAGTGTGGAAAAATGGGTGGTGTCTGATTGGAGGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAAAGTTTTTATGGAACCTAGCACCATGTCTACAGAACTGAACCATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTCAGAATGAAGCTGTGGTTTGGAGGTGTCCCAACGGCTCTG 879

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCCTCTTCTTTGGTGTCTGCAGCTGGTCTTGGATTTTGTATGTCAA 939

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAGGCCTTCCCTTTTACAACAAGAATCAGCAGAGGAATGATCGAAACC 999

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAGGAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAAACT 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCAGAGAGAGTCCAAGAGTCCAAGCAAAAACCTACCGTGCATGCCTGGAAGCT 1119

QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 35
ACA98450
ID ACA98450 standard; cDNA; 2372 BP.
XX
AC ACA98450;
XX
DT 25-JUL-2003 (first entry)
XX
DE Human PRO polynucleotide #3.
XX
KW Human; PRO; gene; ss; affinity purification.
XX
OS Homo sapiens.
XX
PN US2003027993-A1.
XX
PD 06-FEB-2003.
XX
PF 02-MAY-2002; 2002US-00063537.
XX

PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
XX (GETH) GENENTECH INC.
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-417284/39.
DR P-PSDB; ABU96441.
XX
PT New anti-PRO antibody, useful in diagnostic assays for PRO polypeptide or
PT for affinity purification of PRO from the recombinant cell culture or
PT natural source.
XX
PS Disclosure; Fig 5; 236pp; English.
XX
CC The invention relates to an antibody which binds to a PRO polypeptide.
CC The antibody is useful in diagnostic assays for the PRO polypeptide or
CC for affinity purification of PRO from a recombinant cell culture or
CC natural source. Sequences ACA98448-ACA98531 represent cDNA molecules
CC encoding human PRO polypeptides of the invention
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACA98450 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCCAGGTGCTTCAGCTGGTGTCTCATTCCATCTGGACCACGAGGCTCCTG 219

Qy	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	220	GTCCAAAGGCTCTTTGCGTGCAGAAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGG	279
Qy	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	280	ATCACCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC	339
Qy	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAGCT	399
Qy	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	400	AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCATCTCTAGGATT	459
Qy	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	460	AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTGATTTGGAAGTTCCAGTG	519
Qy	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	520	AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGAAGTAACTCGTGCAAT	579
Qy	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATTATCACCCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA	639
Qy	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTTATTGTGAGTGACAGTACCTACTCGTGGCATCCCTTACTCTACAATACCTGCC	699
Qy	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	700	CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	759
Qy	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCAATTGTT	819
Qy	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAAAAATAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG	879
Qy	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGCTTGCTCTCCTCTCTTCTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA	939
Qy	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAATGATCGAAACC	999
Qy	281	LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1000	AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACT	1059
Qy	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTCCGATGCCTGGAAGCT	1119
Qy	321	GluVal	322
Db	1120	GAAAGTT	1125
RESULT	36		
ACA63375			
ID	ACA63375	standard; cDNA; 2372 BP.	
XX	ACA63375;		
AC			
XX			
DT	13-JUN-2003	(first entry)	
XX			

DE		cDNA encoding human PRO polypeptide #3.	
XX			
KW		Human; PRO polypeptide; secreted and transmembrane protein;	
KW		anti-PRO antibody; diagnostic assay; gene expression; gene; ss.	
OS		Homo sapiens.	
XX			
PN		US2003023042-A1.	
XX			
PD		30-JAN-2003.	
XX			
PF		01-MAY-2002; 2002US-00063502.	
XX			
PR		06-DEC-2001; 2001US-00006867.	
XX			
PA		(GETH) GENENTECH INC.	
XX			
PI		Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;	
PI		Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;	
XX			
DR		WPI; 2003-331484/31.	
DR		P-PSDB; ABU72111.	
XX			
PT		Novel monoclonal antibody that binds to secreted and transmembrane	
PT		polypeptide, useful for detecting and purifying the polypeptide and also	
PT		for treating conditions responsive to the antibody.	
XX			
PS		Disclosure; Fig 5; 408pp; English.	
XX			
CC		The present invention relates to the isolation of novel human PRO	
CC		polypeptides, and the polynucleotide sequences encoding them. The PRO	
CC		polypeptides are secreted and transmembrane proteins. The PRO	
CC		polypeptides and polynucleotides are useful for preparing a medicament	
CC		useful in the treatment of a condition responsive to anti-PRO antibody.	
CC		Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting	
CC		its expression in specific cells, tissues or serum, and for affinity	
CC		purification of PRO from recombinant cell culture or natural sources.	
CC		ACA63373-ACA63456 represent cDNA sequences encoding the human PRO	
CC		polypeptides of the invention	
XX			
SQ		Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;	
Alignment Scores:			
Pred. No.:	1-49e-304	Length:	2372
Score:	322.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0
US-10-079-111-1 (1-322) x ACA63375 (1-2372)			
QY	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu	20
Db	160	ATGGCCAGGTGCTTCAGCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGTCCTG	219
QY	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	220	GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG	279
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	280	ATCACCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC	339
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAGCT	399
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	400	AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTCACTCTAGGATT	459
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120

Db	460	AGCCCAACCCCAAGTGTGGAAAAATGGGTGGTGTCTGATTTCGAAGGTTCCAGTG	519
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	520	AGCCGACAGTTTGCAGCCTATTGTTACAACACTCATCTGATACTTGGACTAACTCGTGCATT	579
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATTATCACCAACAAGATCCCATATTCAACACTCAAACCTGCACACAACAACA	639
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTTATTGTAGTGACAGTACCTACTCGTGGCATCCCTTACTCTACAATACCTGCC	699
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	700	CCTACTACTACTCTCTCTGCTCCAGCTTCACATTCTATTCACGGAGAAAAAATTGATT	759
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal	220
Db	760	TGTGTACAGAAAGTTTTTATGGAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCACGGCTCTG	879
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGCTTGCTCTCCTCTTCTTTGGTGTGCAGCTGGTCTTGGATTTGCTATGTCAA	939
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGCCTTCCTTTTACAACAAGAATCAGCAGAAAGGAATGATCGAAACC	999
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1000	AAAGTAGTAAGGAGGAGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAANA	1059
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAACCCAGAAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCGTGAAGCT	1119
QY	321	GluVal 322	
Db	1120	GAAGTT 1125	
RESULT 37			
ACD19807			
ID	ACD19807 standard; cDNA; 2372 BP.		
XX			
AC	ACD19807;		
XX			
DT	22-AUG-2003 (first entry)		
XX			
DE	Human secreted / transmembrane polypeptide PRO263 cDNA.		
XX			
KW	Human; ss; gene; gene therapy; apoptosis; bleeding; tumour; ALS;		
KW	gynaecological disease; hysterectomy; angiogenesis; skin disease; cancer;		
KW	coronary ischaemic condition; gastrointestinal mucosa disorder; asthma;		
KW	mucosal lesion repair; keratinocyte differentiation; psoriasis;		
KW	Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;		
KW	neuropathy; blood coagulation cascade disorder; thrombosis; haemorrhage;		
KW	neurodegenerative disease; endometrial bleeding; wound healing;		
KW	tissue repair; rheumatoid arthritis; multiple sclerosis; tissue typing.		
OS	Homo sapiens.		
XX			
PN	US2003027143-A1.		
XX			
PD	06-FEB-2003.		
XX			
PF	16-JUL-2001; 2001US-00906838.		

XX	17-SEP-1997;	97US-0059113P.
PR	17-SEP-1997;	97US-0059115P.
PR	17-SEP-1997;	97US-0059117P.
PR	17-SEP-1997;	97US-0059119P.
PR	17-SEP-1997;	97US-0059121P.
PR	17-SEP-1997;	97US-0059122P.
PR	17-SEP-1997;	97US-0059184P.
PR	18-SEP-1997;	97US-0059263P.
PR	18-SEP-1997;	97US-0059266P.
PR	15-OCT-1997;	97US-0062125P.
PR	17-OCT-1997;	97US-0062285P.
PR	17-OCT-1997;	97US-0062287P.
PR	21-OCT-1997;	97US-0063486P.
PR	24-OCT-1997;	97US-0062814P.
PR	24-OCT-1997;	97US-0062816P.
PR	24-OCT-1997;	97US-0063045P.
PR	24-OCT-1997;	97US-0063120P.
PR	24-OCT-1997;	97US-0063121P.
PR	24-OCT-1997;	97US-0063127P.
PR	24-OCT-1997;	97US-0063128P.
PR	27-OCT-1997;	97US-0063327P.
PR	27-OCT-1997;	97US-0063329P.
PR	28-OCT-1997;	97US-0063541P.
PR	28-OCT-1997;	97US-0063542P.
PR	28-OCT-1997;	97US-0063544P.
PR	28-OCT-1997;	97US-0063549P.
PR	28-OCT-1997;	97US-0063550P.
PR	28-OCT-1997;	97US-0063564P.
PR	29-OCT-1997;	97US-0063435P.
PR	29-OCT-1997;	97US-0063704P.
PR	29-OCT-1997;	97US-0063732P.
PR	29-OCT-1997;	97US-0063734P.
PR	29-OCT-1997;	97US-0063735P.
PR	29-OCT-1997;	97US-0063738P.
PR	29-OCT-1997;	97US-0064215P.
PR	31-OCT-1997;	97US-0063870P.
PR	31-OCT-1997;	97US-0064103P.
PR	03-NOV-1997;	97US-0064248P.
PR	07-NOV-1997;	97US-0064809P.
PR	12-NOV-1997;	97US-0065186P.
PR	17-NOV-1997;	97US-0065846P.
PR	18-NOV-1997;	97US-0065693P.
PR	21-NOV-1997;	97US-0066120P.
PR	21-NOV-1997;	97US-0066364P.
PR	24-NOV-1997;	97US-0066453P.
PR	24-NOV-1997;	97US-0066466P.
PR	24-NOV-1997;	97US-0066511P.
PR	24-NOV-1997;	97US-0066770P.
PR	24-NOV-1997;	97US-0066772P.
PR	25-NOV-1997;	97US-0066840P.
PR	12-DEC-1997;	97US-0069425P.
PR	04-JUN-1998;	98US-0088026P.
PR	10-SEP-1998;	98US-0099803P.
PR	10-SEP-1998;	98WO-US018824.
PR	14-SEP-1998;	98US-0100262P.
PR	14-SEP-1998;	98WO-US019177.
PR	16-SEP-1998;	98WO-US019330.
PR	17-SEP-1998;	98US-0100858P.
PR	17-SEP-1998;	98WO-US019437.
PR	13-OCT-1998;	98US-0104080P.
PR	20-NOV-1998;	98US-0109304P.
PR	01-DEC-1998;	98WO-US025108.
PR	22-DEC-1998;	98US-0113296P.
PR	07-JUL-1999;	99US-0143048P.
PR	26-JUL-1999;	99US-0145698P.
PR	28-JUL-1999;	99US-0146222P.
PR	08-SEP-1999;	99WO-US020594.
PR	13-SEP-1999;	99WO-US020944.
PR	15-SEP-1999;	99WO-US021090.
PR	15-SEP-1999;	99WO-US021547.
PR	05-OCT-1999;	99WO-US023089.
PR	29-NOV-1999;	99WO-US028214.

PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-417249/39.
DR P-PSDB; AB014839.
XX
PT Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating abnormal bleeding involved in
PT gynecological diseases, skin diseases and neurodegenerative diseases.
XX
PS Claim 2; Fig 73; 467pp; English.
XX
CC The invention relates to an isolated secreted and transmembrane PRO
CC polypeptide. The PRO polypeptides are useful for modulating biological
CC activity of a cell, in diagnosing or treating abnormal bleeding involved
CC in gynaecological diseases e.g. to avoid or lessen the need for
CC hysterectomy, for treating angiogenesis, tumour, coronary ischaemic
CC condition, disorders associated with the preservation and maintenance of
CC gastrointestinal mucosa and the repair of acute and chronic mucosal
CC lesions, skin diseases associated with abnormal keratinocyte
CC differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's
CC disease, amyotrophic lateral sclerosis (ALS), neuropathies, disease
CC related to uncontrolled cell growth (e.g. cancer), blood coagulation
CC cascade disorders, neurodegenerative disease, thrombosis, haemorrhage,
CC endometrial bleeding, wound healing, tissue repair, asthma, rheumatoid
CC arthritis, multiple sclerosis. Nucleic acid encoding PRO polypeptides are
CC useful in molecular biology including uses as hybridisation probes and in
CC the generation of antisense RNA and DNA, for preparing PRO polypeptides,
CC for generating transgenic animals or knockout animals. The PRO
CC polypeptides and their nucleic acids are useful for tissue typing. PRO
CC antibodies are useful for immunohistochemical staining and/or assay of
CC sample fluids. Anti-PRO antibodies are useful in diagnostic assays for
CC PRO e.g. detecting its expression in specific cells, tissues or serum and
CC for affinity purification of PRO from recombinant cell culture or natural
CC sources. The present sequence represents cDNA encoding a human secreted
CC and transmembrane PRO polypeptide
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-079-111-1 (1-322) x ACD19807 (1-2372)

Qy	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu	20
Db	160	ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCATCTGGACCACGAGGCTCCTG	219
Qy	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	220	GTCCAAGGCTCTTTGCGTGAGAAAGAGCTTTCATCCAGTGTCATGCAGAAATTATGGGG	279
Qy	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	280	ATCACCCCTTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTACAGAAGCTAAGGAGCC	339
Qy	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGACCAGTTGAAACAGCCTTGAAAGCT	399
Qy	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	400	AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCTCTAGGATT	459
Qy	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	460	AGCCCAAAACCCCAAGTGTGGAAAAAATGGGTGGTGTCTGTATTTGGAAGGTTCCAGTG	519
Qy	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerSerAspThrTrpThrAsnSerCysIle	140
Db	520	AGCGGACAGTTTGCAGCCCTATTGTTACAACCTCATCTGTACTTGGACTAACTCGTGCAIT	579
Qy	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATTATCACCCACCAAGATCCCATATTCAACACTCAAACTGCAACACAACAACA	639
Qy	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	699
Qy	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	700	CCTACTACTCTCCTCCTGCCAGCTTCCACTTCTATTTCACGGAGAAAAAATTGATT	759
Qy	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTCACAGAAGTTTTTATGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	819
Qy	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG	879
Qy	241	LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTGGTCTTTGGATTGTGCAAA	939
Qy	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCCCTTCCTTTTACAACAAGAATCAGCAGAAGGAATGATCGAAACC	999
Qy	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1000	AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACT	1059
Qy	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAAGCT	1119
Qy	321	GluVal 322	
Db	1120	GAAGTT 1125	
RESULT 38			
ADB29405			
ID ADB29405 standard; cDNA; 2372 BP.			
XX			

AC ADB29405;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted/transmembrane protein cDNA, #40.
XX
KW Human; gene; ss; PRO; secreted; transmembrane; gastrointestinal mucosa;
KW mucosal lesion; skin disease; keratinocyte differentiation; psoriasis;
KW Parkinson's disease; Alzheimer's diseases; amyotrophic lateral sclerosis;
KW ALS; neuropathy; cell growth; cancer; tumour; viral infection;
KW neurodegenerative disease; antithrombotic agent; haemorrhage;
KW endometrial bleeding angiogenesis; kidney tissue; apoptosis; therapeutic;
KW tissue typing; immunohistochemical staining; gene therapy; nootropic;
KW neuroprotective; cytostatic; virucide; anticoagulant.
XX
OS Homo sapiens.
XX
PN US2003092002-A1.
XX
PD 15-MAY-2003.
XX
PF 10-JUL-2001; 2001US-00902615.
XX
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
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PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.

PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005044.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX

(GETH) GENENTECH INC.

Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
Williams PM, Wood WI;

WPI; 2003-765473/72.
P-PSDB; ADB29406.

Novel isolated native PRO polypeptide useful for treating Parkinson's disease, enterocolitis, Zollinger-Ellison syndrome gastrointestinal ulceration, Alzheimer's disease, amyotrophic lateral sclerosis, Usher syndrome.

Claim 2; Fig 73; 469pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. PRO polypeptides are useful for detecting other PRO polypeptides in a sample and for linking a bioactive molecule to a cell expressing a PRO polypeptide. The PRO polypeptide antibodies are useful for modulating the biological activity of a cell expressing PRO polypeptides. PRO polypeptides are also useful for treating disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's

PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX

(GETH) GENENTECH INC.

PA Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
PI

XX WPI; 2003-521820/49.
DR P-PSDB; ADB17063.
DR

XX
PT New secreted and transmembrane PRO polypeptide, useful for preparing a
PT composition for diagnosing or treating cancer and as a molecular weight
PT marker.

XX
PS Disclosure; Fig 5; 235pp; English.

XX
CC This invention relates to a novel isolated and secreted PRO polypeptide.
CC PRO is a transmembrane protein involved in the formation, differentiation
CC and maintenance of multicellular organisms, and more particularly the
CC proliferation, differentiation and migration of individual cells. The
CC invention describes screening compounds to identify PRO polypeptide
CC agonists and antagonists, anti-PRO antibodies, and immunoconjugates
CC comprising an antibody conjugated to a cytotoxic agent. Specifically, the
CC heterologous protein of the chimeric polypeptide is an epitope tag or an
CC Fc region of an immunoglobulin. Through the use of gene therapy, the PRO
CC polypeptide is useful for preparing cytostatic compositions for
CC diagnosing or treating cancer. The polypeptide is also useful as a
CC molecular weight marker for protein electrophoresis purposes. This
CC polynucleotide sequence is a native cDNA clone that encodes human PRO
CC polypeptide, found in the cDNA library of the invention.

XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-079-111-1 (1-322) x ADB17062 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTCCATCTGGACCAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
XX

Db 220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTACAGAGAGCTAAGGAGCC 339
QY 61 CysArgLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAGTTGAAACAGCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAACCCCAAGTGTGGGAAAAAATGGGGTGGGTGCTCTGATTGGAAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACCTTGGACTAACTCGTGCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCCAAAGATCCCATATTTCAACACTCAAACTGCAACACAAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTTATTGTCAGTGACAGTACCTACTCGTGGGCATCCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAAAGTTTTTATGGAACCTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTCTGCTCTCCTCTTTCTTTGGTGTGCTGCAGCTGGTCTTTGGATTGTGCTATGTCAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAACCCAGAAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125
RESULT 40
ACH03578
ID ACH03578 standard; cDNA; 2372 BP.
XX
AC ACH03578;
XX
DT 26-SEP-2003 (first entry)
XX
DE Human secreted/transmembrane polypeptide PRO 263 cDNA.
XX
KW Human; ss; tumour; cancer; tissue typing; gene.

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xx OS Homo sapiens.
xx XX US2003018172-A1.
xx PN
xx XX
xx PD 23-JAN-2003.
xx XX
xx PF 01-MAY-2002; 2002US-00063513.
xx XX
xx PR 06-DEC-2001; 2001US-00006867.
xx XX (GETH ) GENENTECH INC.
xx PA
xx PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
xx PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
xx XX
xx DR WPI; 2003-479475/45.
xx DR P-PSDB; ABO44241.
xx XX
xx PT Isolated antibody specifically binding a PRO polypeptide, useful for the
xx PT diagnosis and treatment of disorders with the aberrant expression or
xx PT activity of the PRO polypeptide, such as tumor conditions and cancer.
xx PS Disclosure; Fig 5; 409pp; English.
xx XX
xx CC The invention relates to an antibody that binds to a fully defined PRO
xx CC polypeptide. The antibody is useful for the diagnosis, prevention and/or
xx CC treatment of disorders associated with the aberrant expression or
xx CC activity of the PRO polypeptide, such as tumour conditions and cancer.
xx CC They can also be used to generate transgenic or knockout animals useful
xx CC in the development and screening of therapeutically useful reagents. The
xx CC PRO polypeptides and encoding nucleic acids can be used as molecular
xx CC weight markers for protein electrophoresis, chromosome identification and
xx CC tissue typing. The antibodies may be used in various diagnostic,
xx CC competitive binding and/or immunoprecipitation assays. The present
xx CC sequence represents cDNA encoding a human secreted and transmembrane PRO
xx CC polypeptide
xx XX
xx SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-079-111-1 (1-322) x ACH03578 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCTGGTGTGCTTCTCACATTCATCTGGACCACGAGGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTCCATCCAGGTGTCATGCAGAAATTATGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAGGCGAACCCAGCAGCTGTAATTTCACAGAAAGCTAAGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTGGCCGGCAAGGACCAGTGTGAACAGCCTTGAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATTGGATTGCTGGTCTATCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAACCCCAAGTGTGGGAAAAAATGGGGTGGGTGCTCTGATTTTGGAAGGTTCCAGTG 519
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QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAATCGTGCATT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAACAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCTCTCTCTTTTGGTGTGCAGCTGGTCTTGGATTTTGGTATGTCAA 939

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAATGATCGAAACC 999

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGGAGGAGGCAATGATAGCAACCTAATGAGGAATCAAAGAAACT 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAACCCAGAGAGTCCCAAGAGTCCAAGCAAAACTACCGTGCATGCGTGAAGCT 1119

QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 41
ADA18261
ID ADA18261 standard; cDNA; 2372 BP.
XX
AC ADA18261;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted/transmembrane protein cDNA, #40.
XX
KW Human; gene; ss; PRO; secreted; transmembrane; gastrointestinal mucosa;
KW mucosal lesion; skin disease; keratinocyte differentiation; psoriasis;
KW Parkinson's disease; Alzheimer's diseases; amyotrophic lateral sclerosis;
KW ALS; neuropathy; cell growth; cancer; tumour; viral infection;
KW neurodegenerative disease; antithrombotic agent; haemorrhage;
KW endometrial bleeding angiogenesis; kidney tissue; apoptosis; therapeutic;
KW tissue typing; immunohistochemical staining; gene therapy; neurotropic;
KW neuroprotective; cytostatic; virucide; anticoagulant.
XX
OS Homo sapiens.
XX
PN US2003039971-A1.
XX
PD 27-FEB-2003.
XX
PF 16-JUL-2001; 2001US-00906646.
XX
PR 17-SEP-1997; 97US-0059113P.
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PR 17-SEP-1997; 97US-00591115P.
PR 17-SEP-1997; 97US-00591117P.
PR 17-SEP-1997; 97US-00591119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 15-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
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PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
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PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.

PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-503392/47.
DR P-PSDB; ADA18262.
XX
PT New secreted and transmembrane polypeptides useful for treating skin,
PT neurodegenerative diseases, asthma, rheumatoid arthritis, psoriasis and
PT multiple sclerosis.
XX
PS Claim 2; SEQ ID NO 200; 471pp; English.
XX
CC The invention discloses isolated PRO secreted/transmembrane polypeptides
CC and the nucleic acid encoding them. The polypeptides can be used to raise
CC antibodies that specifically bind to the PRO polypeptide, for linking a
CC bioactive molecule to a cell expressing a PRO protein and for modulating
CC at least one biological activity of a cell. PRO polypeptides are useful
CC for detecting other PRO polypeptides in a sample and for linking a
CC bioactive molecule to a cell expressing a PRO polypeptide. The PRO
CC polypeptide antibodies are useful for modulating the biological activity
CC of a cell expressing PRO polypeptides. PRO polypeptides are also useful
CC for treating disorders associated with the preservation and maintenance
CC of gastrointestinal mucosa and the repair of acute and chronic mucosal
CC lesions, skin diseases associated with abnormal keratinocyte
CC differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's
CC diseases, amyotrophic lateral sclerosis (ALS), neuropathies and
CC additionally, disease related to uncontrolled cell growth, e.g. cancer.
CC PRO polypeptides also serves as tumour specific antigens which may be
CC exploited as therapeutic targets for anti-tumour drugs, and are also
CC employed therapeutically in vivo for lessening the effects of viral
CC infection. The PRO polypeptides can be also used in assays to determine
CC if it has a role in neurodegenerative diseases or their reversal, as an
CC antithrombotic agent with reduced risk for haemorrhage as compared with
CC heparin, in treating other PRO-associated disorders, in modulating
CC endometrial bleeding angiogenesis, and may also have an effect on kidney
CC tissue. PRO polypeptides and their portions affect the expression of
CC genes which have a role in apoptosis. The polynucleotides are useful in
CC molecular biology including uses as hybridisation probes for cDNA library
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC for preparing PRO polypeptides, for generating transgenic animals or
CC knockout animals which are useful in the development and screening of
CC therapeutically useful reagents, as probes and for the genetic analysis
CC of individuals with genetic disorders as well as for recombinantly
CC expressing the protein and for chromosome identification. The proteins
CC are useful as molecular marker for protein electrophoresis purposes, as
CC therapeutic agents, for screening compounds to identify those that mimic
CC the PRO polypeptide (agonists) or prevent the effect of the PRO
CC polypeptide (antagonists). The polynucleotides and proteins are useful
CC for tissue typing. PRO antibodies are useful for immunohistochemical

CC staining and/or assay of sample fluids. Anti-PRO antibodies are useful in
CC diagnostic assays for PRO e.g. detecting its expression in specific
CC cells, tissues or serum and for affinity purification of PRO from
CC recombinant cell culture or natural sources. The PRO genes may also be
CC used in gene therapy, particularly for replacing a defective gene. The
CC sequence presented is a gene encoding a PRO polynucleotide of the
CC invention.

XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-079-111-1 (1-322) x ADA18261 (1-2372)

QY	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu	20
Db	160	ATGCCCAGGTGCTTCAGCCTGGTGTGCTTCTCACATCCATCTGGACCACGAGGCTCCTG	219
QY	21	ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	220	GTCCAAGGCTCTTTGCGTGCAAGAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG	279
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	280	ATCACCCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC	339
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT	399
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	400	AGCTTTGAAACTTGCAGCTATGGCTGGTGGATGGATCGTGGTCATCTCTAGGATT	459
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	460	AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTGATTTGGAAGGTTCCAGTG	519
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	520	AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCAAT	579
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA	639
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTATTGTGTCAGTGACAGTACCTACTCGTGGCATCCCTTACTCTACAATACCTGCC	699
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	700	CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	759
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTACAGAAAGTTTTTATGGAAAACCTAGCACCATGTCTACAGAAAACCTGAACCATTTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG	879
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGCTTGCTCTCCTCTTCTTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAA	939
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280

Db	940	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAAATGATCGAAACC	999
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1000	AAAGTAGTAAAGGAGGAGGAGGCAATGATGACCAACCTTAATGAGGAATCAAGGAAACT	1059
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAGCT	1119
QY	321	GluVal	322
Db	1120	GAAATT	1125
RESULT 42			
ID	ACD66954	standard; cDNA; 2372 BP.	
XX	AC	ACD66954;	
XX	DT	17-SEP-2003 (first entry)	
XX	DE	Human cDNA encoding secreted/transmembrane protein PRO263.	
XX	XX	Human; ss; gene; PRO; secreted and transmembrane protein; inflammation;	
KW	KW	rheumatoid arthritis; psoriasis; multiple sclerosis; atherosclerosis;	
KW	KW	infertility; birth defect; premature aging; malignancy; cancer; stroke;	
KW	KW	heart attack; hypertension; gastrointestinal ulceration;	
KW	KW	Parkinson's disease; Alzheimer's disease; AIDS; cholesterol uptake;	
KW	KW	wound healing; tissue repair; gene therapy.	
OS	XX	Homo sapiens.	
XX	PN	US2003045693-A1.	
XX	PD	06-MAR-2003.	
XX	PF	11-JUL-2001; 2001US-00903749.	
XX	PR	17-SEP-1997; 97US-0059113P.	
PR	PR	17-SEP-1997; 97US-0059115P.	
PR	PR	17-SEP-1997; 97US-0059117P.	
PR	PR	17-SEP-1997; 97US-0059119P.	
PR	PR	17-SEP-1997; 97US-0059121P.	
PR	PR	17-SEP-1997; 97US-0059122P.	
PR	PR	17-SEP-1997; 97US-0059184P.	
PR	PR	18-SEP-1997; 97US-0059263P.	
PR	PR	18-SEP-1997; 97US-0059266P.	
PR	PR	15-OCT-1997; 97US-0062125P.	
PR	PR	17-OCT-1997; 97US-0062285P.	
PR	PR	17-OCT-1997; 97US-0062287P.	
PR	PR	21-OCT-1997; 97US-0063486P.	
PR	PR	24-OCT-1997; 97US-0062814P.	
PR	PR	24-OCT-1997; 97US-0062816P.	
PR	PR	24-OCT-1997; 97US-0063045P.	
PR	PR	24-OCT-1997; 97US-0063120P.	
PR	PR	24-OCT-1997; 97US-0063121P.	
PR	PR	24-OCT-1997; 97US-0063127P.	
PR	PR	24-OCT-1997; 97US-0063128P.	
PR	PR	27-OCT-1997; 97US-0063327P.	
PR	PR	27-OCT-1997; 97US-0063329P.	
PR	PR	28-OCT-1997; 97US-0063541P.	
PR	PR	28-OCT-1997; 97US-0063542P.	
PR	PR	28-OCT-1997; 97US-0063544P.	
PR	PR	28-OCT-1997; 97US-0063549P.	
PR	PR	28-OCT-1997; 97US-0063550P.	
PR	PR	28-OCT-1997; 97US-0063564P.	
PR	PR	29-OCT-1997; 97US-0063435P.	
PR	PR	29-OCT-1997; 97US-0063704P.	
PR	PR	29-OCT-1997; 97US-0063732P.	
PR	PR	29-OCT-1997; 97US-0063734P.	
PR	PR	29-OCT-1997; 97US-0063735P.	

PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-512316/48.
DR P-PSDB; ABO32791.
XX
PT New genes and secreted and transmembrane polypeptides (e.g. PRO245 or
PT PRO1868), useful for treating or diagnosing e.g. cancers,
PT atherosclerosis, infertility, stroke, AIDS or multiple sclerosis in

PT mammals.
XX
PS Claim 2; Fig 73; 476pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule comprising a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 61 PRO (secreted and transmembrane protein) polypeptides appearing as
CC ABO32756-ABO32816; or (b) any of 61 nucleotide sequences having 50-4053bp
CC fully defined in the specification; or the full length coding sequence of
CC any these 61 nucleotide sequences. Also included are the isolated PRO
CC polypeptide (lacking its associated signal peptide or an extracellular
CC domain of the PRO polypeptide, with or lacking its associated signal
CC peptide), a vector comprising the nucleic acid molecule, a host cell
CC comprising the vector (used to produce the PRO polypeptide), a chimaeric
CC molecule comprising the PRO polypeptide fused to a heterologous amino
CC acid sequence, an anti-PRO antibody, detecting PRO245 or PRO1868
CC polypeptide in a sample suspected of containing any of these PRO
CC polypeptides, linking a bioactive molecule to a cell expressing a PRO245
CC or PRO1868 polypeptide and modulating at least one biological activity of
CC a cell expressing the PRO245 or PRO1868 polypeptide. The PRO polypeptides
CC or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors
CC or bioreactors. These are particularly useful for diagnosing or treating
CC e.g. inflammations, rheumatoid arthritis, psoriasis, multiple sclerosis,
CC atherosclerosis, infertility, birth defects, premature aging, malignancy
CC (e.g. cancers), strokes, heart attacks, hypertension, gastrointestinal
CC ulcerations, Parkinson's diseases, Alzheimer's disease, or AIDS in
CC mammals. These are also useful for modulating cholesterol uptake in the
CC body, and in wound healing or tissue repair. The PRO polypeptides are
CC useful in drug screening. The PRO polypeptides are also useful as
CC molecular weight markers, or for chromosome identification. The PRO genes
CC are useful as hybridisation probes, or for screening libraries of human
CC cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
CC therapy, particularly for replacing a defective gene. The present
CC sequence is a cDNA encoding a PRO polypeptide
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-079-111-1 (1-322) x ACD66954 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTCAGCCTGGTGGTGTGCTTCTCATTCCATCTGGACCACGAGGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGGGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAGCGAACCCAGCAGCTGAATTTCACAGAAAGCTAAGGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGTCATCTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValIleuileTrpLysValProVal 120
Db 460 AGCCCAAACCCCAAGTGTGGGAAAAATGGGTGGGTGGTGTCTGATTGGAGGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

Db 520 AGCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
|||||

Db 580 CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACGCAACACAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
|||||

Db 640 GAAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACTGCC 699

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
|||||

Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
|||||

Db 760 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCAATTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
|||||

Db 820 GAAAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGTCTG 879

QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
|||||

Db 880 CTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAA 939

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
|||||

Db 940 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGATCAGCAGAAAGGAATGATCGAAAC 999

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
|||||

Db 1000 AAAGTAGTAAAGGAGGAGAGAGCCCAATGATAGCAACCTAATGAGGAATCAAAGAAACT 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
|||||

Db 1060 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCATCGCTGGAAGCT 1119

QY 321 GluVal 322
|||||

Db 1120 GAAGTT 1125

RESULT 43

ADA19867
ID ADA19867 standard; cDNA; 2372 BP.

XX

AC ADA19867;

XX

DT 20-NOV-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO263 cDNA.

XX

KW human; PRO; membrane bound protein; membrane bound receptor;

KW cell proliferation; cell migration; cell differentiation;

KW mitogenic factor; survival factor; cytotoxic factor;

KW differentiation factor; neuroptide; hormone; cell receptor;

KW receptor-ligand interaction; cytostatic; chondrocyte; tumour; ss; gene.

XX

OS Homo sapiens.

XX

PN US2003069394-A1.

XX

PD 10-APR-2003.

XX

PF 02-MAY-2002; 2002US-000633567.

XX

PR 30-DEC-1998; 98KR-00062142.

PR 08-MAR-1999; 99WO-US005028.

PR 14-MAY-1999; 99US-00311832.

PR 14-MAY-1999; 99WO-US010733.

PR 25-AUG-1999; 99US-00380137.

PR 25-AUG-1999; 99US-00380138.

PR 25-AUG-1999; 99US-00380139.

PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.

(GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

WPI; 2003-669950/63.
P-PSDB; ADA19868.

New isolated PRO polypeptide, useful in the preparation of a medicament for treating a condition responsive to PRO polypeptide, as therapeutic agent e.g. vaccine, and as molecular weight marker.

Disclosure; Fig 5; 239pp; English.

This invention relates to novel nucleic acids encoding human PRO secreted and transmembrane proteins. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information received from other cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuroptides and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the cDNA sequences encoding them. The novel proteins of the invention may have cytotstatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a tumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present sequence is a cDNA sequence which encodes a human PRO protein of the invention.

Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.49e-304 Length: 2372

Score: 322.00 Matches: 322

Percent Similarity: 100.00% Conservative: 0

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Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 100.00%  Indels: 0
DB: 8  Gaps: 0
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US-10-079-111-1 (1-322) x ADA19867 (1-2372)

QY	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu	20
DB	160	ATGGCCAGGTGCTTCAGCCCTGGTGTGTCTCTCACTTCCATCTGGACCACGAGGCTCCTG	219
QY	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
DB	220	GTCCAAGGCTCTTTGGGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATATATGGG	279
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
DB	280	ATCACCCCTTGTGAGCAAAAAGGGCAACAGCAGCTGAATTTACAGAAAGCTTAAGGAGGCC	339
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
DB	340	TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGACCAAGTTGAAACAGCCTTGAAAGCT	399
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
DB	400	AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCACTCTTAGGATT	459
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
DB	460	AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCTGATTGGAAAGTTCCAGTG	519
QY	121	SerArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
DB	520	AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACCTGGACTAACTCGTGCAAT	579
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
DB	580	CCAGAAATTATCACCCCAAGATCCCATATTCAACACTCAAACCTGCAACACAACAACA	639
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
DB	640	GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	699
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
DB	700	CCTACTACTACTCTCTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	759
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
DB	760	TGTGTACAGAGATTTTATGGAAACTTAGCACCATGTCTACAGAAACTGAACCATTTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
DB	820	GAAAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTGTGGAGGTGTCCTCCACGGCTCTG	879
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
DB	880	CTAGTGCTTGCTCTCTCTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAA	939
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
DB	940	AGGTATGTGAAGCCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAAATGATCGAAACC	999
QY	281	LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
DB	1000	AAAGTAGTAAAGGAGGAGGAGCCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACT	1059
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
DB	1060	GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAACTACCCGTGCGATGCTGGAAAGCT	1119
QY	321	GluVal	322
DB	1120	GAAGTT	1125

Db	220	GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG	279
Qy	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	280	ATCACCCCTTGTGAGCAAAAAGGCGAAACCCAGCAGCTGAATTCACAGAAGCTAAGGAGGCC	339
Qy	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGGCTGCTGGACTAAGTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT	399
Qy	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	400	AGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGGATTCGTGTCATCTCTAGGATT	459
Qy	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	460	AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTGATTTGGAAGGTTCCAGTG	519
Qy	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	520	AGCCGACAGTTTGCAGCCCTATTGTTACAACCTCATCTGATACTTGGACTTAACTCGTGCATT	579
Qy	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATTATCACCCACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACAACA	639
Qy	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTATTGTGAGTACAGTACCTACTCGTGGCATCCCTTACTCTACAATACCTGCC	699
Qy	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	700	CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	759
Qy	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCAATTGTT	819
Qy	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG	879
Qy	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGCTTGCTCTCCCTCTCTTTGTTGCTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA	939
Qy	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCCCTCCCTTTTACAAACAAGAATCAGCAGAGGAAATGATCCGAAACC	999
Qy	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1000	AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACT	1059
Qy	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCT	1119
Qy	321	GluVal 322	
Db	1120	GAA GTT 1125	
RESULT 45			
ACD83115			
ID	ACD83115 standard; cDNA; 2372 BP.		
XX			
AC	ACD83115;		
XX			
DT	22-SEP-2003 (first entry)		
XX			
DE	Human PRO polynucleotide #36.		
XX			

KW	Human; PRO; gene; ss; secreted polypeptide; transmembrane polypeptide;
KW	abnormal bleeding; gynaecological disease; hysterectomy; mucosal lesion;
KW	coronary ischaemic condition; gastrointestinal mucosa; skin disease; ALS;
KW	keratinocyte differentiation; psoriasis; Parkinson's disease; asthma;
KW	Alzheimer's disease; rheumatoid arthritis; multiple sclerosis; cancer;
KW	amyotrophic lateral sclerosis; neuropathy; uncontrolled cell growth.
XX	
OS	Homo sapiens.
XX	
PN	US2003044793-A1.
XX	
PD	06-MAR-2003.
XX	
PF	11-JUL-2001; 2001US-00903786.
XX	
PR	17-SEP-1997; 97US-0059113P.
PR	17-SEP-1997; 97US-0059115P.
PR	17-SEP-1997; 97US-0059117P.
PR	17-SEP-1997; 97US-0059119P.
PR	17-SEP-1997; 97US-0059121P.
PR	17-SEP-1997; 97US-0059122P.
PR	17-SEP-1997; 97US-0059184P.
PR	18-SEP-1997; 97US-0059263P.
PR	18-SEP-1997; 97US-0059266P.
PR	15-OCT-1997; 97US-0062125P.
PR	17-OCT-1997; 97US-0062285P.
PR	17-OCT-1997; 97US-0062287P.
PR	21-OCT-1997; 97US-0063486P.
PR	24-OCT-1997; 97US-0062814P.
PR	24-OCT-1997; 97US-0062816P.
PR	24-OCT-1997; 97US-0063045P.
PR	24-OCT-1997; 97US-0063120P.
PR	24-OCT-1997; 97US-0063121P.
PR	24-OCT-1997; 97US-0063127P.
PR	24-OCT-1997; 97US-0063128P.
PR	27-OCT-1997; 97US-0063327P.
PR	27-OCT-1997; 97US-0063329P.
PR	28-OCT-1997; 97US-0063541P.
PR	28-OCT-1997; 97US-0063542P.
PR	28-OCT-1997; 97US-0063544P.
PR	28-OCT-1997; 97US-0063549P.
PR	28-OCT-1997; 97US-0063550P.
PR	28-OCT-1997; 97US-0063564P.
PR	29-OCT-1997; 97US-0063435P.
PR	29-OCT-1997; 97US-0063704P.
PR	29-OCT-1997; 97US-0063732P.
PR	29-OCT-1997; 97US-0063734P.
PR	29-OCT-1997; 97US-0063735P.
PR	29-OCT-1997; 97US-0063738P.
PR	29-OCT-1997; 97US-0064215P.
PR	31-OCT-1997; 97US-0063870P.
PR	31-OCT-1997; 97US-0064103P.
PR	03-NOV-1997; 97US-0064248P.
PR	07-NOV-1997; 97US-0064809P.
PR	12-NOV-1997; 97US-0065186P.
PR	17-NOV-1997; 97US-0065846P.
PR	18-NOV-1997; 97US-0065693P.
PR	21-NOV-1997; 97US-0066120P.
PR	21-NOV-1997; 97US-0066364P.
PR	24-NOV-1997; 97US-0066453P.
PR	24-NOV-1997; 97US-0066466P.
PR	24-NOV-1997; 97US-0066511P.
PR	24-NOV-1997; 97US-0066770P.
PR	24-NOV-1997; 97US-0066772P.
PR	25-NOV-1997; 97US-0066840P.
PR	12-DEC-1997; 97US-0069425P.
PR	04-JUN-1998; 98US-0088026P.
PR	10-SEP-1998; 98US-0099803P.
PR	10-SEP-1998; 98WO-US018824.
PR	14-SEP-1998; 98US-0100262P.
PR	14-SEP-1998; 98WO-US019177.
PR	16-SEP-1998; 98WO-US019330.
PR	17-SEP-1998; 98US-0100858P.

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220 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279

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41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
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280 ATCACCCCTTGTGAGCAAAAAGGCGAAACCCAGCAGCTGAATTCACAGAAGCTAAGGAGGCC 339

|||||
61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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340 TGTAGGCTGCTGGACTAAGTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

|||||
81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
|||||
400 AGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGGATTCGTGTCATCTCTAGGATT 459

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101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
|||||
460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTGATTTGGAAGGTTCCAGTG 519

|||||
121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
|||||
520 AGCCGACAGTTTGCAGCCCTATTGTTACAACCTCATCTGATACTTGGACTTAACTCGTGCATT 579

|||||
141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
|||||
580 CCAGAAATTATCACCCACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACAACA 639

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161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
|||||
640 GAATTATTGTGAGTACAGTACCTACTCGTGGCATCCCTTACTCTACAATACCTGCC 699

|||||
181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
|||||
700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

|||||
201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
|||||
760 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCAATTGTT 819

|||||
221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
|||||
820 GAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879

|||||
241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
|||||
880 CTAGTGCTTGCTCTCCCTCTCTTTGTTGCTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA 939

|||||
261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
|||||
940 AGGTATGTGAAGGCCCTCCCTTTTACAAACAAGAATCAGCAGAGGAAATGATCCGAAACC 999

|||||
281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
|||||
1000 AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACT 1059

|||||
301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
|||||
1060 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCT 1119

|||||
321 GluVal 322
|||||
1120 GAA GTT 1125

PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-492256/46.
DR P-PSDB; ABO34851.
XX
PT Novel secreted and transmembrane PRO polypeptides and polynucleotides
PT encoding them, useful for treating abnormal bleeding involved in
PT gynecological diseases, skin diseases and neurodegenerative diseases.
XX
PS Claim 2; Fig 73; 475pp; English.
XX
CC The invention relates to human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the PRO polynucleotides encoding them.
CC The PRO polypeptides and polynucleotides can be used in diagnosing or
CC treating abnormal bleeding involved in gynaecological diseases e.g. to
CC avoid or lessen the need for hysterectomy. They can also be used in
CC treating coronary ischaemic conditions, disorders associated with the
CC preservation and maintenance of gastrointestinal mucosa and the repair of
CC acute and chronic mucosal lesions, skin diseases associated with abnormal
CC keratinocyte differentiation (e.g. psoriasis), Parkinson's disease,
CC Alzheimer's disease, asthma, rheumatoid arthritis, multiple sclerosis,
CC amyotrophic lateral sclerosis (ALS), neuropathies and diseases related to
CC uncontrolled cell growth, such as cancer. This sequence represents a
CC human PRO polynucleotide of the invention
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 8 Gaps: 0
US-10-079-111-1 (1-322) x ACD83115 (1-2372)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Dbb 160 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCATTCCATCTGGACACGAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Dbb 220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTCCATCCAGGTGTCTATGAGAATTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Dbb 280 ATCACCCCTTGTGAGCAAAAAGCGCAACCAGCAGCTGAATTTACACAGAAGCTAAGGAGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Dbb 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValIleSerArgIle 100
Dbb 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTTCGTGGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Dbb 460 AGCCCAACCCCAAGTGTGGGAAAATGGGGTGGTGTCTCTGATTTCGAAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Dbb 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCAAT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Dbb 580 CCAGAAATTATCACCAACCAAGATCCCATATTCACACTCAAACTGCAACACACAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Dbb 640 GAATTTATTGTGAGTGACAGTACCTACTCGTGGCATCCCTTTACTTACAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Dbb 700 CCTACTACTACTCCTCTCTGCTCCAGCTTCCACTTCTATTCCACGAGAGAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Dbb 760 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Dbb 820 GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Dbb 880 CTAGTGCTTGCTCTCTCTCTTTGGTGTGCTGCAGCTGGTCTTGGATTTGCTATGTCAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Dbb 940 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Dbb 1000 AAAGTAGTAAAGGAGGAGAGGCAATGATAGCAACCTTAATGAGGAATCAAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Dbb 1060 GATAAAACCAGAGAGTCCAGAGTCCAGCAAACTACCGTGGATGCCTGGAAGCT 1119
QY 321 GluVal 322
Dbb 1120 GAAGTT 1125
RESULT 46

CC of a cell expressing PRO polypeptides. The PRO polypeptides or
CC polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or
CC bioreactors. These are useful for stimulating hypertrophy of neonatal
CC heart, inhibiting vascular endothelial growth factor (VEGF)-stimulated
CC proliferation of endothelial cells, modulating the proliferation of
CC stimulated T-lymphocytes, enhancing the survival or proliferation of
CC retinal neurons or rod photoreceptor cells, inducing c-fos in endothelial
CC cells, modulating glucose or FFA uptake, inducing proliferation and/or re
CC differentiation of chondrocytes. In particular, these are useful for
CC detecting or treating cardiac insufficiency disorders, wounds, cancerous
CC tumours, retinal disorders or injuries (e.g. loss of sight due to
CC retinitis pigmentosa), obesity, diabetes, hyperinsulinaemia,
CC hypoinsulinaemia, or bone or cartilage disorders (e.g. sports injuries or
CC arthritis) in mammals. PRO polypeptides and their portions affect the
CC expression of genes which have a role in cell death. The polynucleotides
CC are useful in molecular biology including uses as hybridisation probes
CC for cDNA library to isolate the full-length PRO cDNA or to isolate other
CC cDNAs, in chromosome and gene mapping, in the generation of antisense RNA
CC and DNA, for preparing PRO polypeptides, for generating transgenic
CC animals or knockout animals which are useful in the development and
CC screening of therapeutically useful reagents, as probes and for the
CC genetic analysis of individuals with genetic disorders as well as for
CC recombinantly expressing the protein and for chromosome identification.
CC The proteins are useful as molecular marker for protein electrophoresis
CC purposes, as therapeutic agents, for screening compounds to identify
CC those that mimic the PRO polypeptide (agonists) or prevent the effect of
CC the PRO polypeptide (antagonists). The polynucleotides and proteins are
CC useful for tissue typing. PRO antibodies are useful for
CC immunohistochemical staining and/or assay of sample fluids. Anti-PRO
CC antibodies are useful in diagnostic assays for PRO e.g. detecting its
CC expression in specific cells, tissues or serum and for affinity
CC purification of PRO from recombinant cell culture or natural sources. The
CC PRO genes may also be used in gene therapy, particularly for replacing a
CC defective gene. The sequence presented is a gene encoding a PRO
CC polynucleotide of the invention.

XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-079-111-1 (1-322) x ADA16236 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCTGGTGTTCACCTCCATCTGGACCACGAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAAGGCTCTTTGCGTGCAGAGAGCTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAAGCGAACACAGCAGCTGAATTCACAGAAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAACAGCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTGGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

Db 520 AGCCGACAGTTTGACGCCTATTGTTACAACCTCATCTGATCTTGGACTAAACTCGTGCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTTATCACCAACCAAGATCCCATATTCAACACTCAAACCTGCAACAAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTCAGTGACAGTACCTACTCCGTGGCATCCCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyLeuGlyPheCysTyrValLys 240
Db 820 GAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGAGGTGTCCTCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyValAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCTCTCTTTGGTGCTGCAGCTGGTCTTGGAATTTGCTATGTCAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGAGGCCCATGATAGCAACCTTAATGAGGAATCAAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCACAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGGCATGCCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125
RESULT 47
ADA20039
ID ADA20039 standard; cDNA; 2372 BP.
XX
AC ADA20039;
XX
DT 20-NOV-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO263 cDNA.
XX
KW human; PRO; membrane bound protein; membrane bound receptor;
KW cell proliferation; cell migration; cell differentiation;
KW mitogenic factor; survival factor; cytotoxic factor;
KW differentiation factor; neuropeptide; hormone; cell receptor;
KW receptor-ligand interaction; cytostatic; chondrocyte; tumour; ss; gene.
XX
OS Homo sapiens.
XX
PN US2003055222-A1.
XX
PD 20-MAR-2003.
XX
PF 02-MAY-2002; 2002US-00063534.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.

PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.

(GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

WPI; 2003-521866/49.
P-PSDB; ADA20040.

New antibody that binds to a secreted protein, designated as PRO
polypeptide, useful as pharmaceuticals, diagnostics, biosensors and
bioreactors.

Disclosure; Fig 5; 235pp; English.

This invention relates to novel nucleic acids encoding human PRO secreted
and transmembrane proteins. Extracellular proteins play important roles
in the formation, differentiation and maintenance of multicellular
organisms. The fate of many individual cells (for example proliferation,
migration or differentiation) is typically governed by information
received from other cells and the immediate environment. The information
is often transmitted by secreted polypeptides (for example mitogenic
factors, survival factors, cytotoxic factors, differentiation factors,
neuropeptides and hormones) which are received and interpreted by diverse
cell receptors or membrane bound proteins. These membrane bound proteins
and receptors may be of use as pharmaceutical and diagnostic agents, such
as in the blocking of receptor-ligand interactions. The current invention
provides the amino acid sequences of novel human membrane bound receptors
and proteins, along with the cDNA sequences encoding them. The novel
proteins of the invention may have cytostatic activities through the
stimulation of chondrocytes. The nucleic acids of the invention may be
useful for the manufacture of a medicament for diagnosing or treating a
tumour in a mammal. In addition, they may be useful for measuring or
detecting the expression of a tumour associated gene. The present
sequence is a cDNA sequence which encodes a human PRO protein of the
invention.

SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0
US-10-079-111-1 (1-322) x ADA20039 (1-2372)			
QY	1	MetAlaArgCysPheSerIleuValLeuLeuLeuThrSerIleTrrPThrThrArgLeuLeu	20
Db	160	ATGGCCAGGTGCTTCAGCCTGGTGTGTTCTTCTCACATCTCGACCACGAGGCTCTGTG	219
QY	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	220	GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG	279
QY	41	IleThrLeuValSerLysLysAlaAAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	280	ATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC	339
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGGCTGTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT	399
QY	81	SerPheGluThrCysSerTyrGlyTrrPValGlyAspGlyPheValIleSerArgIle	100
Db	400	AGCTTTGAAACTTGCAGCTATGGCTGGTGGATGGATCGTGGTCATCTCTAGGATT	459
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	460	AGCCCAAACCCCAAGTGTGGAAAAAATGGGTGGGTGCTCTGATTTGAAGGTTCCAGTG	519
QY	121	SerArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	520	AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGGATT	579
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAAATTATCACCCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA	639
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC	699
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	700	CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	759
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTGTACAGAAACTGAACCATTTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG	879
QY	241	LeuValLeuAlaLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAA	939
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAATGATCGAAACC	999
QY	281	LysValValLysGluLysAlaAAsnAspSerAsnProAsnGluGluSerLysThr	300
Db	1000	AAAGTAGTAAAGGAGGAGGACCAATGATAGCAACCTTAATGAGGAATCAAAAGAAACT	1059
QY	301	AspLysAsnProGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAACCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCTTGGAGCT	1119
QY	321	GluVal 322	

Db 1120 GAAGTT 1125

RESULT 48

ACD82092

ID ACD82092 standard; cDNA; 2372 BP.

XX

AC ACD82092;

XX

DT 19-SEP-2003 (first entry)

XX

DE Human secreted/transmembrane polypeptide PRO 263 cDNA.

XX

KW Human; ss; gene therapy; cancer; tissue typing; gene.

XX

OS Homo sapiens.

XX

PN US2003060601-A1.

XX

PD 27-MAR-2003.

XX

PF 02-MAY-2002; 2002US-00063541.

XX

PR 30-DEC-1998; 98KR-00062142.

PR 08-MAR-1999; 99WO-US005028.

PR 14-MAY-1999; 99US-00311832.

PR 14-MAY-1999; 99WO-US010733.

PR 25-AUG-1999; 99US-00380137.

PR 25-AUG-1999; 99US-00380138.

PR 25-AUG-1999; 99US-00380139.

PR 25-AUG-1999; 99US-00380142.

PR 15-SEP-1999; 99US-00397342.

PR 18-OCT-1999; 99US-00403297.

PR 12-NOV-1999; 99US-00423844.

PR 30-DEC-1999; 99WO-US031274.

PR 18-FEB-2000; 2000WO-US004341.

PR 01-MAR-2000; 2000WO-US005601.

PR 02-MAR-2000; 2000WO-US005841.

PR 21-MAR-2000; 2000WO-US007532.

PR 22-MAY-2000; 2000WO-US014042.

PR 02-JUN-2000; 2000WO-US015264.

PR 22-AUG-2000; 2000US-00644848.

PR 24-AUG-2000; 2000WO-US023328.

PR 18-SEP-2000; 2000US-0064610.

PR 18-SEP-2000; 2000US-00665350.

PR 08-NOV-2000; 2000US-00709238.

PR 10-NOV-2000; 2000WO-US030873.

PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.

PR 20-DEC-2000; 2000WO-US034956.

PR 28-FEB-2001; 2001WO-US006520.

PR 22-MAR-2001; 2001US-00816744.

PR 10-MAY-2001; 2001US-00854208.

PR 10-MAY-2001; 2001US-00854280.

PR 30-MAY-2001; 2001US-00870574.

PR 01-JUN-2001; 2001WO-US017800.

PR 05-JUN-2001; 2001US-00874503.

PR 29-JUN-2001; 2001US-00869599.

PR 18-JUL-2001; 2001US-00908827.

PR 06-DEC-2001; 2001US-00006867.

XX

PA (GETH) GENENTECH INC.

XX

PI Eaton DL, Filvaroff E, Gerritsen MB, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

XX

DR WPI; 2003-521927/49.

DR P-PSDB; ABO34169.

XX

PT New PRO polypeptide, useful for preparing a composition for diagnosing or treating cancer or for tissue typing.

PT

XX

PS Disclosure; Fig 5; 236pp; English.

XX

CC The invention relates to an isolated PRO polypeptide. The polypeptide is useful for preparing a composition for diagnosing or treating cancer or for tissue typing. The present sequence represents cDNA encoding a human secreted/transmembrane PRO polypeptide

XX

SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.49e-304 Length: 2372

Score: 322.00 Matches: 322

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 8 Gaps: 0

US-10-079-111-1 (1-322) x ACD82092 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20

Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACACGAGGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

Db 220 GTCCAAGGCTCTTTGCGTGCAGAAAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60

Db 280 ATCACCCCTTGTGAGCAAAAGCGAACCCAGCAGCTGAATTTTCACAGAAGCTAAGGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100

Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGTCATCTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

Db 460 AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTGGAAAGGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCAAT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

Db 580 CCAGAAATTATCACCCCAAGATCCCATATTCAACACTCAACTCAACTCAACACAAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

Db 640 GAATTTATTGTCAGTGACAGTACCCTACTCGGTGGCATTCCCCCTTACTCTACAATACCTGCC 699

QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

Db 760 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTTGT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240

Db 820 GAAAAATAAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260

Db 880 CTAGTGCTTGCTCTCCTCTTTCTTTGGTGTGCTGCAGTGGTCTTGGATTTTGTATGTCAAA 939

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280

Db 940 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAAATCAGCAGAAAGAAATGATCGAAACC 999

XX Claim 2; SEQ ID NO 200; 479pp; English.

PS

XX

CC The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. PRO polypeptides are useful for detecting other PRO polypeptides in a sample and for linking a bioactive molecule to a cell expressing a PRO polypeptide. The PRO polypeptide antibodies are useful for modulating the biological activity of a cell expressing PRO polypeptides. PRO polypeptides are also useful for treating disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's diseases, amyotrophic lateral sclerosis (ALS), neuropathies and additionally, disease related to uncontrolled cell growth, e.g. cancer. PRO polypeptides also serves as tumour specific antigens which may be exploited as therapeutic targets for anti-tumour drugs, and are also employed therapeutically in vivo for lessening the effects of viral infection. The PRO polypeptides can be also used in assays to determine if it has a role in neurodegenerative diseases or their reversal, as an antithrombotic agent with reduced risk for haemorrhage as compared with heparin, in treating other PRO-associated disorders, in modulating endometrial bleeding angiogenesis, and may also have an effect on kidney tissue. PRO polypeptides and their portions affect the expression of genes which have a role in apoptosis. The polynucleotides are useful in molecular biology including uses as hybridisation probes for cDNA library to isolate the full-length PRO cDNA or to isolate other cDNAs, in chromosome and gene mapping, in the generation of antisense RNA and DNA, for preparing PRO polypeptides, for generating transgenic animals or knockout animals which are useful in the development and screening of therapeutically useful reagents, as probes and for the genetic analysis of individuals with genetic disorders as well as for recombinantly expressing the protein and for chromosome identification. The proteins are useful as molecular marker for protein electrophoresis purposes, as therapeutic agents, for screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). The polynucleotides and proteins are useful for tissue typing. PRO antibodies are useful for immunohistochemical staining and/or assay of sample fluids. Anti-PRO antibodies are useful in diagnostic assays for PRO e.g. detecting its expression in specific cells, tissues or serum and for affinity purification of PRO from recombinant cell culture or natural sources. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequence presented is a gene encoding a PRO polynucleotide of the invention.

XX SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.49e-304	Length:	2372
Score:	322.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0

US-10-079-111-1 (1-322) x ADA42381 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
|||||
Db 160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219
|||||
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
|||||
Db 220 GTCCAAGGCTCTTTGCGTGCAGAGAGCTTCCATCCAGGTGTCATGCAGAATTATGGGG 279
|||||
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
|||||
Db 280 ATCACCTGTGTAGCAAAAGCGCAACAGCAGCTGAATTCACAGAAGCTAAGGAGGCC 339
|||||

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
|||||
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAACAGCCTTGAAAGCT 399
|||||
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
|||||
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGTCATCTCTAGGATT 459
|||||
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
|||||
Db 460 AGCCCAACCCCAAGTGTGGGAAAAATGGGTTGGGTGCTCTGATTGTGAAGGTTCCAGTG 519
|||||
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
|||||
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACCTGGACTAACTCGTGCAATT 579
|||||
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
|||||
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACGTGCAACACAACA 639
|||||
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaAlaSerProTyrSerThrIleProAla 180
|||||
Db 640 GAATTTATGTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699
|||||
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
|||||
Db 700 CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
|||||
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
|||||
Db 760 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
|||||
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
|||||
Db 820 GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCACCGGCTCTG 879
|||||
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
|||||
Db 880 CTAGTGCTTGCTCTCTCTTCTTTGGTGTGCAGCTGGTCTTGGATTGCTATGTCAAA 939
|||||
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
|||||
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAAATGATCGAAACC 999
|||||
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
|||||
Db 1000 AAAGTAGTAAAGGAGGAGAGGCAATGATAGCAACCTAATGAGGAATCAAAGAAACT 1059
|||||
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
|||||
Db 1060 GATAAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCT 1119
|||||
QY 321 GluVal 322
|||||
Db 1120 GAAGTT 1125
|||||
RESULT 50
ACD23293
ID ACD23293 standard; cDNA; 2372 BP.
XX
AC ACD23293;
XX
DT 26-AUG-2003 (first entry)
XX
DE Human PRO polynucleotide #36.
XX
KW Human; PRO; gene; ss; Parkinson's disease; Alzheimer's disease; ALS;
KW amyotrophic lateral sclerosis; neuropathy; cancer; viral infection; AIDS;
KW Usher's syndrome; haemorrhage; enterocolitis; Zollinger-Ellison syndrome;
KW gastrointestinal ulceration; congenital microvillus atrophy; psoriasis;
KW skin disease; endometrial bleeding; angiogenesis; ischaemic condition;
KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disease;
KW atherosclerosis; infertility; birth defect; premature aging; stroke;

KW diabetetic complication.
XX
OS Homo sapiens.
XX
PN US2003064367-A1.
XX
PD 03-APR-2003.
XX
PF 13-JUL-2001; 2001US-00904485.
XX
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063354P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.

PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-567176/53.
DR P-PSDB; ABO17529.
XX
PT Novel isolated PRO polypeptides e.g. PRO245 and PRO1868, useful for
PT treating e.g. Parkinson's disease, Alzheimer's disease, amyotrophic
PT lateral sclerosis, cancer, neuropathies, diabetes and psoriasis.
XX
PS Claim 2; Fig 73; 477pp; English.
XX
CC The invention relates to human PRO polypeptides and the polynucleotides
CC encoding them. The polypeptides and polynucleotides are used for treating
CC diseases related to growth or survival of nerve cells such as Parkinson's
CC disease, Alzheimer's disease, amyotrophic lateral sclerosis (ALS) and
CC neuropathies, diseases related to uncontrolled cell growth such as
CC cancer, viral infections, Usher's syndrome, haemorrhage, enterocolitis,
CC Zollinger-Ellison syndrome, gastrointestinal ulceration, congenital
CC microvillus atrophy, skin diseases such as psoriasis and epithelial
CC cancers, endometrial bleeding, angiogenesis, ischaemic conditions,
CC asthma, rheumatoid arthritis, multiple sclerosis, inflammatory diseases,
CC atherosclerosis, cardiac injury, infertility, birth defects, premature
CC aging, AIDS, stroke and diabetic complications. The polynucleotides are
CC also useful in chromosome and gene mapping. This sequence represents a
CC human PRO polynucleotide of the invention
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
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US-10-079-111-1 (1-322) x ACD232293 (1-2372)

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QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	280	ATCACCCCTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC	339
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAGTTGAAACAGCCTTGAAAGCT	399
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle	100
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QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	460	AGCCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCTCTGATTGGAAGGTTCCAGTG	519
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
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QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATTATCACCCCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACAACA	639
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTTACAATAACCTGCC	699
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	700	CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	759
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal	220
Db	760	TGTGTACACAGAAGTTTATTGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
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QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGCTTGCTCTCCTCTTCTTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAA	939
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAAATGATCGAAACC	999
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
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QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAACCCAGAGAGTCCAAAGAGTCCAAGCAAAACTACCGTGCATGCTGGAAGCT	1119
QY	321	GluVal	322
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GenCore version 5.1.6
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Run on: September 15, 2004, 21:23:25 ; Search time 2278 Seconds
(without alignments)
713.467 Million cell updates/sec

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Ygapop 60.0 , Ygapext 60.0
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Searched: 3327077 seqs, 2523723180 residues

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Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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86	322	100.0	2372	13	US-10-305-654-31	Sequence 31, Appl
87	322	100.0	2372	13	US-10-448-923-200	Sequence 200, App
88	322	100.0	2372	14	US-10-006-867-5	Sequence 5, Appli
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ALIGNMENTS

RESULT 1
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; Sequence 2, Application US/10079111
; Publication No. US20030124543A1
; GENERAL INFORMATION:
; APPLICANT: Stuart, Susan G.
; APPLICANT: Streeter, David G.
; TITLE OF INVENTION: BREAST CANCER MARKER
; FILE REFERENCE: PC-0053 CIP
; CURRENT APPLICATION NUMBER: US/10/079,111
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 09/232,160
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 2029
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124543A1 3044710CB1
US-10-079-111-2

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Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

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QY	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	243	GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCTATGCAGAATATATGGG	302

QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	303	ATCACCCCTGTGAGCAAAAAGCGCAACAGCAGCTGAATTTACAGAAAGTAAGGAGGCC	362
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	363	TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT	422
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle	100
Db	423	AGCTTTGAAACTTGCAGCTATGGCTGGTGGATGGATTTCGTGGTCACTCTTAGGATT	482
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	483	AGCCCAACCCCAAGTGTGGGAAAATGGGTGGTGCTCTGATTGGAAAGGTTCCAGTG	542
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	543	AGCCGACAGTTGCAGCCTATTGTTACAACTCATCTGATACCTTGGACTAACTCGTGCA	602
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
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Db	843	GAAAAATAAGCAGCATTCAAGAAATGAAGTGTCTGGGTTTGGAGGTGTCCCCACGGCTCTG	902
QY	241	LeuValLeuAlaLeuLeuPhePheGlyValAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	903	CTAGTGTCTTGTCTCTCTTCTTTTGGTGTGCAGCTGGTCTTGGATTTTGTATGTCAAA	962
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	963	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAAGGAATGATCGAAACC	1022
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Db	1023	AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCTAATGAGGAATCAAAGAAACT	1082
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RESULT 2
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; Sequence 200, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
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; PRIOR FILING DATE: 1999-09-15
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; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-909-320-200

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Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
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US-10-079-111-1 (1-322) x US-09-909-320-200 (1-2372)

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QY 81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100
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Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGTGGATGGATTGCTGGTTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
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Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATCTTGACTAATCCTCGTGATT 579
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QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
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Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
|||
Db 760 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTGTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
|||
Db 820 GAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
|||
Db 880 CTAGTGCTTGCTCTCCTTCTTTTGGTGTGTCAGCTGGTCTTGGATTTTGTATGTCAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
|||
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAAACAAGAATCAGCAGAGGAAGGAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
|||
Db 1000 AAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
|||
Db 1060 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAAACCTACCGTGCATGCCTGGAAGCT 1119
QY 321 GluVal 322
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Db 1120 GAAGTT 1125
RESULT 3
US-09-909-088B-200
; Sequence 200, Application US/09909088B
; Patent No. US20020146709A1


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; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,088B
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-909-088B-200
Alignment Scores:
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Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-079-111-1 (1-322) x US-09-909-088B-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrrPThrThrArgLeuLeu 20
Db 160 ATGCCCAGGTGCTTCAGCCTGGTGTGGTTCTCATTCCATCTGGACCAGAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGGGTGCAGAAAGAGCTTTCCATCCAGGTGTCTGCAGAAATTATGGGG 279
QY 41 IleThrLeuValSerLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTTGTAGCAAAAAGGCGAACCCAGCAGCTGAATTTTCACAGAAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCGAAGGACCAAGTTGAACAGAGCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrrPValGlyAspGlyPheValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrrPlysValProVal 120
Db 460 AGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCCTGATTGGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrrPThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCAAT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCCAAAGATCCCATATTCAACACTCAAACACTGCAACACAAACAACA 639
QY 161 GluPheIleValSerAspSerThrTrrSerValAlaSerProTrrSerThrIleProAla 180
Db 640 GAAATTTATTGTGTCAGTGACAGTACCTACTCGTGGCATCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCCTGCTCCAGTTCACACTTCTATTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db 760 TGTGTACAGAAAGTTTTTATGGAACTAGCACCATTGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATATAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCCTCTTTTGGTGTGCTGCAGTGGTCTTGGAATTTTGCTATGTCAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAAACAAGAAATCAGCAGAAGGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTACTAAAGGAGGAGAGGCCCAATGATAGCAACCTTAATGAGGAATCAAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAACTACCGTGGCATGCCTGGAAGCT 1119
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QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 4

US-09-905-291A-200
; Sequence 200, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05

; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-905-291A-200
Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9
US-10-079-111-1 (1-322) x US-09-905-291A-200 (1-2372)
Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCATTCCATCTGGACCACGAGGCTCCTG 219
Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCGAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTCACAGAAGCTAAGGAGGCC 339
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 459
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAACCCCAAGTGTGGAAAAAATGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 519
Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerSerSerSerSerSerSerSerSer 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAATCGTGCATT 579
Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCCACCAAGATCCCATATTTCACACTCAAACTGCAACACACAAACAACA 639
Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACTGCC 699
Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 759
Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 879
Qy 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 939
Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC 999

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
|||||
Db 1000 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAAGAACT 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
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Db 1060 GATAAAAACCCAGAAAGAGTCCAAGAGTCCAAGCAAAAACCTACCGTGCATGCCTGGGAAGCT 1119

QY 321 GluVal 322
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Db 1120 GAAGTT 1125

RESULT 5
US-09-902-853-200
; Sequence 200, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-902-853-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-079-111-1 (1-322) x US-09-902-853-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
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Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCATTCCATCTGGACCACGAGGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
|||||
Db 220 GTCCAAGGCTCTTTGCGTGCAGAGAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
|||||
Db 280 ATCACCCCTGTGAGCAAAAAGCGCAACCAAGGAGCTGAATTTTCACAGAAGCTAAGGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
|||||
Db 340 TGTAGGCTGCTGGGACTAAGTTTGCGCGCAAGGACCAAGTTGAAACAGACCTTGAAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgile 100
|||||
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTTCGTGGTCATCTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
|||||
Db 460 AGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTTGGAAAGGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerSerAspThrTrpThrAsnSerCysile 140
|||||
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACCTTGGACTAACTCGTGCAIT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
|||||
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
|||||
Db 640 GAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC 699

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuile 200
|||||
Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
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Db 760 TGTGTCAAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
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Db 820 GAAATAAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879

Db 700 CCTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCCTCTCTTTTGGTGTGCAGCTGGTCTTGGATTGTGCTATGTCAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCAGAGAGTCCAAGAGTCCAAGCAAAACTACCCGTGGATGCCTGGAAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 7

US-09-907-841-200
; Sequence 200, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-841-200
Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-10-079-111-1 (1-322) x US-09-907-841-200 (1-2372)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCAATGAGGCTTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCTTGTGAGCAAAAGGCGAACCAACGACGCTGAATTTTCAGAAAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCTGGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuLeuTrpLysValProVal 120
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTTAACCTCGTGCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTCAAACTGCAACACAAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATGTGTCAGTGACAGTACTACTCGTGGCATCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCTCTCTCCAGTTCCTACTTCTATTTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

Db 640 GAATTTATTGTCAAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db 760 TGTGTACACAGAAGTTTTTATGGAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTCTGCTCTCCTCTCTTTTGGTGTGCAGCTGGTCTTGGATTTTGTATGTCAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCTAATGAGGAATCAAGAAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCAGAGAGTCCAGAGTCCAAGCAAAACTACCGTGCATGCCCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 9

US-09-906-742-200
; Sequence 200, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-906-742-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-906-742-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCATTCCATCTGGACCACGAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCATCCAGGTGTCTGCAGAAATTATGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnLysLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTGTGAGCAAAAGGCCAACCAGCAGCTGAATTTTCAGAAAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGGTCTCTTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCCAAACCCCAAGTGTGGGAAAAAATGGGGTGGGTGCTCTGTGATTGGAAAGGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTTGTACAACTCATCTGATACTTGGACTAACTCGTCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTATTGTGAGTACAGTACCTACTCGTGGCATCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db 760 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCCTCTCTTTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCTTTTACAAACAAGATCAGCAGAGGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCTAATGAGGAATCAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGAGTCCAAGCAAACTACCGTCCGATGCCGTGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 10
US-09-906-838-200
; Sequence 200, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,838
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-906-838-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-906-838-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCTGGTGTGTCTTCTCCATCTGGACCAGAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTGCCTGTCAGAGAGCTTCCATCCAGGTGTCTATCAGAAATTATGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTGTGAGCAAAAGCGCAACCCAGCAGCTGAATTTTCACAGAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAAGCT 399
Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAAACCTTGCAGCTATGGCTGGGTGGAGATGGATTCTGTGTCATCTCTAGGATT 459
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTGGAAGGTTCCAGTG 519
Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACITGGACTAACTCGTGCATT 579
Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 639
Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699
Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATTGATT 759
Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db 760 TGTGTCTCAGAGAAGTTTATTGGAACACTAGCACCATGTCTACAGAACTGAACCATTTGTT 819
Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
Qy 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCCTCTTCTTTGGTGTCTGCAGCTGGTCTTGGATTTTGCTATGTCAA 939
Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAAACAAGAATCAGCAGAGGAATAATGATCGAAACC 999
Qy 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGGAGGCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT 1059
Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAACCCAGAAGAGTCCCAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCT 1119
Qy 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 11

US-09-907-613-200
; Sequence 200, Application US/09907613
; Publication No. US20030027145A1
; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,613
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
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; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-613-200

Alignment Scores:

Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-907-613-200 (1-2372)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTCCATCTGGACCAAGGCTCCTG 219
Qy 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40

Db 220 GTCCAAGGCTCTTTGGCTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAAGCGAACACAGCAGCTGAATTTTCAGAAAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAACACAGCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCACTCTTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCCTGATTGGAAAGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGGAATACTCGTGCAAT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTTACAATACTGCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCCTCGTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTCACAGAAAGTTTATTGGAAGTACGACCATGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 820 GAAAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCCTCTTCTTTGGTGTGTCAGCTGGTCTGGATTTTGTATGTCAAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCGCTTCCCTTTTACAAACAAGATCAGCAGAGGAATGATCGAAACC 999
QY 281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGGAGGCAATGATAGCAACCTAATGAGGAATCAAGAAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAACTACCGTGGATGCCTGGAAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 12

US-09-907-942-200
; Sequence 200, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,942
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-942-200

Alignment Scores:

Pred. No.: 0
Score: 322.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 10
Length: 2372
Matches: 322
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-079-111-1 (1-322) x US-09-907-942-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCACGGTCTTCAGCCTGGTGTCTCTCACTTCATCTGGACCACGAGGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAAGGTCTTTGCGTGCAGAAGAGCTTCCATCCAGGTGTCTGCAGAATTATGGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTTGTGAGCAAAAAGGCAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGTGGTCACTCTTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCCAAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCTGATTTGGAAGGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTGCAGCCCTATTGTTACAACACTCATCTGATACTTGGACTAACTCGTGCATT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTTATACCACCAAGATCCCATATTCACACTCAAACTGCAACACAAACAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTCAGTGACAGTACCTACTCGTGGCATCCCCTTACTCTACAATACCTGCC 699

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCCTGTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTCAAGAAATGAAGCTGTGGTTTGGAGGTGTCCCCACGGCTCTG 879

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCCTCTCTTTTGGTGTCTGCAGCTGGTCTTGGATTTTGTATGTCAA 939

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAAATGATCGAAACC 999

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACT 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAAACCCAGAGAGTCCAAAGAGTCCAAAGAAAACTACCGTGGATGCTGGAAGCT 1119

QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 13
US-09-904-859-200

; Sequence 200, Application US/09904859
; Publication No. US20030036060A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,859
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA


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; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-909-204-200

Alignment Scores:
Pred. No.:      0      Length:      2372
Score:          322.00    Matches:      322
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match:      100.00%    Indels: 0
DB:              10      Gaps: 0

US-10-079-111-1 (1-322) x US-09-909-204-200 (1-2372)

QY      1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db      160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219

QY      21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      220 GTCCAAAGGCTCTTTGCGTGCAGAAAGCTTTCCATCCAGGTGTCTATGCAGAAATTATGGGG 279

QY      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      280 ATCACCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 339

QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

QY      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
Db      400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGIGTCACTCTTAGGATT 459

QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCTCTGATTGGAAGGTTCCAGTG 519

QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520 AGCCGCAGAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAATCGTGCATT 579

QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580 CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639

QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTTACAATACCTGCC 699

QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      700 CCTACTACTACTCCTCTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db      760 TGTGTACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      820 GAAATATAAGCAGCATTCGAAGATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879

QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      880 CTAGTGCTTGCTCTCCTCTTCTTTGGTGGCTGCAGCTGGTCTTGGATTTTGCTATGTCAA 939
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QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAAGAAATGATCGAAACC 999

QY      281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db      1000 AAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAAGAAACT 1059

QY      301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db      1060 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAACTACCGTGGATGCCTGGAAGCT 1119

QY      321 GluVal 322
Db      1120 GAAGTT 1125

RESULT 15
US-09-904-820-200
; Sequence 200, Application US/09904820
; Publication No. US20030036094A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,820
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
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; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-820-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-904-820-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCTGGTGTGCTTCTCACATCCATCTGGACCACGAGGTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAAGGCTCTTTGGCTGCAGAAAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAGGCGAACCAGCAGCTGAATTTACAGAAAGCTAAAGGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAAGTTTGGCCGCAAGGCAAGTTGAAACAGCCTTGAAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGGATTTCGTGGTCATCTTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAACCCCAAGTGGGAAAATGGGGTGGTGTCTCTGATTGGGAAGGTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT 579

QY 141 ProGluIleIleThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACAAAGATCCCATATTCAACACTCAAACCTGCAACACAAACAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTATTGTGAGTGACAGTACCTACTCGGTGGATCCCTTACTCTACATACTGCTGCC 699

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

Db 760 TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATTGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 820 GAAAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTGGAGGTGTCCCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCCTCTTCTTTGGTGTGTCAGCTGGTCTTGGATTTTGTATGTCAAA 939
QY 261 ArgTyrValLysAlaPhePropheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCTTAATGAGGAATCAAGAAAACT 1059
QY 301 AspLysAsnProGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAAACTACCGTGGATGCCITGGAAAGCT 1119

QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 16
US-09-904-786-200
; Sequence 200, Application US/09904786
; Publication No. US20030039969A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,786
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-786-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0
US-10-079-111-1 (1-322) x US-09-904-786-200 (1-2372)			
QY	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrrPThrThrArgLeuLeu	20
Db	160	ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG	219
QY	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	220	GTCCAAAGGCTCTTTGCGTGCAGAGAGAGCTTTCCATCCAGGTGTATGCAGAATTATGGGG	279
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	280	ATCACCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC	339
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAACAGACGCTTGAAGCT	399
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	400	AGCTTTTGAACCTTGACGCTATGGCTGGTGGATGGATTCTGTCATCTCTAGGATT	459
QY	101	SerProAnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	460	AGCCCAACCCCAAGTGTGGGAAAAATGGGTGGTGTCTCTGATTGGAAGGTTCCAGTG	519
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	520	AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGTATCTTGGACTAACTCGTGCA	579
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA	639
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTTATTTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACATACTGCC	699
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	700	CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATTGATT	759
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAACTGAACCATTTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAATAAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG	879
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGTGTGCTCTCCTCTCTTTTGGTGCTGCAGCTGGTCTTGGATTGTGCTATGTCAA	939
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAATGATCGAAACC	999
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluSerLysLysThr	300
Db	1000	AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACT	1059
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAACCCAGAGAGTCCAAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCT	1119
QY	321	GluVal 322	

Db	1120	GAAGTT 1125
RESULT 17		
US-09-906-646-200		
; Sequence 200, Application US/09906646		
; Publication No. US20030039971A1		
; GENERAL INFORMATION:		
; APPLICANT: Genentech, Inc.		
; APPLICANT: Ashkenazi, Avi		
; APPLICANT: Botstein, David		
; APPLICANT: Desnoyers, Luc		
; APPLICANT: Eaton, Dan L.		
; APPLICANT: Ferrara, Napoleone		
; APPLICANT: Filvaroff, Ellen		
; APPLICANT: Fong, Sherman		
; APPLICANT: Gao, Wei-Qiang		
; APPLICANT: Gerber, Hanspeter		
; APPLICANT: Gerritsen, Mary E.		
; APPLICANT: Goddard, A.		
; APPLICANT: Godowski, Paul J.		
; APPLICANT: Grimaldi, Christopher J.		
; APPLICANT: Gurney, Austin L.		
; APPLICANT: Hillan, Kenneth, J.		
; APPLICANT: Kljavin, Ivar J.		
; APPLICANT: Mather, Jennie P.		
; APPLICANT: Pan, James		
; APPLICANT: Paoni, Nicholas F.		
; APPLICANT: Roy, Margaret Ann		
; APPLICANT: Stewart, Timothy A.		
; APPLICANT: Tumas, Daniel		
; APPLICANT: Williams, P. Mickey		
; APPLICANT: Wood, William, I.		
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic		
; TITLE OF INVENTION: Acids Encoding the Same		
; FILE REFERENCE: 10466-14		
; CURRENT APPLICATION NUMBER: US/09/906,646		
; CURRENT FILING DATE: 2002-01-22		
; PRIOR APPLICATION NUMBER: PCT/US00/04414		
; PRIOR FILING DATE: 2000-02-22		
; PRIOR APPLICATION NUMBER: US 60/143,048		
; PRIOR FILING DATE: 1999-07-07		
; PRIOR APPLICATION NUMBER: US 60/145,698		
; PRIOR FILING DATE: 1999-07-26		
; PRIOR APPLICATION NUMBER: US 60/146,222		
; PRIOR FILING DATE: 1999-07-28		
; PRIOR APPLICATION NUMBER: PCT/US99/20594		
; PRIOR FILING DATE: 1999-09-08		
; PRIOR APPLICATION NUMBER: PCT/US99/20944		
; PRIOR FILING DATE: 1999-09-13		
; PRIOR APPLICATION NUMBER: PCT/US99/21090		
; PRIOR FILING DATE: 1999-09-15		
; PRIOR APPLICATION NUMBER: PCT/US99/21547		
; PRIOR FILING DATE: 1999-09-15		
; PRIOR APPLICATION NUMBER: PCT/US99/23089		
; PRIOR FILING DATE: 1999-10-05		
; PRIOR APPLICATION NUMBER: PCT/US99/28214		
; PRIOR FILING DATE: 1999-11-29		
; PRIOR APPLICATION NUMBER: PCT/US99/28313		
; PRIOR FILING DATE: 1999-11-30		
; PRIOR APPLICATION NUMBER: PCT/US99/28564		
; PRIOR FILING DATE: 1999-12-02		
; PRIOR APPLICATION NUMBER: PCT/US99/28565		
; PRIOR FILING DATE: 1999-12-02		
; PRIOR APPLICATION NUMBER: PCT/US99/30095		
; PRIOR FILING DATE: 1999-12-16		
; PRIOR APPLICATION NUMBER: PCT/US99/30911		
; PRIOR FILING DATE: 1999-12-20		
; PRIOR APPLICATION NUMBER: PCT/US99/30999		
; PRIOR FILING DATE: 1999-12-20		
; PRIOR APPLICATION NUMBER: PCT/US00/00219		
; PRIOR FILING DATE: 2000-01-05		
; NUMBER OF SEQ ID NOS: 423		
; SEQ ID NO 200		


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;   LENGTH: 2372
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-906-646-200

Alignment Scores:
Pred. No.:      0      Length: 2372
Score:          322.00  Matches: 322
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:      100.00%  Indels: 0
DB:               10      Gaps: 0

US-10-079-111-1 (1-322) x US-09-906-646-200 (1-2372)

QY      1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db      160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219

QY      21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      220 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279

QY      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      280 ATCACCCCTTGTAGCAAAAAGGCGAACCAGCAGCTGAATTTACAGAAGCTAAGAGGCC 339

QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      340 TGTAGGCTGCTGGGACTAAAGTTTGGCCGGCAAGGCAAGTTGAAACAGCCCTGAAAGCT 399

QY      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db      400 AGCTTTGAAACTTGACGCTATGGCTGGGTTGGAGATGGATTTCGTGGTCATCTCTAGGATT 459

QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      460 AGCCCAAACCCCAAGTGTGGAAAAATGGGGTGGGTGCTCCTGATTTTGGAAGGTTCCAGTG 519

QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTTAACCTCGTGCAAT 579

QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580 CCAGAAATTATCACCCACCAAGATCCCATATTCAACACTCATCTGATACTTGGACTTAACCTCGTGCAAT 639

QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640 GAATTTATTGTGTCAGTGACAGTACCTACTCGGTGGGATCCCTTACTCTACAAATACCTGCC 699

QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      700 CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluThrPropheVal 220
Db      760 TGTGTCACAGAAGTTTATTATGGAACCTAGCACCATGTCTACAGAACTGAACCATTTGTT 819

QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      820 GAAAAATAAGCAGCAATCAAGAATGAAGCTGCTGGGTTGGAGGTGTCGCCACGGCTCTG 879

QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      880 CTAGTGCTTGCTCTCCTCTTCTTTGGTGTGTCAGCTGGTCTTGGATTTTGTGATGTCAAA 939

QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      940 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAATGATCGAAACC 999

QY      281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
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Db      1000 AAAGTAGTAAAGGAGAGAGCCCAATGATAGCAACCCTAATGAGGAATCAAAAGAAACT 1059

QY      301 AspLysAsnProGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db      1060 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCCTGGAGACT 1119

QY      321 GluVal 322
Db      1120 GAAGTT 1125

RESULT 18
US-09-906-700-200
; Sequence 200, Application US/09906700
; Publication No. US20030039972A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,700
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
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; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-906-700-200

Alignment Scores:
Pred. No.:      0      Length:      2372
Score:          322.00      Matches:      322
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels: 0
DB:              10      Gaps: 0

US-10-079-111-1 (1-322) x US-09-906-700-200 (1-2372)

Qy      1  MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db      160 ATGCCAGGTGCTTCAGCCCTGGTGTGCTTCTCACTTCATCTGACACACGAGGCTCCTG 219

Qy      21  ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      220 GTCCAGGCTCTTTGCGTGCAGAGAGCTTCCATCCAGGTGTATGCAGAAATTATGGGG 279

Qy      41  IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      280 ATCACCTTGTGAGCAAAAGGCGAACACGACGAGCTGAATTTACAGAAAGCTAAGGAGGCC 339

Qy      61  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      340 TGTAGGCTGTGGGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

Qy      81  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db      400 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCTCGTTCATCTCTAGGATT 459

Qy      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      460 AGCCCCAAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCTCTGATTGGAAGGTTCCAGTG 519

Qy      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520 AGCCGACAGTTTGCAGCCTATTGTACAACTCATCTGATACTTGGACTAACTCGTGCATT 579

Qy      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580 CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639

Qy      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640 GAATTATTGTTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC 699

Qy      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

Qy      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      760 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

Qy      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      820 GAAATAAAGCAGCATTCAAGAATGAAGTGTGGGTTTGGAGGTGTCCCCACGGCTCTG 879

Qy      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
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Db      880 CTAGTGCTTGCTCTCCTCTCTTCTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAA 939

Qy      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAAATGATCGAAACC 999

Qy      281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db      1000 AAAGTAGTAAAGGAGGAGAGAGGCAATGATAGCAACCTAATGAGGAATCAAAGAAACT 1059

Qy      301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db      1060 GATAAAAACCCAGAGAGTCCAGAGTCCAAAGCAAAACTACCGTGGATGCCTGGAAGCT 1119

Qy      321 GluVal 322
Db      1120 GAAGTT 1125

RESULT 19
US-09-903-786-200
; Sequence 200, Application US/09903786
; Publication No. US20030044793A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: ROY, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/903,786
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
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; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-903-786-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-903-786-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCATCTGGACCACGAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGAGAAAGAGCTTTCCATCCAGGTGTCTATGAGAAATTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAGCGGAACCAAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 339
QY 61 CysArgLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGGATTGCTGGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeulleTrpLysValProVal 120
Db 460 AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTGCTGATTGGAAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACACTCATCTGATACTTGGACTAACTCGTGCAAT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCCATAATTCAACACTCAAACTGCAACACAAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeulle 200
Db 700 CCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 820 GAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCCTCTTCTTTTGGTGCTGCAGTGGTCTTTGGATTTTGTATGTCAAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGATCAGCAGAAGGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCTTAATGAGGAATCAAAGAAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAAACTACCGTGGATGCCCTGGAGACT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125
RESULT 20
US-09-902-903-200
; Sequence 200, Application US/09902903
; Publication No. US20030044839A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,903
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-903-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-902-903-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAAGCTCTTTCGCTGCAGAAAGCGAACAGCAGCTGAATTCACAGAAGCTAAGGAGGCC 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTGTGTAGCAAAAGCGAACAGCAGCTGAATTCACAGAAGCTAAGGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCITTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGTGTCATCTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCCTGATTGGAAGGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGTACTTGGACTAACTCGTGCATT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACCTGCAACCAACAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAAATTTATGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC 699

QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db 760 TGTGTACAGAAAGTTTTTATGAAACTAGCACCATTGTCTACAGAAACTGAACCATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCCTCTCTTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAA 939

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAAATGATCGAAACC 999

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCTTAATGAGGAATCAAAGAAACT 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTCCGATGCCTGGAAGCT 1119

QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 21
US-09-903-749A-200
; Sequence 200, Application US/09903749A
; Publication No. US20030045693A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/903,749A
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22

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; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-903-749A-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-903-749A-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCCTGGTGTGCTTCTCACITCCATCTGGACCACGAGGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGGCTGCAGAAAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAACAGCCTTGAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATGGATTCGTGGTCATCTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAAATGGGGTGGGTGCTCCTGATTTGGAAGGTTCCAGTG 519
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QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAATCGTGCATT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGCTTACAGAAACTGAACCATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCCTCTTCTTTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAAA 939

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAATGATCGAAACC 999

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAAC 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAAACTACCGTGCATGCCCTGGAAGCT 1119

QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 22
US-09-904-119-200
; Sequence 200, Application US/09904119
; Publication No. US20030049621A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
```

```
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,119
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-119-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-904-119-200 (1-2372)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219

Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgileMetGly 40
Db 220 GTCCAAAGGCTCTTTGCGTGCAGAGAGCTTCCATCCAGGTGTGTCAGAAATTATGGGG 279

Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAGCGAACAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 339

Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACACACCTTGAAAGCT 399
Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgile 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTTCGTGGTCACTCTTAGGATT 459
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCCTGATTGGAAAGGTTCCAGTG 519
Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysile 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACACTCATCTGATACTTGGACTAACTCGTGCA 579
Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATATCACCAACCAAGATCCCATATTTCAACACTCAAACCTGCAACACAAACA 639
Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTTATGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC 699
Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db 760 TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879
Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCTCTCTTTTGGTGTGCTGCAGCTGGTCTTGGATTTTGTATGTCAA 939
Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAAATGATCGAAACC 999
Qy 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGGAGGCCCAATGATAGCAACCTTAATGAGGAATCAAAGAAACT 1059
Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCTCCAAGCAAAACTACCGTCCGATGCCTGGAAGCT 1119

Qy 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 23
US-09-904-956-200
; Sequence 200, Application US/09904956
; Publication No. US20030049622A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
```



```
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,956
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-904-956-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-904-956-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCCTGGTGTGCTTCTCACITCCATCTGGACCACGAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
|||||
```

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Db 220 GTCCAAGGCTCTTTGGCGTCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
|||||
Db 280 ATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
|||||
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
|||||
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGGATTCGTGGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
|||||
Db 460 AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTTGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
|||||
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAATCTGTCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
|||||
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
|||||
Db 640 GAATTTATTGTCAGTGACGTACCTACTCGGTGGCATCCCTTTACTCTACAATACCTGCC 699
QY 181 ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
|||||
Db 700 CCTACTACTCTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
|||||
Db 760 TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
|||||
Db 820 GAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
|||||
Db 880 CTAGTGCTTGCTCTCCTCTTCTTTTGGTGTGCTGAGCTGGTCTTTGGATTTTGTCTATAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
|||||
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAGAATCAGCAGAGGAATAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
|||||
Db 1000 AAAGTAGTAAAGGAGAGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
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Db 1060 GATAAAAACCCAGAGAGTCCAAGAGTCCCAAGCAAAAACTACCGTGCATGCCTTGAAGCT 1119
QY 321 GluVal 322
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Db 1120 GAAGTT 1125

RESULT 24
US-09-902-736-200
; Sequence 200, Application US/09902736
; Publication No. US20030049676A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
```

```
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,736
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-902-736-200

Alignment Scores:
Pred. No.: 0
Score: 322.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%

Length: 2372
Matches: 322
Conservative: 0
Mismatch: 0
Indels: 0
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DB: 10 Gaps: 0
US-10-079-111-1 (1-322) x US-09-902-736-200 (1-2372)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Dbb 160 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCATTCCATCTGGACACGAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Dbb 220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTCCATCCAGGTGTCATGCAGAAATTATGGG 279
QY 41 ileThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Dbb 280 ATCACCCCTTGTGAGCAAAAAGGCGAACCCAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGlnThrAlaLeuLysAla 80
Dbb 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Dbb 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Dbb 460 AGCCCAAAACCCCAAGTGTGGGAAAATGGGGTGGGTGTCCTGATTGGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCystTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Dbb 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCAAT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Dbb 580 CCAGAAATTATCACCAACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Dbb 640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTTACAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Dbb 700 CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Dbb 760 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATTGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Dbb 820 GAAATAAAGCAGCATTTCAAGATGAAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Dbb 880 CTAGTGCTTGCTCTCCTCTTCTTTGGTGTGTCAGCTGGTCTTGGATTTTGTATGTCAAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Dbb 940 AGGTATGTGAAGGCCTTCCCTTTTACAAAACAAGAAATCAGCAGAGGAAATGATCGAAACC 999
QY 281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Dbb 1000 AAAGTAGTAAAGGAGGAGAGGCGCAATGATAGCAACCCTAATGAGGAATCAAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Dbb 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAACTACCGTCGATGCCTGGAAGCT 1119
QY 321 GluVal 322
Dbb 1120 GAAGTT 1125
RESULT 25
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US-09-907-794-200
; Sequence 200, Application US/09907794
; Publication No. US20030049677A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-907-794-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-907-794-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTCAGCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTTCACAGAAGCTAAGGAGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGTGGAGATGGATTCTGGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTyrLysValProVal 120
Db 460 AGCCCAAACCCCAAGTGTGGGAAAAAATGGGGTGGTGTCTCTGATTGGGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAATCTCGTGCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACAAAGATCCCATATTCAAACTCAAACACAAACAACAAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTCAGTCACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACTCGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCCTCGCTCCAGCTTCCACTTCTATTTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 820 GAAAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTCTGCTCTCTCTTCTTTTGGTGTCTGAGCTGGTCTTTGGATTTTGTATGTCAAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGAGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAGAAACT 1059
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Db 880 CTAGTGCCTGCTCTCCTCTCTTTTGGTGGCTGCAGCTGGTCTTGGATTGTGCTATGTCAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCCTTCCTTTTACAAACAAGAAATCAGCAGAGGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGGAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 27

US-09-904-462-200
; Sequence 200, Application US/09904462
; Publication No. US20030054351A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,462
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-462-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-904-462-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCTATGCAGAATTATGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTTGTGAGCAAAAAGCCAAACCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTTAAGTTGGCCGCAAGGACCACCACTTGAAACAGCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGATGGATGGTGCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAACCCCAAGTGTGGAAAAATGGGTGGGTGCTCTGTGATTGGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaIaTyrCysTyrAsnSerSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAATCGTGCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACCTGCAACACACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeulle 200
Db 700 CCTACTACTCTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
DB	760	TGTGTACAGAAAGTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu	240
DB	820	GAAAAATAAGCAGCAATCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG	879
QY	241	LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
DB	880	CTAGTGCTTGCTCTCTCTCTTTGGTGCTGCAGCTGGTCTTGATTTTGTATGTCAAA	939
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
DB	940	AGGTATGTGAAGGCTTCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC	999
QY	281	LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
DB	1000	AAAGTAGTAAAGGAGAGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACT	1059
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
DB	1060	GATAAAAACCCAGAGAGTCCAGAGTCCAGCAAAACTACCGTGGATGCCTGGAGCT	1119
QY	321	GluVal	322
DB	1120	GAAGTT	1125

RESULT 28

US-09-907-925-200
; Sequence 200, Application US/09907925
; Publication No. US20030054352A1

; GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/907,925

; CURRENT FILING DATE: 2001-07-17

; PRIOR APPLICATION NUMBER: 09/665,350

; PRIOR FILING DATE: 2000-09-18

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

;
; PRIOR APPLICATION NUMBER: US 60/143,048

;; PRIOR FILING DATE: 1999-07-07
PRIOR PUBLICATION NUMBER: US

;; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26

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; PRIOR FILING DATE: 1999=0/-28
; PRIOR APPLICATION NUMBER: IIS

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; PRIOR APPLICATION NUMBER: US 60/146,222

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; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-907-925-200

```

Alignment Scores:

Pred. NO.:	0	Length:	2372
Score:	322.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-079-111-1 (1-322) x US-09-907-925-200 (1-2372)

QY	1	Met	Ala	Arg	Cys	Phe	Ser	Leu	Val	Leu	Leu	Leu	Leu	Thr	Ser	Ile	Trp	Thr	Thr	Arg	Leu	Leu	20	
DB	160	AT	GGC	CAG	GT	GCT	T	CAG	CT	GGT	GT	GCT	T	T	C	ACT	T	CC	AT	CT	CG	ACC	ACGAGGCTCCTG	219
QY	21	Val	Gln	Gly	Ser	Leu	Arg	Ala	Glu	Glu	Leu	Ser	Ile	Gln	Val	Ser	Cys	Arg	Ile	Met	Gly	40		
DB	220	GT	CCA	AGG	CT	CT	T	T	CG	GT	CGA	AG	AGCTT	T	CCA	T	CC	AGG	TGT	CAT	GC	AGAA	TATATGGGG	279
QY	41	Ile	Thr	Leu	Val	Ser	Lys	Lys	Ala	A	Asn	Gln	Gln	Leu	Asn	Phe	Thr	Glu	Ala	Lys	Glu	Ala	60	
DB	280	AT	CAC	CTT	TGT	GAG	CAAAA	AGG	CAAA	CC	CAG	CAG	CT	GA	ATT	T	CA	CAG	AA	GC	TAA	GAGAGGCC	339	
QY	61	Cys	Arg	Leu	Leu	Gly	Leu	Ser	Leu	Ala	Gly	Lys	Asp	Gln	Val	Glu	Thr	Ala	Leu	Lys	Ala	80		
DB	340	TGT	AGG	CT	GCT	GGA	CTA	AGT	TT	TGG	CCG	CAAG	CAAG	CAAG	TT	TG	AA	CAG	GC	CTT	TG	AAAGCT	399	
QY	81	Ser	Phe	Glu	Thr	Cys	Ser	Tyr	Gly	Trp	Val	Gly	Asp	Gly	Phe	Val	Val	Ile	Ser	Arg	Ile	100		
DB	400	AG	CTT	TG	AACT	TGC	AGCT	AT	GGCT	GGGT	TG	GAG	TGG	ATT	CG	TGGT	CAT	CT	C	TAG	GATT	459		
QY	101	Ser	Pro	Asn	Pro	Lys	Cys	Gly	Lys	Asn	Gly	Val	Gly	Val	Leu	Ile	Trp	Lys	Val	Pro	Val	120		
DB	460	AG	CCCAA	ACCC	CAAG	TGT	GGG	AAAA	AT	GGG	TGG	TGCT	CT	GATT	T	CG	AGG	TT	CC	AGT	G	519		
QY	121	Ser	Arg	Gln	Phe	Ala	Ala	Tyr	Cys	Tyr	Asn	Ser	Ser	Asp	Thr	Trp	Thr	Asn	Ser	Cys	Ile	140		
DB	520	AG	CCG	AC	AG	TTT	GC	AGC	CT	ATT	GT	TACA	AACT	CAT	CT	GATA	CT	TGG	ACT	TAA	CTCGTGCATT	579		
QY	141	Pro	Glu	Ile	Ile	Thr	Thr	Lys	Asp	Pro	Ile	Phe	Asn	Thr	Gln	Thr	Ala	Thr	Gln	Thr	Thr	160		

Db 580 CCAGAAATTATCACCAACAAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCTGCTCCAGCTTCCACITTCATTCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTCACAGAAAGTTTTTATGGAACTAGCACCATGTCTACAGAAACTGAACCAATTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCCTCTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAATGATCGAAACC 999
QY 281 LysValValLysGluGlyLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCTAATGAGGAATCAAGAAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAACCCAGAGAGTCCAAAGAGTCCAAGCAAACTACCGTGGATGCCCTGGAAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 29

US-09-902-692-200
; Sequence 200, Application US/09902692
; Publication No. US20030054400A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,692

; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-692-200

Alignment Scores:

Pred. No.:	0	Length:	2372
Score:	322.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-079-111-1 (1-322) x US-09-902-692-200 (1-2372)

QY	1	MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu	20
Db	160	ATGGCCAGGTGCTTCAGCCTGGTGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG	219
QY	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	220	GTCCAAGGCTCTTTGGTGCAGAGAGCTTTCCATCCAGGTGTCATGCAGATTATGGGG	279
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	280	ATCACCCCTTGTGAGCAAAAAGCGCAACACGACGCTGAATTTTCACAGAAGCTAAGGAGGCC	339
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGGCTGTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT	399
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	400	AGCTTTGAAACTTGACGCTATGGCTGGTGGAGATGGATTCTGGTGCATCTCTAGGATT	459
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120

Db 460 AGCCCAAACCCCAAGTGTGGAAAAATGGGTGGGTGCTCCTGATTTGGAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysile 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCACACTCAAACCTGCAACACAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTGACGTGACAGTACCTACTCGTGGCATCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuile 200
Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAAGTTTTTATGGAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCCTCTTCTTTGGTGCTCAGCTGGTCTTGGATTTTGTATGTCAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGCATGCCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 30
US-09-903-520-200
; Sequence 200, Application US/09903520
; Publication No. US20030054401A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/903,520
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-903-520-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-903-520-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCCTGGTGTGTTCTTCTCATTCCATCTGGACCACGAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCTATGCAGAAATTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTTGTGAGCAAAAAGCGAAACCAAGCAGCTGAATTTTCACAGAAAGCTAAGGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGGATTCGTGGTCATCTTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTGATTGGGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCCTATGTGTACAACCTCATCTGATACTTGGACTAACTCGTGCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATATATCACCAACCAAGATCCCATATTCAACACTCAACTGATACTTGGACTAACTCGTGCATT 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCCTCTCTTGTGGTGCTGCAGCTGGTCTTGGATTTTGTATGTCAAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGATCAGCAGAAGGAATGATCGAAACC 999
QY 281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAACTACCGTGCATGCCTGGAACT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 31
US-09-905-056-200
; Sequence 200, Application US/09905056
; Publication No. US2003005441A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,056
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-905-056-200

Alignment Scores:			
Pred. No.:	0	Length:	2372
Score:	322.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-079-111-1 (1-322) x US-09-905-056-200 (1-2372)

QY 1 MetAlaArgCysPheSerIleValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCCTGGTGTGTTCTTCTCATTCCATCTGGACCACGAGGCTCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db |||||
220 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGG 279

QY 41 IleThrLeuValSerIysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db |||||
280 ATCACCCCTTGTCAGCAAAAAGCGAACCAGCAGCTGAATTTACAGAAAGCTTAAGGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db |||||
340 TGTAGGCTGCTGGACTAAGTTTGGCCGCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db |||||
400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCACTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db |||||
460 AGCCCAAAACCCCAAGTGTGGAAAAAATGGGGTGGGTGCTCCTGATTTGGAAAGGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db |||||
520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db |||||
580 CCAGAAATTATACCAACCAAGATCCCATATTCAACTCAAACTGCAACACAAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db |||||
640 GAATTTATTGTCAGTGACAGTACCTACTCGTGGCATCCCTTACTCTACAAATACCTGCC 699

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db |||||
700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db |||||
760 TGTGTACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db |||||
820 GAAATAAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGCTCCACGGCTCTG 879

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db |||||
880 CTAGTGCTTGCTCTCCTCTCTTTGCTGCTGAGCTGGTCTTGGATTTGCTATGTCAA 939

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db |||||
940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAAATGATCGAAACC 999

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db |||||
1000 AAAGTAGTAAAGGAGGAGAGGCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACT 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db |||||
1060 GATAAAAACCCAGAGAGTCCAGAGTCCAGCAAAACTACCCTGCGATGCCTGGAAAGCT 1119

QY 321 GluVal 322
Db |||||
1120 GAAGTT 1125

RESULT 32

US-09-909-064-200
; Sequence 200, Application US/09909064
; Publication No. US20030059772A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David

Alignment Scores:

Pred. No.: 0
Score: 322.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Length: 2372
Matches: 322
Conservative: 0
Mismatches: 0

; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,064
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-909-064-200

Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0
US-10-079-111-1 (1-322) x US-09-909-064-200 (1-2372)			
Qy	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu	20
Db	160	ATGGCCAGGTGCTTACGCTGGTGTGCTTCTACATCCATCTGGACCACGAGGCTCCTG	219
Qy	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	220	GTCCAAGGCTCTTTCGCTGCAGAAAGAGCTTCCATCCAGGTGTCTATGCAGAAATATGGGG	279
Qy	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	280	ATCACCCCTGTGACAAAAAGCGAACCCAGCAGCTGAATTTTCACAGAAGCTAAGGAGGCC	339
Qy	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGGCTGCTGGACTAAGTTTGGCCGGCAAGCACCAAGTTGAAACAGCCCTTGAAGCT	399
Qy	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	400	AGCTTTGAACCTGCAGCTATGGCTGGGTGGAGATGGATTCTGTGGTCACTCTTAGGATT	459
Qy	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	460	AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTTGAAGGTTCCAGTG	519
Qy	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	520	AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACCTTGGACTAACTCGTGCAAT	579
Qy	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACGCAACACAAACAACA	639
Qy	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTTATTGTCTAGTGACAGTACCTACTCGGTGGCATCCCTTTACTCTACAATACCTGCC	699
Qy	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeulle	200
Db	700	CCTACTACTCTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	759
Qy	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTACAGAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCAATTGTT	819
Qy	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu	240
Db	820	GAAAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG	879
Qy	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGCTTGCTCTCTCTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGTCTATGTCAA	939
Qy	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAAATGATCGAAACC	999
Qy	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluSerLysLysThr	300
Db	1000	AAAGTAGTAAAGGAGGAAAGGCCAATGATAGCAACCTAATGAGGAATCAAAGAAAACT	1059
Qy	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAAACCCAGAAAGACTCCAAGAGTCCAAGCAAAACTACCGTCCGATGCCTGGAGCT	1119
Qy	321	GluVal	322
Db	1120	GAAGTT	1125

; ORGANISM: Homo sapiens									
US-09-904-553-200									
Alignment Scores:									
Pred. No.:	0	Length:	2372						
Score:	322.00	Matches:	322						
Percent Similarity:	100.00%	Conservative:	0						
Best Local Similarity:	100.00%	Mismatches:	0						
Query Match:	100.00%	Indels:	0						
DB:	10	Gaps:	0						
US-10-079-111-1 (1-322) x US-09-904-553-200 (1-2372)									
QY	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTIpThrThrArgLeuLeu	20						
Db	160	ATGCCAGGTGCTTCAGCCTGGTGTTCCTCACTTCCATCTGGACCAAGGCTCCTG	219						
QY	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40						
Db	220	GTCCAAGGCTCTTTCGCTGCAGAAAGACTTTCATCCAGGTGTCATGCAGAATTATGGG	279						
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60						
Db	280	ATCACCCCTTGTAGCAAAAAGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGCC	339						
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80						
Db	340	TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT	399						
QY	81	SerPheGluThrCysSerTyrGlyTIpValGlyAspGlyPheValValIleSerArgIle	100						
Db	400	AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGGTCATCTCTAGGATT	459						
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTIpLysValProVal	120						
Db	460	AGCCCCAAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCTGTGATTTGGAAGGTTCCAGTG	519						
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTIpThrAsnSerCysIle	140						
Db	520	AGCCGACAGTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCAATT	579						
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160						
Db	580	CCAGAAATTATCACCACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACAACA	639						
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180						
Db	640	GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	699						
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200						
Db	700	CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTTCACGGAGAAAAAATTGATT	759						
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal	220						
Db	760	TGTGTACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	819						
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240						
Db	820	GAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG	879						
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260						
Db	880	CTAGTGCTTGCTCTCCTCTTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAA	939						
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280						
Db	940	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC	999						
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluSerLysLysThr	300						
Db	1000	AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT	1059						

QY	301	AspLysAsnProGluSerLysSerProSerLysThrValArgCysLeuGluAla	320
Db	1060	GATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCTTGGAGCT	1119
QY	321	GluVal	322
Db	1120	GAAGTT	1125
RESULT 34			
US-09-905-381-200			
; Sequence 200, Application US/09905381			
; Publication No. US20030059829A1			
; GENERAL INFORMATION:			
; APPLICANT: Genentech, Inc.			
; APPLICANT: Ashkenazi, Avi			
; APPLICANT: Botstein, David			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Eaton, Dan L.			
; APPLICANT: Ferrara, Napoleone			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Fong, Sherman			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Gerber, Hanspeter			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, A.			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, Christopher J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Hillan, Kenneth, J.			
; APPLICANT: Kljavin, Ivar J.			
; APPLICANT: Mather, Jennie P.			
; APPLICANT: Pan, James			
; APPLICANT: Paoni, Nicholas F.			
; APPLICANT: Roy, Margaret Ann			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Williams, P. Mickey			
; APPLICANT: Wood, William, I.			
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
; TITLE OF INVENTION: Acids Encoding the Same			
; FILE REFERENCE: 10466-14			
; CURRENT APPLICATION NUMBER: US/09/905,381			
; CURRENT FILING DATE: 2001-07-13			
; PRIOR APPLICATION NUMBER: 09/665,350			
; PRIOR FILING DATE: 2000-09-18			
; PRIOR APPLICATION NUMBER: PCT/US00/04414			
; PRIOR FILING DATE: 2000-02-22			
; PRIOR APPLICATION NUMBER: US 60/143,048			
; PRIOR FILING DATE: 1999-07-07			
; PRIOR APPLICATION NUMBER: US 60/145,698			
; PRIOR FILING DATE: 1999-07-26			
; PRIOR APPLICATION NUMBER: US 60/146,222			
; PRIOR FILING DATE: 1999-07-28			
; PRIOR APPLICATION NUMBER: PCT/US99/20594			
; PRIOR FILING DATE: 1999-09-08			
; PRIOR APPLICATION NUMBER: PCT/US99/20944			
; PRIOR FILING DATE: 1999-09-13			
; PRIOR APPLICATION NUMBER: PCT/US99/21090			
; PRIOR FILING DATE: 1999-09-15			
; PRIOR APPLICATION NUMBER: PCT/US99/21547			
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; PRIOR FILING DATE: 1999-10-05			
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; PRIOR APPLICATION NUMBER: PCT/US99/28313			
; PRIOR FILING DATE: 1999-11-30			
; PRIOR APPLICATION NUMBER: PCT/US99/28564			
; PRIOR FILING DATE: 1999-12-02			
; PRIOR APPLICATION NUMBER: PCT/US99/28565			
; PRIOR FILING DATE: 1999-12-02			
; PRIOR APPLICATION NUMBER: PCT/US99/30095			
; PRIOR FILING DATE: 1999-12-16			


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; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-905-381-200

Alignment Scores:
Pred. No.:      0      Length:      2372
Score:          322.00    Matches:      322
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:      100.00%  Indels: 0
DB:              10      Gaps: 0

US-10-079-111-1 (1-322) x US-09-905-381-200 (1-2372)

Qy      1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db      160 ATGGCAGGTCCTTCAGCCTGGTGTGCTTCTCACTTCCATCGGACCACGAGGCTCCTG 219

Qy      21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      220 GTCCAGGCTCTTTGCGTGCAGAAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGG 279

Qy      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      280 ATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 339

Qy      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      340 TGTAGCGTCTGGGACTAAGTTTGGCCGCGCAAGGACCAAGTTGAAACAGCCTTTGAAAGCT 399

Qy      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db      400 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCTGGTTCATCTCTAGGATT 459

Qy      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCCTGATTGGAAAGTTCCAGTG 519

Qy      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACITGGACTAACTCGTGCAATT 579

Qy      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580 CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639

Qy      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640 GAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC 699

Qy      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATTGATT 759

Qy      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      760 TGTGTGCAGAGAAGTTTATTGGAACCTAGCACCATGTCTACAGAACTGAACCATTTGTT 819

Qy      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      820 GAAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879

Qy      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
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Db      880 CTAGTGCTTGCTCTCCTCTCTTTGGTGTCTGCAGCTGGTCTTGGAATTTTGCTATGTCAA 939

Qy      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
      |||||
Db      940 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAATGATCGAAACC 999

Qy      281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
      |||||
Db      1000 AAAGTAGTAAAGGAGGAGGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT 1059

Qy      301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
      |||||
Db      1060 GATAAAAACCCAGAAAGAGTCTCAAGAGTCCAAGCAAAACTACCGTGGATGCCCTGGAAGCT 1119

Qy      321 GluVal 322
      |||||
Db      1120 GAAGTT 1125

RESULT 35
US-09-905-088-200
; Sequence 200, Application US/09905088
; Publication No. US20030073077A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,088
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
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; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-905-088-200

Alignment Scores:
Pred. No.:      0      Length:      2372
Score:          322.00      Matches:      322
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels: 0
DB:              10      Gaps: 0

US-10-079-111-1 (1-322) x US-09-905-088-200 (1-2372)

QY      1  MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrrPThrThrArgLeuLeu 20
Db      160 ATGCCAGGTCGTTTCAGCCTGGTGTGTTCTTCTCACTTCCATCTGGACCAGAGGCTCCTG 219

QY      21  ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCATCCAGGTGTCATGCAGAATTATGGGG 279

QY      41  IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      280 ATCACCCCTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTACAGAACTTAAGGAGGCC 339

QY      61  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLysAla 80
Db      340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 399

QY      81  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db      400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCACTCTTAGGATT 459

QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      460 AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTGGAAGGTTCCAGTG 519

QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520 AGCCGACAGTTTGCAGCCTATTGTTACAACACTCATCTGATACCTGGACTAATCGTGCATT 579

QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580 CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 639

QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640 GAATTTATGTCAAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC 699

QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
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QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      760 TGTGTCACAGAGTTTTTATGGAAACTAGCACCATTGTCTACAGAAACTGAACCATTTGTT 819

QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      820 GAAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCACGGCTCTG 879

QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      880 CTAGTGTCTGCTCTCCTCTTCTTTTGGTGTGCTGAGCTGGTCTTGGATTTTGGTATGTCAA 939

QY      261 ArgTyrValLysAlaPhePropheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      940 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAAATGATCGAAACC 999

QY      281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db      1000 AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCTTAATGAGGATCAAAAGAAACT 1059

QY      301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db      1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGACTCCAAGCAAAACTACCGTCCGATGCTGGA 1119

QY      321 GluVal 322
Db      1120 GAAGTT 1125

RESULT 36
US-09-907-575-200
; Sequence 200, Application US/09907575
; Publication No. US20030073079A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,575
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
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; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-575-200

Alignment Scores:

Pred. No.:	0	Length:	2372
Score:	322.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-079-111-1 (1-322) x US-09-907-575-200 (1-2372)

QY	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu	20
Db	160	ATGCCAGGTGCTTCAGCCCTGGTGTGCTTCTCACCTCCATCTGGACCACGAGGCTCTG	219
QY	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	220	GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGCATGCAGAAATTATGGG	279
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	280	ATCACCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTCACAGAAGCTAAGGAGCC	339
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGGCTGCTGGACTAAGTTGGCCGGCAAGGACCAAGTTCGAAACAGCCTTGAAAGCT	399
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	400	AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGGTGCATCTCTAGGATT	459
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValIleTrpLysValProVal	120
Db	460	AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCCTGATTGGAAAGTTCCAGTG	519
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	520	AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCAATT	579
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAAACTGCAACACAACA	639

QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	699
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	700	CCTACTACTCCTCCTCGCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT	759
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu	240
Db	820	GAAAAATAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG	879
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGCTTGCTCTCCTCTTCTTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAA	939
QY	261	ArgTyrValLysAlaPhePropheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAATGATCGAAACC	999
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1000	AAAGTAGTAAAGGAGGAGGAGGCCCAATGATAGCAACCTAATGAGGAATCAAAGAAAACT	1059
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAAACCCAGAGAGTCCAAAGAGTCCAAAGCAAAACTACCGTCCGATGCCTGGAGCT	1119
QY	321	GluVal	322
Db	1120	GAAATT	1125
RESULT 37			
US-09-905-075-200			
; Sequence 200, Application US/09905075			
; Publication No. US20030077583A1			
; GENERAL INFORMATION:			
; APPLICANT: Genentech, Inc.			
; APPLICANT: Ashkenazi, Avi			
; APPLICANT: Botstein, David			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Eaton, Dan L.			
; APPLICANT: Ferrara, Napoleone			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Fong, Sherman			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Gerber, Hanspeter			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, A.			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, Christopher J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Hillan, Kenneth, J.			
; APPLICANT: Kljavin, Ivar J.			
; APPLICANT: Mather, Jennie P.			
; APPLICANT: Pan, James			
; APPLICANT: Paoni, Nicholas F.			
; APPLICANT: Roy, Margaret Ann			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Williams, P. Mickey			
; APPLICANT: Wood, William, I.			
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
; TITLE OF INVENTION: Acids Encoding the Same			
; FILE REFERENCE: 10466-14			
; CURRENT APPLICATION NUMBER: US/09/905,075			
; CURRENT FILING DATE: 2001-07-13			
; Prior application data removed. Check file wrapper or PALM.			
; NUMBER OF SEQ ID NOS: 423			


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; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-905-075-200

Alignment Scores:
Pred. No.:      0      Length:      2372
Score:          322.00  Matches:      322
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:      100.00%  Indels: 0
DB:              10      Gaps: 0

US-10-079-111-1 (1-322) x US-09-905-075-200 (1-2372)

QY      1  MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db      160  ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCAGGCTCCTG 219

QY      21  ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      220  GTCCAAGGCTCTTTGGCGTCAGAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG 279

QY      41  IleThrLeuValSerLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      280  ATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 339

QY      61  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      340  TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGACCAAGTTGAAACAGCCTTGAAAGCT 399

QY      81  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
Db      400  AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGTGTCATCTTAGGATT 459

QY      101  SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      460  AGCCCAAAACCCCAAGTGTTGGGAAAAATGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG 519

QY      121  SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520  AGCCGACAGTTTGCAGCCTATTGTTACRACTCATCTGTACTTGGACTAACTCGTGCAAT 579

QY      141  ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580  CCAGAAATTATACCAACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACA 639

QY      161  GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640  GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTTACTACAATACCTGCC 699

QY      181  ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      700  CCTACTACTCTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY      201  CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db      760  TGTGTACAGAAAGTTTTTATGGAAGCTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

QY      221  GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      820  GAAATAAAGCAGCATTCAAGAATGAAGTGTCTGGGTTTGGAGGTGCCCCACGGCTCTG 879

QY      241  LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      880  CTAGTGCTTGCTCTCCTCTCTTCTTTGGTGTGCAGCTGGTCTTGGATTGTGCTATGTCAA 939

QY      261  ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      940  AGGATGTGAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAAGGAATGATCGAAACC 999

QY      281  LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
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Db      1000  AAAGTAGTAAAGGAGGAGAGCCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACT 1059

QY      301  AspLysAsnProGluGluSerLysSerProSerLysThrValArgCysLeuGluAla 320
Db      1060  GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCTGGAAGCT 1119

QY      321  GluVal 322
Db      1120  GAAGTT 1125

RESULT 38
US-09-902-759-200
; Sequence 200, Application US/09902759
; Publication No. US20030077654A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,759
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
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; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-902-634-200

Alignment Scores:
Pred. No.:      0      Length:      2372
Score:          322.00      Matches:      322
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels: 0
DB:              10      Gaps: 0

US-10-079-111-1 (1-322) x US-09-902-634-200 (1-2372)

QY      1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db      160 ATGCCAGGCTCTTCAGCCTGGTGTCTCTCACTTCCATCTGGACGAGGCTCCTG 219

QY      21 ValGlnGlySerLeuArgAlaGluGluSerIleGlnValSerCysArgIleMetGly 40
Db      220 GTCCAAGGCTCTTTCGCTGCAGAGAGCTTCCATCCAGGTGTCATCGAGAATTATGGG 279

QY      41 ileThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      280 ATCACCCCTGTGAGCAAAAGCGCAACGACGAGCTGAATTCACAGAAGCTAAGGAGGCC 339

QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      340 TGTAGGCTGTGGGACTAAGTTTGGCCGCGCAAGGCCAAGTTTGAACAGCCTTGAAAGCT 399

QY      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db      400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGTCATCTCTAGGATT 459

QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      460 AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGAAGGTTCCAGTG 519

QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520 AGCCGACAGTTTGCAGCCTATTGTTACAACACTCATCTGATACTTGACTAATCGTGCATT 579

QY      141 ProGluIleIleThrThrLysAspProfilePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580 CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAACAACA 639

QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699

QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
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Db      760 TGTGTCACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      820 GAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCACGGCTCTG 879

QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      880 CTAGTGTCTGCTCTCTCTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA 939

QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      940 AGGTATGTGAAGGCCTTCCCTTTTACAAAACAAGAATCAGCAGAAGGAATGATCGAAACC 999

QY      281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysThr 300
Db      1000 AAAGTAGTAAGGAGGAGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAAAGAAACT 1059

QY      301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db      1060 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCAGATGCCTGGAAGCT 1119

QY      321 GluVal 322
Db      1120 GAAGTT 1125

RESULT 40
US-09-902-713-200
; Sequence 200, Application US/09902713
; Publication No. US20030082541A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,713
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
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; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-902-713-200

Alignment Scores:
Pred. No.:      0      Length:      2372
Score:          322.00  Matches:      322
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:      100.00%  Indels: 0
DB:              10      Gaps: 0

US-10-079-111-1 (1-322) x US-09-902-713-200 (1-2372)

QY      1  MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db      160 ATGCCAGGTGCTTCAGCCCTGGTGTGCTTCTCACTTCATCTGGACCACGAGGCTCCTG 219

QY      21  ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      220 GTCCAAGGCTCTTTGCGTGCAAGAGAGCTTTCCATCCAGGTGCATGCAGAAATTATGGGG 279

QY      41  IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      280 ATCACCTTGTGAGCAAAAAGCGGAACCAAGCAGCTGAATTCACAGAAGCTAAGGAGGCC 339

QY      61  CysArgLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      340 TGTAGGCTGCTGGGACTAAGTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

QY      81  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db      400 AGCTTTGAAACTTGCAGCTATGCGTGGGTGGAGATGGATTGCTGGTGCATCTCTAGGATT 459

QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuilleTrpLysValProVal 120
Db      460 AGCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCCTGATTGGAAGGTTCCAGTG 519

QY      121 SerArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520 AGCCGACAGTTTGCAGCCTATTGTTACAACACTCATCTGATACTTGGACTTAACTCGTGCATT 579

QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580 CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAAACTGCAACAAACACA 639
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QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699

QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      700 CCTACTACTACTCTCTCTCTCCAGCTTCCACATCTTATTCACGGAGAAAAAATTGATT 759

QY      201 CysValThrGluValPheMetGluThrSerThrSerThrMetSerThrGluThrGluProPheVal 220
Db      760 TGTGTCAACAGAAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      820 GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879

QY      241 LeuValLeuAlaLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      880 CTAGTGTCTGCTCTCTCTCTTTTGGTGTGCTGCAGTGGTCTTGGATTTTGTCTATGTCAAA 939

QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      940 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC 999

QY      281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db      1000 AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCTTAATGAGGAATCAAAGAAACT 1059

QY      301 AspLysAsnProGluGluSerLysSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db      1060 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAAACCTACCGTGGATGCCTGGAGCT 1119

QY      321 GluVal 322
Db      1120 GAAGTT 1125

RESULT 41
US-09-907-979-200
; Sequence 200, Application US/09907979
; Publication No. US20030082542A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,979
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
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; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-979-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-907-979-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAAAGCTTTCCATCCAGGTGTCTGAGAAATTATGGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAAGCGCAACCAAGCAAGTTGAAACAGCCTTGAAGGCT 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTTAAGTTTGGCCGCAAGCAAGTTGAAACAGCCTTGAAGGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCTGGTCTATCTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTCTGATTGGGAAGGTTCCAGTG 519
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QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACATCATCTGATACCTTGGACTAACTCGTGCAAT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCACCAAGATCCCATATTCACACTCAAACTGCAACACAAACAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC 699

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTCTCTCTCTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAAAATAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTCTGCTCTCTCTCTTTTGGTGTGCTGCAGCTGGTCTTTGGATTTTGTATGTCAA 939

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAAACAAGAAATCAGCAGAGGAAATGATCGAAACC 999

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAGGAGGAGAGGCCCAATGATAGCAACCTAATGAGGAATCAAAGAAAACT 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAACCCAGAAAGAGTCCCAAGAGTCCAAAGCAAAACTACCGTGGCATGCCTGGAAGCT 1119

QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 42
US-09-902-615-200
; Sequence 200, Application US/09902615
; Publication No. US20030092002A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hallan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
```

```
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,615
; CURRENT FILING DATE: 2001-12-14
; Prior application data removed. Check file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-615-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-902-615-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTCAGCCCTGGTGTGCTTCTCACITTCATCTGGACCACGAGGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGGGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTTGTAGCAAAAGGCGAACCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCGTGGTCATCTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTGATTTGGAAAGGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACTGCC 699

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCAGGAGAAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
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QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCCTCCTCTCTTTTGGTGCTGCAGTGGTCTTGGATTTTGCATGTCAA 939

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAAATGATCGAAACC 999

QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGAGAGAGGCCAATGATAGCAACCACTAATGAGGAATCAAGAAACT 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGGAGTCCAAGCAAACTACCGTGCATGCCTGGAAGCT 1119

QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 43
US-09-903-925-200
; Sequence 200, Application US/09903925
; Publication No. US20030096233A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/903,925
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
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; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-903-925-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-903-925-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTCCATCTGGACCAGAGGTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAAGGCTCTTTGCGTGCAGAAAGAGCTTCCATCCAGGTGTCATGCAGAAATTATGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTCCACAGAGCTAAAGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGTGGGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCCTGATTGGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

Db 700 CCTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTTCAAGAAATGAAGCTGGTGGGTTTGGAGGTGTCCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTCTCTCTCTCTCTTTTGGTGTGCAGCTGGTCTTGGATTGTGCTATGTCAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCTTAATGAGGAATCAAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125
RESULT 44
US-09-906-760A-200
; Sequence 200, Application US/09906760A
; Publication No. US20030096340A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,760A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28


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; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-903-823-200

Alignment Scores:
Pred. No.:          0      Length:      2372
Score:              322.00  Matches:      322
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:        100.00%  Indels: 0
DB:                  10      Gaps: 0

US-10-079-111-1 (1-322) x US-09-903-823-200 (1-2372)

QY      1  MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db      160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCAAGGCTCCTG 219

QY      21  ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      220 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279

QY      41  IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      280 ATCACCCCTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 339

QY      61  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAAGCT 399

QY      81  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
Db      400 AGCTTTGAAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCCGTGGTCATCTCTAGGATT 459

QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

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Db      460 AGCCCAAAACCCCAAGTGTGGGAAAAAATGGGGTGGTGTCTTGATTGGGAAGGTTCCAGTG 519
QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACCTTGGACTAACTCGTGCAAT 579
QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580 CCAGAAATTATCACCCAAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639
QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640 GAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699
QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      700 CCTACTACTACTCCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      760 TGTGTCAAGAAAGTTTATTGGAAGTACGACCATGTCTACAGAAACTGAACCATTTGTT 819
QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      820 GAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      880 CTAGTGCTTGTCTCTCTCTTCTTTGGTGTGCTGCAGTGGTCTTGGATTTTGTATGTCAA 939
QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      940 AGGTATGTGAAGGCCCTTCCCTTTTACAAAACAAGAAATCAGCAGAGGAAATGATCGAAACC 999
QY      281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db      1000 AAAGTAGTAAAGGAGGAGGAGCAATGATAGCAACCCTAATGAGGAATCAAAGAAACT 1059
QY      301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db      1060 GATAAAAACCCAGAGAGTCCACAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAAGCT 1119
QY      321 GluVal 322
Db      1120 GAAGTT 1125

RESULT 46
US-09-907-652-200
; Sequence 200, Application US/09907652
; Publication No. US2003010469A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.

```



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; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,652
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-652-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-907-652-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCGTGGTGTGCTTCTCACTCCATCTGGACCACGAGGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAAGCGAACCAGCAGCTGAATTCACAGAAGCTAAGGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGGTCAATCTTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTGATTTGGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCCACCAAGATCCCATATTTCACACTCAAACTGCAACACACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTCAACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 820 GAAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTCTGCTCTCTCTCTTTTGGTGTGTCAGCTGGTCTTTGGATTTTGGCTATGTCAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCCTCCCTTTTACAAACAAGAAATCAGCAGAAGGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAGGAGAGAGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAGAAACT 1059
QY 301 AspLysAsnProGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAACCCAGAGAGTCCAAGAGTCCAGCAAAAACCTACCGTGCATGCCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 47
US-09-902-572A-200
; Sequence 200, Application US/09902572A
; Publication No. US20030108983A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,572A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-572A-200

Alignment Scores:
Pred. No.:      0      Length:      2372
Score:          322.00      Matches:      322
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels: 0
DB:              10      Gaps: 0

US-10-079-111-1 (1-322) x US-09-902-572A-200 (1-2372)

QY      1  MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db      160 ATGCCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219

QY      21  ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTCCATCCAGGTGTCATGCAGAATTATGGGG 279

QY      41  IleThrLeuValSerLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      280 ATCACCCCTGTGAGCAAAAGGCGAACACGAGCTGAATTTACAGAGCTAAGGAGGCC 339

QY      61  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGACGCTTGAAGCT 399

QY      81  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db      400 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGGTCATCTCTAGGATT 459
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QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuLeuTrpLysValProVal 120
Db      460 AGCCCAAAACCCCAAGTGTGGGAAAAAATGGGGTGGGTGCTCCTGATTGGAAAGGTTCCAGTG 519

QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520 AGCCGACAGTTTGCAGCCTATTGTACAACTCATCTGATACTTGGACTAACTCGTGCATT 579

QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580 CCAGAAATTATCACCCAAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639

QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC 699

QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      700 CCTACTACTACTCCTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759

QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      760 TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      820 GAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879

QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      880 CTAGTGCTTGCTCTCTCTCTTTTGGTGTGCTGCAGCTGGTCTTGGATTGCTATGTCAA 939

QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      940 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAAATGATCGAAACC 999

QY      281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysThr 300
Db      1000 AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCTAATAGGAATCAAAGAAACT 1059

QY      301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db      1060 GATAAAAAACCCAGAAAGAGTCCAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAAGCT 1119

QY      321 GluVal 322
Db      1120 GAAGTT 1125

RESULT 48
US-09-902-979-200
; Sequence 200, Application US/09902979
; Publication No. US20030113718A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
```

```

; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,979
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-902-979-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-902-979-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCTGGTGTGTTCTCACTCCATCTGGACCACGAGGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGG 279

QY 41 IleThrLeuValSerLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAAGGGCAACCAGCAGCTGAATTTCACAGAAGCTAAGGAGGCC 339
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QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCTGGTTCATCTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTTGGAAGGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCACTGATACCTTGGACTAATCGTGCATT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACTGCC 699

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCTGCTCCAGCTTCCACCTTATTTCCACGGAGAAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTCACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACATTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAAAATAAAGCAGCAATCAAGAATGAAGCTGCTGGGTTTGAGGTTGTCCCCACGGGCTCG 879

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCCTCTTCTTTGGTGTCTGCAGCTGGTCTTGGATTTTGCATATGTCAA 939

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC 999

QY 281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT 1059

QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAAACCTACCGTCCGATGCCCTGGAAGCT 1119

QY 321 GluVal 322
Db 1120 GAAAGTT 1125

RESULT 49
US-09-905-125-200
; Sequence 200, Application US/09905125
; Publication No. US20030113719A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-905-125-200
Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-10-079-111-1 (1-322) x US-09-905-125-200 (1-2372)
Qy 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
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Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 219
Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGGGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGATTATGGGG 279
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTTCAGAAAGCTAAGGAGGCC 339
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGACGCTATGGCTGGGTGGAGATGGATTTCGTGGTCATCTCTAGGATT 459
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAATGGGGTGGGTGCTCCTGATTGGAAGGTTCCAGTG 519
Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCAAT 579
Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCCCAAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639
Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTCAGTGACAGTACCTACTCGTGGTGGCATCCCCCTTACTCTACAATACCTGCC 699
Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCCTCGTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTTGATT 759
Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACACAGAAAGTTTTTATGGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 819
Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCCTCTTCTTTGGTGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAA 939
Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCCTTCCCTTTTACAACAAGAAATCAGCAGAGGAAATGATCGAAACC 999
Qy 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGAGGCCCAATGATAGCAACCTTATGAGGAATCAAAGAAACT 1059
Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAAACCCAGAGAGTCCCAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCT 1119
Qy 321 GluVal 322
Db 1120 GAAGTT 1125
RESULT 50
US-09-906-815A-200
; Sequence 200, Application US/09906815A
; Publication No. US20030113838A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,815A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-906-815A-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322

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Db 1120 GAAGTT 1125

Search completed: September 16, 2004, 05:29:16
Job time : 2347 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: September 15, 2004, 03:45:39 ; Search time 7898 Seconds
(without alignments)
11134.846 Million cell updates/sec

Title: US-10-079-111-2
Perfect score: 2029
Sequence: 1 ccttgacaagtcagaagctt.....aaacattttaaaaaaaaaa 2029

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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7:	gb_ph:*		
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39:	em_htgo_hum:*		
40:	em_htgo_mus:*		
41:	em_htgo_other:*		

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2029	100.0	2029	6	AR204700	AR204700 Sequence
2	2029	100.0	2029	6	BD222718	BD222718 Human sig
3	1994	98.3	2372	6	AR410761	AR410761 Sequence
4	1994	98.3	2372	6	AX092274	AX092274 Sequence
5	1994	98.3	2372	6	AX454446	AX454446 Sequence
6	1994	98.3	2372	6	AX490924	AX490924 Sequence
7	1994	98.3	2372	6	AX697609	AX697609 Sequence
8	1994	98.3	2372	6	BD075532	BD075532 Secretary
9	1994	98.3	2372	6	BD172392	BD172392 Secreted
10	1994	98.3	2372	6	BD172711	BD172711 Secreted
11	1994	98.3	2372	6	BD173030	BD173030 Secreted
12	1994	98.3	2372	6	BD173349	BD173349 Secreted
13	1994	98.3	2372	6	BD175383	BD175383 Secretary
14	1994	98.3	2372	9	AY358925	AY358925 Homo sapi
15	1907.2	94.0	2313	9	AF118108	AF118108 Homo sapi
16	1876.8	92.5	2282	9	BC026231	BC026231 Homo sapi
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22	927.2	45.7	1613	4	AY372937	AY372937 Bos tauru
23	654.8	32.3	716	6	AX136529	AX136529 Sequence
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25	631	31.1	2027	10	BC038653	BC038653 Mus muscu
26	631	31.1	2027	10	BC038892	BC038892 Mus muscu
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C 28	499.4	24.6	516	6	AX331191	AX331191 Sequence
C 29	499.4	24.6	516	6	AX331600	AX331600 Sequence
C 30	499.4	24.6	516	6	AX332298	AX332298 Sequence
C 31	499.4	24.6	516	6	AX333352	AX333352 Sequence
C 32	499.4	24.6	516	6	AX333777	AX333777 Sequence
C 33	499.4	24.6	516	6	AX407467	AX407467 Sequence
C 34	458.8	22.6	591	6	AX136672	AX136672 Sequence
C 35	458.8	22.6	591	6	BD123912	BD123912 Secretary
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37	386.2	19.0	603	4	AY304537	AY304537 Sus scrof
38	354.8	17.5	373	6	BD073800	BD073800 5'EST of
39	343	16.9	363	6	BD077623	BD077623 5'EST of
40	261.4	12.9	506	6	AX156239	AX156239 Sequence
C 41	239	11.8	241	6	AR280816	AR280816 Sequence
C 42	239	11.8	241	6	AR283312	AR283312 Sequence
C 43	239	11.8	241	6	AR344080	AR344080 Sequence
C 44	239	11.8	241	6	AR351281	AR351281 Sequence
C 45	239	11.8	241	6	AX303004	AX303004 Sequence

ALIGNMENTS

RESULT 1					
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LOCUS	AR204700	2029 bp	DNA	linear	PAT 20-JUN-2002
DEFINITION	Sequence 13 from patent US 6368794.				
ACCESSION	AR204700				
VERSION	AR204700.1	GI:21502094			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 2029)				
AUTHORS	Daniel,S., Gilmore,J., Stuart,S.G. and Stuve,L.L.				
TITLE	Detection of altered expression of genes regulating cell proliferation				
JOURNAL	Patent: US 6368794-A 13 09-APR-2002;				

RESULT 2
BD222718
LOCUS
DEFINITION Human signal peptide-containing protein.
ACCESSION BD222718
VERSION BD222718.1 GI:33032488
KEYWORDS JP 2002519030-A/64.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2029)
AUTHORS Lal,P., Tang,Y.T., Gorgone,G.A., Corley,N.C., Guegler,K.J.,
Baughn,M.R., Akerblom,I.E., Young,J.A., Yue,H., Patterson,C.,
Reddy,R., Hillman,J.L. and Bandman,O.
TITLE Human signal peptide-containing protein
JOURNAL Patent: JP 2002519030-A 64 02-JUL-2002;
INCYTE PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002519030-A/64
PD 02-JUL-2002
PF 25-JUN-1999 JP 2000557363
PR 26-JUN-1998 US 60/090762,31-JUL-1998 US 60/094983 PR
01-OCT-1998 US 60/102686,11-DEC-1998 US 60/112129 PI PREETI
LAL,Y TOM TANG,GINA A GORGONE,NEIL C CORLEY,KARL J PI GUEGLER,
PI MARIAH R BAUGHN,INGRID E AKERBLOM,JANICE AU YOUNG,HENRY YUE,
PI CHANDRA PATTERSON,ROOPA REDDY,JENNIFER L HILLMAN,OLGA BANDMAN
PC C12N15/09,A61K38/00,A61K39/395,A61K45/00,A61P9/00,A61P15/00,
PC A61P25/00,
PC A61P29/00,A61P35/00,A61P43/00,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/68//C12P21/08, PC
C12N15/00,
PC A61K37/02,C12N5/00
CC Incyte Clone No: 3044710
FH Key Location/Qualifiers
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FT /organism='Homo sapiens (human)'.
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Best local Similarity 100.0%; Pred. No. 0;
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RESULT 3
AR410761
LOCUS AR410761 2372 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 200 from patent US 6635468.
ACCESSION AR410761
VERSION AR410761.1 GI:40162261
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 2372)
Ashkenazi,A., Botstein,D., Desnovers,L., Eaton,D.L., Ferrara,N.,
Filvaroff,E., Fong,S., Gao,W.-Q., Gerber,H., Gerritsen,M.E.,
Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Hillan,K.J.,
Kljamin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A.,
Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: US 6635468-A 200 21-OCT-2003;
FEATURES Location/Qualifiers
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ORIGIN
Query Match 98.3%; Score 1994; DB 6; Length 2372;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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1 AGCAGGGAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60
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RESULT 4	
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LOCUS	AX092274
DEFINITION	Sequence 5 from Patent WO0116318.
ACCESSION	AX092274
VERSION	AX092274.1
KEYWORDS	GI:13444451
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1

AUTHORS	Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and Wood,W.I.									
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same									
JOURNAL	Patent: WO 0116318-A 5 08-MAR-2001; Genentech, Inc. (US)									
FEATURES	Location/Qualifiers									
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AX454446
LOCUS AX454446 2372 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 31 from Patent WO0208284.
ACCESSION AX454446
VERSION AX454446.1 GI:21713847
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS
Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.
TITILE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0208284-A 31 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)
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VERSION	AX490924.1	GI:22323799	
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I. and Ye,W.		
TITLE	Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis		
JOURNAL	Patent: WO 0200690-A 31 03-JAN-2002; Genentech, Inc. (US)		
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SOURCE      Homo sapiens (human)
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             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
             Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
             Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
             and Ye,W.
TITLE       Compositions and methods for the diagnosis and treatment of
             disorders involving angiogenesis
JOURNAL     Patent: WO 0200690-A 31 03-JAN-2002;
             Genentech, Inc. (US)
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Db 1981 TTCAACAAAACATTTGCTGAATA 2002

RESULT 7
AX697609
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

AX697609
Sequence 200 from Patent WO0104311.
AX697609
AX697609.1 GI:29498705
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Ashkenazi,A.J., Botstein,D., Desnovers,L., Eaton,D.L., Ferrara,N.,
Filvaroff,E., Fong,S., Gao,W.Q., Gerber,H., Gerritsen,M.E.,

Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Hillan,K.J.,
Kljavin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A.,
Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I.
TITLE
Secreted and transmembrane polypeptides and nucleic acids encoding
the same

JOURNAL
Patent: WO 0104311-A 200 18-JAN-2001;
Genentech Inc. (US)
FEATURES
Location/Qualifiers
source
1. .2372
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ORIGIN

Query Match 98.3%; Score 1994; DB 6; Length 2372;
Best Local Similarity 99.8%; Pred. No. 0;
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Db	181	GTGTTGCTTCTC	ACTTCCATCTGGAC	CACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA	240
QY	264	GAAGAGCTTTCCATCCAGG	TGTCAGAAATTATGGGGAT	CACCCCTTGTGAGCAAAAAG	323
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QY	1164	TGAGGAGACACACCTGAG	GGTGGTTTCTTTCAIGCT	CCTTACCCTGCCCGCAGCTGGGAA	1223
Db	1141	TGAGGAGACACACCTGAG	GGTGGTTTCTTTTCAIGCT	CCTTACCCTGCCCGCAGCTGGGAA	1200
QY	1224	ATCAAAAGGGCCAAAGAA	ACCAAGAGAAAGTCCAC	CCCTGGTTCCTAACTGGAATCAGC	1283
Db	1201	ATCAAAAGGGCCAAAGAA	ACCAAGAGAAAGTCCAC	CCCTGGTTCCTAACTGGAATCAGC	1260
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Db	1261	TCAGGACTGCCATTGGAC	TATGGAGTGCACCAAG	AGAAATGCCCTTCTCCTTATTGTAAC	1320
QY	1344	CCTGTCTGGATCCTATC	CTCTCTACCTCCAAAG	CTTCCACGGCCTTTCTAGCCTGGCTAT	1403
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Db 1981 TTCAACAACAATTTGCTGAATA 2002

LOCUS BD172392 2372 bp DNA linear PAT 18-FEB-2003

DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding the same.

ACCESSION BD172392

VERSION BD172392.1 GI:28413692

KEYWORDS JP 2002223786-A/165.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2372)

AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: JP 2002223786-A 165 13-AUG-2002; GENENTECH INC

COMMENT OS Homo sapiens (human)

PN JP 2002223786-A/165

PD 13-AUG-2002

PF 18-DEC-2001 JP 2001385135

PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR

17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR

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17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR

18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR

17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR

21-OCT-1997 US 60/063486,24-OCT-1997 US 60/062816 PR

24-OCT-1997 US 60/062814,24-OCT-1997 US 60/063127 PR

24-OCT-1997 US 60/063120,24-OCT-1997 US 60/063121 PR

24-OCT-1997 US 60/063045,24-OCT-1997 US 60/063128 PR

27-OCT-1997 US 60/063329,27-OCT-1997 US 60/063327 PR

28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR

28-OCT-1997 US 60/063550,28-OCT-1997 US 60/063542 PR

28-OCT-1997 US 60/063544,28-OCT-1997 US 60/063564 PR

29-OCT-1997 US 60/063734,29-OCT-1997 US 60/063738 PR

29-OCT-1997 US 60/063704,29-OCT-1997 US 60/063435 PR

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07-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR

17-NOV-1997 US 60/065846,18-NOV-1997 US 60/065693 PR

21-NOV-1997 US 60/066120,21-NOV-1997 US 60/066364 PR

24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066466 PR

24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR

24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI

WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI

JIAN ZHENG,

PI JEAN YUAN

PC C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC C12N5/10,

PC C12P21/02//C12P21/08,(C12P21/02,C12R1:19),(C12P21/02,C12R1:91), PC (C12P21/02,C12R1:645),C12N15/00,C12N5/00

CC Secreted and transmembrane polypeptides and nucleic CC acids encoding the same

FH Key Location/Qualifiers

FT source 1. .2372

FT Location/Qualifiers

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FEATURES

source

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ORIGIN

Query Match 98.3%; Score 1994; DB 6; Length 2372;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 1 AGCAGGGAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60

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Db	61	GTTCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGGC	120
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QY	204	GTGTTGCTTCTCACTTCATCTGGACCAACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA	263
Db	181	GTGTTGCTTCTCACTTCATCTGGACCAACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA	240
QY	264	GAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAG	323
Db	241	GAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAG	300
QY	324	GCGAACCCAGCAGCTGAATTCACAGAAGCTAAGGAGCCCTGTAGGCTGCTGGACTAAGT	383
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QY	384	TTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT	443
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RESULT 10
BD172711
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BD172711 2372 bp DNA linear PAT 18-FEB-2003
Secreted and transmembrane polypeptides and nucleic acids encoding
the same.

BD172711
BD172711.1 GI:28414015
JP 2002238586-A/165.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.


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AUTHORS
  Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
  Yuan,J.
TITLE
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VERSION	BD173349.1		GI:28414660			
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ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and Yuan, J.					
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same					
JOURNAL	Patent: JP 2002238588-A 165 27-AUG-2002;					
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WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI		
JIAN ZHENG,		
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AY358925

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DEFINITION Homo sapiens clone DNA34431 XLKD1 (UNQ230) mRNA, complete cds.
ACCESSION AY358925
VERSION AY358925.1 GI:37182967
KEYWORDS FLI CDNA.

SOURCE
ORGANISM

Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2372)

REFERENCE
AUTHORS

Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
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Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:

TITLE

A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)

JOURNAL
PUBMED

REFERENCE
AUTHORS

TITLE
JOURNAL

FEATURES
source

12975309
2 (bases 1 to 2372)
Clark,H.F.
Direct Submission
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA

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AF118108
LOCUS
DEFINITION Homo sapiens lymphatic endothelium-specific hyaluronan receptor
LYVE-1 mRNA, complete cds.
ACCESSION AF118108
VERSION AF118108.1 GI:5359672
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2313)
AUTHORS Banerji,S., Ni,J., Wang,S.X., Clasper,S., Su,J., Tammi,R., Jones,M.
and Jackson,D.G.
TITLE LYVE-1, a new homologue of the CD44 glycoprotein, is a
lymph-specific receptor for hyaluronan
JOURNAL J. Cell Biol. 144 (4), 789-801 (1999)
MEDLINE 99156989
PUBMED 10037799
REFERENCE 2 (bases 1 to 2313)
AUTHORS Jackson,D.G., Banerji,S. and Ni,J.
TITLE Direct Submision
JOURNAL Submitted (06-JAN-1999) MRC Human Immunology Unit, Univ. of Oxford,
John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK
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B/ank

GenCore version 5.1.6
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Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
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2: em_esthum:*
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25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description
C 1	1053.4	51.9	1143 9	AL574194
2	1043.8	51.4	1154 9	AL550279
3	991.6	48.9	1201 9	AL550621
C 4	954.6	47.0	1073 9	AL552625

C 5	954.4	47.0	1201 9	AL546590
6	943.8	46.5	1015 9	AL552299
C 7	937.8	46.2	1157 9	AL575514
8	936	46.1	1201 13	BX366718
C 9	933	46.0	1007 9	AL575633
10	932.8	46.0	1201 9	AL547774
11	925.8	45.6	1201 9	AL546669
12	924.2	45.5	1172 9	AL552127
13	914	45.0	1116 9	AL552661
C 14	907.6	44.7	973 9	AL574433
15	907.2	44.7	1201 9	AL546623
16	905.4	44.6	1201 9	AL544430
C 17	899.8	44.3	978 9	AL573693
18	893.4	44.0	1151 9	AL550829
19	891.6	43.9	1074 9	AL552777
20	890.4	43.9	1201 13	BX402505
C 21	885.4	43.6	1201 9	AL571928
22	881	43.4	970 9	AL550615
23	878.6	43.3	1172 9	AL550911
24	877.2	43.2	1201 9	AL551020
25	872.8	43.0	1014 9	AL553858
C 26	854.4	42.1	1161 9	AL550876
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C 28	848.4	41.8	1201 9	AL570563
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30	834.8	41.1	913 13	BX459046
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32	826.8	40.7	1201 13	BX366589
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37	788	38.8	863 12	BI761420
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39	774.4	38.2	839 9	AL546217
40	755	37.2	960 9	AL553920
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C 43	728	35.9	987 13	BX418210
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ALIGNMENTS

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LOCUS	AL574194	Homo sapiens	PLACENTA COT 25-NORMALIZED	Homo sapiens	cdna	
DEFINITION	clone CS0DI039YJ06 3-PRIME, mrna sequence.					
ACCESSION	AL574194					
VERSION	AL574194.2	GI:31295529				
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.					
TITLE	Full-length cDNA libraries and normalization					
JOURNAL	Unpublished (2001)					
COMMENT	On Feb 16, 2001 this sequence version replaced gi:12934166. Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r For more information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI039DE03NP1&cluster=5952.r. Contact : Feng Liang Email : fliang@lifetech.com URL :					

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http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI039DE03NP1.
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        /note="1st strand cDNA was primed with a NotI-oligo(dT)
        primer. Five prime end enriched, double-strand cDNA was
        digested with Not I and cloned into the Not I and EcoR V
        sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
    Query Match
    Best Local Similarity 51.9%; Score 1053.4; DB 9; Length 1143;
    Matches 1083; Conservative 8; Mismatches 20; Indels 2; Gaps 2;
QY 769 GAAAAAAATTGATTGTGTCACAGAAAGTTTATGGAAACTAGCAACATGTCTACAGAAA 828
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Db 665 AGAAAGTCCACCCCTTGGTTCTTAAGTGAATCAGCTCAGGACTGCCATTTGGACTATGGAG 606
QY 1309 TGCACCAAGAGAAATGCCCTTCTCCTTTATTTAAACCCCTGTCTGGATCCTATCCTCCTACC 1368
Db 605 TGCACCAAGAGAAATGCCCTTCTCCTTTATTTAAACCCCTGTCTGGATCCTATCCTCCTACC 546
QY 1369 TCCAAAGCTTCCACGGCCCTTTCTAGCCTGGCTATGTCCTAATAATATATCCACTGGGAGA 1428
Db 545 TCCAAAGCTTCCACGGCCCTTTCTAGCCTGGCTATGTCCTAATAATATATCCACTGGGAGA 486
QY 1429 AAGGAGTTTTCGAAAGTGCAGGACCTTAAACATCTCATCAGTATCCAGTGGTAAAGG 1488
Db 485 AAGGAGTTTTCGAAAGTGCAGGACCTTAAACATCTCATCAGTATCCAGTGGTAAAGG 426
QY 1489 CCTCTGGCTGTCTGAGGCTAGGTGGTTGAAAGCCCAAGGAGTCACTGAGACCAAGGCTT 1548
Db 425 CCTCTGGCTGTCTGAGGCTAGGTGGTTGAAAGCCCAAGGAGTCACTGAGACCAAGGCTT 366
QY 1549 TCTCTACTGATTCGCGAGCTCAGACCCCTTTCTTCAGCTCTCGAAAGAGAAACACGTATCCC 1608
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Db 305 KCCTGACATGTCCTTCTTGAGCCCGGTAAGAGCAAAAGAAATGGKGGDARRGTTTAGCCCK 246
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QY 1729 TAGAACAAAGCTGAGGATACGACAGTACACTGTGAGCAGGACTGTAAACACAGACAGGG 1788
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AL550279 1154 bp mRNA linear EST 31-MAY-2003
AL550279 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI039YJ06 5-PRIME, mRNA sequence.
AL550279
AL550279.2 GI:31272096
EST.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1154)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12887098.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI039DE03QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI039DE03QP1.
FEATURES
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        /note="1st strand cDNA was primed with a NotI-oligo(dT)
        primer. Five prime end enriched, double-strand cDNA was
        digested with Not I and cloned into the Not I and EcoR V
        sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
    Query Match
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    Matches 1057; Conservative 4; Mismatches 6; Indels 2; Gaps 1;
QY 125 CTCTCATATCACCAGTGGCCATCTGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCACGAT 184
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Db 64 CTCTCATATCACCAGTGGCCATCTGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCAGGAT 123

QY 185 GGCCAGGTGCTTCAGCCTGGTGTGTTGCTTCTCATTCCATCTGGACCACGAGGCTCCTGGT 244

Db 124 GGCCAGGTGCTTCAGCCTGGTGTGTTGCTTCTCATTCCATCTGGACCACGAGGCTCCTGGT 183

QY 245 CCAAGGCTCTTTGCGTGCAAGAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGGAT 304

Db 184 CCAAGGCTCTTTGCGTGCAAGAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGGAT 243

QY 305 CACCCTTGTGAGCAAAAAGGCGAAACCAGCAGCTGAAATTTACAGAAAGCTAAGGAGGCTG 364

Db 244 CACCCTTGTGAGCAAAAAGGCGAAACCAGCAGCTGAAATTTACAGAAAGCTAAGGAGGCTG 303

QY 365 TAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAG 424

Db 304 TAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAG 363

QY 425 CTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTGCTGGTCATCTCTAGGATTAG 484

Db 364 CTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTGCTGGTCATCTCTAGGATTAG 423

QY 485 CCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGAATTTGGAAGGTTCCAGTGAG 544

Db 424 CCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGAATTTGGAAGGTTCCAGTGAG 483

QY 545 CCGACAGTTTGCAGCCTAATGTTTACAACTCATCTGATACTGGACTAACTCGTGCAATCC 604

Db 484 CCGACAGTTTGCAGCCTAATGTTTACAACTCATCTGATACTGGACTAACTCGTGCAATCC 543

QY 605 AGAAATTATCACCCACCAAGATCCCATATTTCAACACTCAAACCTGCAACACAAACACAGA 664

Db 544 AGAAATTATCACCCACCAAGATCCCATATTTCAACACTCAAACCTGCAACACAAACACAGA 603

QY 665 ATTTATTTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCC 724

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Db 964 AGTAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1023

QY 1085 TAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAAGCTGA 1144

Db 1024 TAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAAGCTGA 1083

QY 1145 AGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGTTCTTT 1193

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LOCUS AL550621 1201 bp mRNA linear EST 31-MAY-2003

DEFINITION AL550621 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI058YN14 5-PRIME, mRNA sequence.

ACCESSION AL550621

VERSION AL550621.2 GI:31272438

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1201)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On Feb 15, 2001 this sequence version replaced gi:12887768.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 5952.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI058DG07QPI&cluster=5952.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ InvitroGen Corporation 1600

Paraday Avenue Genoscope sequence ID : CS0DI058DG07QPI.

Location/Qualifiers

1. .1201

/organism="Homo sapiens"

/mol_type="mRNA"

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/clone="CS0DI058YN14"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES

source

ORIGIN

Query Match 48.9%; Score 991.6; DB 9; Length 1201;

Best Local Similarity 98.5%; Pred. No. 4.8e-190;

Matches 989; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

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Db 65 GAACTCTCCATCCGACTAGTATTAGCATCTGCCTCTCATATCACCAGTGGCCATCTG 124

QY 150 AGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG 209

Db 125 AGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG 184

QY 210 CTTCTCACTTCCATCTGACACGAGGCTCCTGTCGAAGGCTCTTTGCCGTGCAGAGAG 269

Db 185 CTTCTCACTTCCATCTGACACGAGGCTCCTGTCGAAGGCTCTTTGCCGTGCAGAGAG 244

QY 270 CTTTCCATCCAGGTGTCATGCAGAAATTATGGGGATCACCTTGTGAGCAAAAAGGCGAAC 329

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QY 330 CAGCAGCTGAATTTACAGAAAGCTAAGGAGGCTCTAGGCTGCTGGACTAAGTTTGGCC 389

Db 305 CAGCAGCTGAATTTACAGAAAGCTAAGGAGGCTCTAGGCTGCTGGACTAAGTTTGGCC 364

QY 390 GGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGCTGG 449

Db 365 GGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGCTGG 424

QY 450 GTTGAGATGGATTTCGTGTCATCTCTAGGATTAGCCAAACCCCAAGTGTGGGAAAAAT 509

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Db 203 ACCTAATCTCTGTAAAGCTAAATAAAGAAATAGAACAGGCTGAGGATACGACGTACA 144

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QY 1878 TTCTCTAGGAAATATACTTTTAC 1900

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RESULT 5

AL546590/c

LOCUS

DEFINITION AL546590 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI029YM23 3-PRIME, mRNA sequence.

ACCESSION AL546590

VERSION AL546590.2 GI:31268423

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On Feb 15, 2001 this sequence version replaced gi:12879852.

Contact: Genoscope

Genoscope - Centre National de Sequencage

Bp 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 5952.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI029AG12NP1&cluster=5952.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ InvitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DI029AG12NP1.

FEATURES

source

1. .1201

/organism="Homo sapiens"

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/clone="CS0DI029YM23"

/tissue type="PLACENTA COT 25-NORMALIZED"

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/note="1st strand cDNA was primed with a NotI-oligo (dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 47.0%; Score 954.4; DB 9; Length 1201;

Best Local Similarity 96.9%; Pred. No. 1.6e-182;

Matches 997; Conservative 13; Mismatches 14; Indels 5; Gaps 4;

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QY 1008 GAAATGATCGAAACCCAAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCCCTAATGAG 1067

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QY 1427 GAAAGGAGTTTTCGAAAGTCAAGGACCTAAACATCTCATCAGTATCCAGTGGTAAAAA 1486

Db 489 GAAAGGAGTTTTCGAAAGTCAAGGACCTAAACATCTCATCAGTATCCAGTGGTAAAAA 430

QY 1487 GGCCTCCTGGCTGCTCGAGGCTAGGTGGGTTGAAAGCCCAAGGAGTCACTGAGACCAAGGC 1546

Db 429 GGCCTCCTGGCTGCTCGAGGCTAGGTGGGTTGAAAGCCCAAGGAGTCACTGAGACCAAGGC 370

QY 1547 TTTCTCTACTGATCCGCAGCTCAGACCCCTTTCTTCAGCTCTGAAAGAGAAACACGTATC 1606

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QY 1607 CCACCTGACATGTCCTTCTGAGCCCGGTAAAGACAAAAGAAATGGCAGAAAAGTTTAGCCC 1666

Db 309 CCMCCTGACATGTCCTTCTGAGCCCGGTAAAGACAAAAGAAATGGCAGAAAAGTTTAGCCC 250

QY 1667 CTGAAAGCCATGGAGATTCTCATAACTTGAGACCTTAATCTCTGTAAGCTAAAAATAAGA 1726

Db 249 CTGAAAGCCATGGAGATTCTCATAACTTGAGACCTTAATCTCTGTAAGCTAAAAATAAGA 190

QY 1727 AATAGAACAAGGCTGAGGATACGACAGTACACTGTCTCAGCAGGGACTGTAACACACAGACAG 1786

Db 189 AATAGAACAAGGCTGAGGATACGACAGTACACTGTCTCAGCAGGGACTGTAACACACAGACAG 130

QY 1787 GGTCAAAGTGTCTTCTCTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACACTT 1846

Db 129 GGTCAAAGTGTCTTCTCTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACACTT 70

QY 1847 ACTTTTCTGCTCTACCACTGCTGATATTTCTCTAGGAAATATATCTTTTACAAGTAA 1906

Db 69 ACTTTTCTGCTCTACCACTGCTGATATTTNCTCTAGGAAATATATCTTTTACAAGTAA 10

QY 1907 CAAAAATAA 1915

Db 9 NNWNWGAW 1

RESULT 6

AL552299

LOCUS

DEFINITION AL552299 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI069YN02 5-PRIME, mRNA sequence.

ACCESSION AL552299

VERSION AL552299.2 GI:31274114

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 1015)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12891068.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI069DG01QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI069DG01QP1.
Location/Qualifiers
1. .1015
/organism="Homo sapiens"
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/clone="CS0DI069YN02"
/tissue_type="PLACENTA COT 25-NORMALIZED"
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/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES source
1. .1015
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI069YN02"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 46.5%; Score 943.8; DB 9; Length 1015;
Best Local Similarity 99.8%; Pred. No. 2.2e-180;
Matches 945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 101 CCGGACTAGTATTAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGTGTTTCCC 160
Db 62 CGGATTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGTGTTTCCC 121
QY 161 TGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACATTC 220
Db 122 TGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACATTC 181
QY 221 CATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCA 280
Db 182 CATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCA 241
QY 281 GGTGTCATGCAGAAATTATGGGATCACCCCTTGTGAGCAAAAAGCGAACCCAGCAGCTGAA 340
Db 242 GGTGTCATGCAGAAATTATGGGATCACCCCTTGTGAGCAAAAAGCGAACCCAGCAGCTGAA 301
QY 341 TTTCACAGAAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCCGGAAGGACCA 400
Db 302 TTTCACAGAAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCCGGAAGGACCA 361
QY 401 AGTTGAAACAGCCTTGAAAGCTAGCTTTGAAAACCTTGCAACTTGCAGCTATGGCTGGGTGGAGATGG 460
Db 362 AGTTGAAACAGCCTTGAAAGCTAGCTTTGAAAACCTTGCAACTTGCAGCTATGGCTGGGTGGAGATGG 421
QY 461 ATTCTGGTGCATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGGAAAAAATGGGTGGGTGT 520
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QY 521 CCTGATTGGAGGTTCCAGTGAGCCGACAGTTTGCAGCCCTATGTTACAACTCATCTGA 580
Db 482 CCTGATTGGAGGTTCCAGTGAGCCGACAGTTTGCAGCCCTATGTTACAACTCATCTGA 541
QY 581 TACTTGAACTAACTCGTGCATTTCCAGAAATTATCACCACCAGATCCCATATTTCAACAC 640
Db 542 TACTTGAACTAACTCGTGCATTTCCAGAAATTATCACCACCAGATCCCATATTTCAACAC 601
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Db 602 TCAAACTGCAACACACAAACAACAGAAATTATTGTGTCAGTGACAGTACTCGGTGGCATC 661
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QY 821 TACAGAAACTGAACCATTTTGTGAAAAATAAAGCAGCATTTCAAGATGAAGCTGCTGGGTT 880
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Db 842 TGGAGGTGTCCTCCACGGCTCTGCTAGTGTCTCTCCTCTTCTTTGGTGTGCAGCTGG 901
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Db 962 GCAGAGGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAGGCCA 1008

RESULT 7
AL575514/c
LOCUS AL575514 1157 bp mRNA linear EST 01-JUN-2003
DEFINITION AL575514 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI059YA12 3-PRIME, mRNA sequence.
ACCESSION AL575514
VERSION AL575514.2 GI:31313822
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1157)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 16, 2001 this sequence version replaced gi:12936752.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI059BA06NP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI059BA06NP1.
Location/Qualifiers
1. .1157
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI059YA12"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES source
1. .1157
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 46.2%; Score 937.8; DB 9; Length 1157;
Best Local Similarity 95.1%; Pred. No. 3.6e-179;

Matches		960;	Conservative	23;	Mismatches	23;	Indels	3;	Gaps	2;
QY	915	CTCCTCTCTTTGGTGTG	CAGCTGGTCTTGGATT	TTGCTATGTCAAAAGG	TATGTGAAG	974				
Db	1006	STKSTCYCTYTTTGGKSTCCGCTKGTCTTGATTGTTGCTWTGTCAAAARGKTATGTRA--	949							
QY	975	GCCTTCCCTTTTACAAACAAGAAATCAGCAGAAAGGAATGATCGAAACCAAGTAGTAAAG	1034							
Db	948	GGCCTTCCTTTTACAAACAARAATCAGCAG-ARGAATRATCGAAMCCAAAGTAGTAAAG	890							
QY	1035	GAGGAGAAAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAAACTGATAAAACCCA	1094							
Db	889	GAGGAGAAAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAAACTGATAAAACCCA	830							
QY	1095	GAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCTGAAGTTAGATG	1154							
Db	829	GAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCTGAAGTTAGATG	770							
QY	1155	AGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCCTGCCCCA	1214							
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QY	1215	GCTGGGGAATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCCCTTGGTTCTTA	1274							
Db	709	GCTGGGGAATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCCCTTGGTTCTTA	650							
QY	1275	GGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCT	1334							
Db	649	GGAATCAGCTCAGAACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCT	590							
QY	1335	TATTGTAACCTGTCTGGATCCTATCCTCCTACCTCCAAGCTTCCCACGGCCTTCTTAG	1394							
Db	589	TATTGTAACCTGTCTGGATCCTATCCTCCTACCTCCAAGCTTCCCACGGCCTTCTTAG	530							
QY	1395	CCTGGCTATGTCTTAATAATATCCACTGGGAGAAAGAGTTTTGCAAAGTGCAAGGACC	1454							
Db	529	CCTGGCTATGTCTTAATAATATCCACTGGGAGAAAGAGTTTTGCAAAGTGCAAGGACC	470							
QY	1455	TAAACATCTCATCAGTATCCAGTGGTAAAGGGCCTCTCGGTGTCTGAGGCTAGGTGG	1514							
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QY	1515	GTTGAAAGCCAAAGGACTACTGAGACCAAGGCTTTCTACTGATTCGGCAGCTCAGACC	1574							
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QY	1575	CTTTCTTCAGCTCTGAAAGAGAAACACGTATCCACCTGACATGTCTTCTGAGCCCGGT	1634							
Db	349	CTTTCTTCAGCTCTGAAAGAGAAACACGTATCCACCTGACATGTCTTCTGAGCCCGGT	290							
QY	1635	AAGAGCAAAAGAAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTT	1694							
Db	289	AAGAGCAAAAGAAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTT	230							
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Db	229	GAGACCTAATCTCTGTAAAGCTAAAATAAAGAAATAGAAAGGCTGAGGATACGACAGT	170							
QY	1755	ACACTGTCAGCAGGACTGTAAACACAGACAGGCTCAAAGTGTTTTTCTCTGAACACATTG	1814							
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QY	1815	AGTTGGAATCACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGAT	1874							
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QY	1875	ATTTTCTCTAGGAAATATACTTTACAAGTAACAAAATAFAAAAACTCTT	1923							
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LOCUS	BX366718	1201 bp	mRNA	linear	EST 08-MAY-2003
DEFINITION	BX366718 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI040YD03 5-PRIME, mRNA sequence.				
ACCESSION	BX366718				
VERSION	BX366718.1	GI:30451557			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1201)				
AUTHORS	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CS0AI040CB02QP1&cluster=5952.r. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0AI040CB02QP1.				
FEATURES	Location/Qualifiers				
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	/tissue_type="PLACENTA COT 25-NORMALIZED"				
	/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"				
	/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."				
ORIGIN					
Query Match	46.1%;	Score 936;	DB 13;	Length 1201;	
Best Local Similarity	97.6%;	Pred. No. 8.2e-179;			
Matches	953;	Conservative 15;	Mismatches 6;	Indels 2;	Gaps 2;
QY	35	CGGGATGTCTCGGTTATGAAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGTTCAGAACT	94		
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QY	95	CTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGTG	154		
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QY	155	TTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCT	214		
Db	184	TTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCT	243		
QY	215	CAC TTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTC	274		
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QY	275	CATCCAGGTGTCTATGCAGAAATTATGGGGATCACCCCTGTGAGCAAAAAGCGCAACCCAGCA	334		
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QY	335	GCTGAATTTACAGAAGCTAAGGAGGCTGTGAGGCTGTGGACTTAAGTTTGGCCGGCAA	394		
Db	364	GCTGAATTTACAGAAGCTAAGGAGGCTGTGAGGCTGTGGACTTAAGTTTGGCCGGCAA	423		
QY	395	GGACCAAGTTGAAACAGACCTTGAAAGCTAGCTTTGAAACTTTCAGCTATGGCTGGGTGG	454		
Db	424	GGACCAAGTTGAAACAGACCTTGAAAGCTAGCTTTGAAACTTTCAGCTATGGCTGGGTGG	483		
QY	455	AGATGGATTCTGGTTCATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGGT	514		

REFERENCE

1 (bases 1 to 1201)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:12880008.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
[http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI029CE05QP1&cluster=5952.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI029CE05QP1&cluster=5952.r). Contact :
Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI029CE05QP1.

FEATURES

Location/Qualifiers

1..1201

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI029YJ09"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dt)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

```

Db      591  GCAACACAAACACAGAATTATTGTTCAGTGACACTACCTACTCGGTGGCATCCCTTAC 650
QY      708  TCTACAAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTTCCACCTTCTATTCCACGG 767
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QY      768  AGAAAAAAATTTGATTGTGTGCACAGAAAGTTTTTATGGAAACTAGCACCATGCTGTACAGAA 827
Db      711  AGAAAAAAATTTGATTGTGTGCACAGAAAGTTTTTATGGAAACTAGCACCATGCTGTACAGAA 770
QY      828  ACTGAACCAATTTGTTGAAATAAAAGCAGCAATTCARGAATGAAGCTGCTGGGTTGGAGGT 887
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QY      888  GTCCCCACGGCTCTGCTAGTGTCTTGCTCTCCTCTTCTTTTGGTGTGCAGCTGGTCTTGA 947
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QY      948  TTTTGCTATGTCAAAAAGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAATCAGCAGAAG 1007
Db      891  TTTTGCTATGTCAAAAAGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAATCAGCAGAAG 950
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Db      951  GAAATGATCGAAACCAAGTAGTAAAGGAGGAGGAGCCCAATGATAGCAACCTTAATGAG 1005
QY      1068  GAATCAAAGAAACTGATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTG 1127
Db      1006  GRGGATCAAAGAAACTGATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTTMCCTG 1062
QY      1128  CGATGCCTGGA 1138
Db      1063  CGATGCTCGGA 1073

RESULT 12
AL552127
LOCUS
DEFINITION
AL552127 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI059YA12 5-PRIME, mRNA sequence.
ACCESSION
AL552127
VERSION
AL552127.2 GI:31273943
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1172)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12890728.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI059BA06QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI059BA06QP1.
Location/Qualifiers
1. .1172
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CS0DI059YA12"
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
FEATURES
source

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primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match		45.5%;	Score 924.2;	DB 9;	Length 1172;
Best Local Similarity		89.8%;	Pred. No. 2e-176;		
Matches 994;		Conservative 26;	Mismatches 83;	Indels 4;	Gaps 3;
QY	2	CTTGACAAAGTCAGAAAGCTTGAAAGCAGGGAAATCCGGATGTCTCGTTATGAAGTGGAGC	61		
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QY	62	AGTGAGTGTGAGCCTCAACATAGTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATC	121		
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QY	182	GATGGCCAGGTGCTTCAGCCTGGTGTGTTGCTTCTCACTTCCATCTGGACCCAGGCTCCT	241		
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Db	301	GGTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCATCCAGGTGTCAATGCAGAATTATGGG	360		
QY	302	GATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTTCACAGAAGCTAAGGAGGC	361		
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QY	542	GAGCCGACAGTTTGGAGCCTATTGTTACAACCTCATCTGATACCTTGGACTAACTCGTGAT	601		
Db	601	GAGCCGACAGTTTGGAGCCTATTGTTACAACCTCATCTGATACCTTGGACTAACTCGTGAT	660		
QY	602	TCCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAAACTGCAACACAAACAAC	661		
Db	661	TCCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAAACTGCAACACAAACAAC	720		
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QY	722	CCCTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGAT	781		
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Db	899	TTGAAATAAAGCAGCATTTCAAGAATGAAGCTGTGGGTTTGGAGGTGTCCCCACGGCTCT	958		
QY	902	GCTAGTGCTTGCTCTCCTCTTCTTTTGGTGCTGCAGCTGGTCTTGGAATTTTGCTATGTCAA	961		
Db	959	TCTAGTGCTTGCTCTTCTTCTTTTKGTGCTGCACTCGGTC-TKGAATTTTKCTATGTY-A	1016		

QY	962	AAGGTATGTGAAGGCTTCCCTTTTACAAAACAGAATCAGCAGAAGGAAATGATCGAAAC	1021		
Db	1017	AARGTATTTTAAGGCTTCCYTTTAYAAACAAATARCAGARGRAATGATCAAAACAAATA	1076		
QY	1022	CAAAGTAGTAAAGGAGAGGCGCAATGATAGCAACCCCTAATGAGGAATCAAAGGAAAC	1081		
Db	1077	GTAAGGGGGAGGCATGATAGMMCCYYATGAGGATMARAAAAAYGBWAAAAACMRAGAKCC	1136		
QY	1082	TGATAAAAACCCAGAGAGTCCAAGAG	1108		
Db	1137	ARRTCMRVAAATACGKGDKCKGRRVK	1163		

RESULT 13
AL552661
LOCUS
DEFINITION
AL552661 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI067YG15 5-PRIME, mRNA sequence.
ACCESSION
AL552661
VERSION
AL552661.2 GI:31274476
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1116)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12891779.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI067AD08QP1&cluster=5952.r. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DI067AD08QP1.

FEATURES
source

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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 45.0%; Score 914; DB 9; Length 1116;
Best Local Similarity 98.0%; Pred. No. 2.3e-174;
Matches 972; Conservative 5; Mismatches 10; Indels 5; Gaps 5;

QY	2	CTTGACAAGTCAGAAGCTTGAAAGCAGGGAATCCGGATGTCTCGGTATGAAGTGGAGC	61		
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QY	62	AGTGAGTGTGAGCCTCAACATAGTTCAGAACTCTCCATCCGGACTAGTTATTGAGCATC	121		
Db	128	AGTGAGTGTGAGCCTCAACATAGTTCAGAACTCTCCATCCGGACTAGTTATTGAGCATC	187		
QY	122	TGCCTCTCATATCACCAGTGGCCATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCAC	181		
Db	188	TGCCTCTCATATCACCAGTGGCCATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCAC	247		
QY	182	GATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCCAGGCTCCT	241		

QY 1692 CTTGAGACCTAATCTCTGTAAAGCTAAATAAAGAAATAGAAACAAGGCTGAGGATACGAC 1751
Db |||||
QY 1752 AGTACACTGTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTCTCTGAAACACA 1811
Db |||||
QY 1812 TTGAGTTGGAATCACTGTTTAGAACACACACACTTACTTTTCTGCTCTCTACCACTGCT 1871
Db |||||
QY 1872 GATATTTTCTTAGGAAATATACCTTTTACAAGTAACAAAAATAAAAACTCTTATAAATT 1931
Db |||||
QY 1932 CTATTTTATCTGAGTTACAGAAATGATTACTA-AGGAAGATTAC-TCAGTAATTTGTTT 1989
Db |||||
QY 1990 AAAAAAGTAATAAAAT 2004
Db |||||
QY 1990 AAAAAAGTAATAAAAT 2004
Db |||||

AL546623 1201 bp mRNA linear EST 31-MAY-2003
AL546623 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI029YM23 5-PRIME, mRNA sequence.
AL546623
AL546623.2 GI:31268456
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12879917.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI029AGI2QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI029AGI2QP1.
Location/Qualifiers

FEATURES
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/clone="CS0DI029YM23"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dt)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 44.7%; Score 907.2; DB 9; Length 1201;
Best Local Similarity 96.8%; Pred. No. 5.4e-173;
Matches 976; Conservative 11; Mismatches 14; Indels 7; Gaps 6;

QY 1 CCTTGACAAGTCAGAAGCTTGAAAGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAG 60
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QY 107 CCTTGACAAGTCAGAAGCTTGAAAGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAG 166
Db |||||
QY 61 CAGTGAGTGTGAGCCTCAACATAGTTCAGAACTCTCCATCCGGACTAGTTATTGAGCAT 120
Db |||||
QY 167 CAGTGAGTGTGAGCCTCAACATAGTTCAGAACTCTCCATCCGGACTAGTTATTGAGCAT 226
Db |||||
QY 121 CTGCTCTCATATCACCAGTGGCCATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCA 180
Db |||||
QY 227 CTGCTCTCATATCACCAGTGGCCATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCA 286
Db |||||
QY 181 CGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCC 240
Db |||||
QY 287 CGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCC 346
Db |||||
QY 241 TGGTCCAAGGCTCTTTGGCTGCAGAAAGAGCTTTCCATCCAGGTGTATGCAGAAATTATGG 300
Db |||||
QY 347 TGGTCCAAGGCTCTTTGGCTGCAGAAAGAGCTTTCCATCCAGGTGTATGCAGAAATTATGG 406
Db |||||
QY 301 GGATCACCCCTTGTGAGCAAAAAGCGCAACCCAGCAGCTGAATTTTACAGAAAGCTAAGGAGG 360
Db |||||
QY 407 GGATCACCCCTTGTGAGCAAAAAGCGCAACCCAGCAGCTGAATTTTACAGAAAGCTAAGGAGG 466
Db |||||
QY 361 CCTGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAAACAGCCTTGAAAAG 420
Db |||||
QY 467 CCTGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAAACAGCCTTGAAAAG 526
Db |||||
QY 421 CTAGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCTGTTGATCTCTTAGGA 480
Db |||||
QY 527 CTAGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCTGTTGATCTCTTAGGA 586
Db |||||
QY 481 TTAGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTGGAAGGTTCCAG 540
Db |||||
QY 587 TTAGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTGGAAGGTTCCAG 646
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Db |||||
QY 647 TGAGCCGACAGTTTGCAGCCTATTGTTACAATCATCTGATCTTGGACTAATCGTGCA 706
Db |||||
QY 601 TTCCAGAAATTATCACCACCAAGATCCCAATTCACAACTCAAACTGCAACACAAACAA 660
Db |||||
QY 707 TTCCAGAAATTATCACCACCAAGATCCCAATTCACAACTCAAACTGCAACACAAACAA 766
Db |||||
QY 661 CAGAAATTTATTGTCAGTGACAGTACCTACTCGTGGGCATCCCTTACTCTCAATACCTG 720
Db |||||
QY 767 CAGAAATTTATTGTCAGTGACAGTACCTACTCGTGGGCATCCCTTACTCTCAATACCTG 826
Db |||||
QY 721 CCCCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGA 780
Db |||||
QY 827 CCCCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGA 886
Db |||||
QY 781 TTTGTGTACACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTG 840
Db |||||
QY 887 TTTGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTG 946
Db |||||
QY 841 TTGAAAAATAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTC 900
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QY 947 TTG-AAATAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGT-CCCMCGGCTC 1004
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QY 901 TGCTAGTGTGCTCTCTCTCTTCTTTGGTGTGCTGAGCTGGTCTTGGATTTGCTATGTCA 960
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QY 961 AAAGTATGTGAAGGCTTCCCTTTTACAAAACAAGAAATCAGCAGAAAGG 1008
Db |||||
QY 1062 AAAGK--AKKGRAGGCTTCCCTTTTMAAAAAGAAATARCYGAGGAWTG 1107
Db |||||

Search completed: September 15, 2004, 11:23:59
Job time : 5297 secs

B/ank

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 09:52:54 ; Search time 964 Seconds
(without alignments)
10590.207 Million cell updates/sec

Title: US-10-079-111-2
Perfect score: 2029
Sequence: 1 ccttgacaagtgcagaagctt.....aaacatttaaaaaaaaaa 2029

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2029	100.0	2029	15	US-10-079-111-2	Sequence 2, Appli
2	2005	98.8	2404	9	US-09-833-381-849	Sequence 849, App
3	2005	98.8	2404	9	US-09-833-381-853	Sequence 853, App
4	1994	98.3	2372	9	US-09-909-320-200	Sequence 200, App
5	1994	98.3	2372	9	US-09-909-089B-200	Sequence 200, App
6	1994	98.3	2372	9	US-09-905-291A-200	Sequence 200, App
7	1994	98.3	2372	9	US-09-902-853-200	Sequence 200, App
8	1994	98.3	2372	9	US-09-907-824-200	Sequence 200, App
9	1994	98.3	2372	9	US-09-907-841-200	Sequence 200, App
10	1994	98.3	2372	10	US-09-904-011-200	Sequence 200, App
11	1994	98.3	2372	10	US-09-906-742-200	Sequence 200, App
12	1994	98.3	2372	10	US-09-906-838-200	Sequence 200, App
13	1994	98.3	2372	10	US-09-907-613-200	Sequence 200, App
14	1994	98.3	2372	10	US-09-907-942-200	Sequence 200, App

15	1994	98.3	2372	10	US-09-904-859-200	Sequence 200, App
16	1994	98.3	2372	10	US-09-909-204-200	Sequence 200, App
17	1994	98.3	2372	10	US-09-904-820-200	Sequence 200, App
18	1994	98.3	2372	10	US-09-904-786-200	Sequence 200, App
19	1994	98.3	2372	10	US-09-906-646-200	Sequence 200, App
20	1994	98.3	2372	10	US-09-906-700-200	Sequence 200, App
21	1994	98.3	2372	10	US-09-903-786-200	Sequence 200, App
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25	1994	98.3	2372	10	US-09-904-956-200	Sequence 200, App
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27	1994	98.3	2372	10	US-09-907-794-200	Sequence 200, App
28	1994	98.3	2372	10	US-09-903-943-200	Sequence 200, App
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31	1994	98.3	2372	10	US-09-902-692-200	Sequence 200, App
32	1994	98.3	2372	10	US-09-903-520-200	Sequence 200, App
33	1994	98.3	2372	10	US-09-905-056-200	Sequence 200, App
34	1994	98.3	2372	10	US-09-909-064-200	Sequence 200, App
35	1994	98.3	2372	10	US-09-904-553-200	Sequence 200, App
36	1994	98.3	2372	10	US-09-905-381-200	Sequence 200, App
37	1994	98.3	2372	10	US-09-905-088-200	Sequence 200, App
38	1994	98.3	2372	10	US-09-907-575-200	Sequence 200, App
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40	1994	98.3	2372	10	US-09-902-759-200	Sequence 200, App
41	1994	98.3	2372	10	US-09-902-634-200	Sequence 200, App
42	1994	98.3	2372	10	US-09-902-713-200	Sequence 200, App
43	1994	98.3	2372	10	US-09-907-979-200	Sequence 200, App
44	1994	98.3	2372	10	US-09-902-615-200	Sequence 200, App
45	1994	98.3	2372	10	US-09-903-925-200	Sequence 200, App

ALIGNMENTS

RESULT 1
US-10-079-111-2
; Sequence 2, Application US/10079111
; Publication No. US20030124543A1
; GENERAL INFORMATION:
; APPLICANT: Stuart, Susan G.
; APPLICANT: Streeter, David G.
; TITLE OF INVENTION: BREAST CANCER MARKER
; FILE REFERENCE: PC-0053 CIP
; CURRENT APPLICATION NUMBER: US/10/079,111
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 09/232,160
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 2029
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124543A1 3044710CB1
US-10-079-111-2

Query Match 100.0%; Score 2029; DB 15; Length 2029;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2029; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 |||||CTGCCCTCATATCACCAGTGGCCATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCA 180
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Qy 361 CCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAAG 420
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Qy 1081 CTGATAAAACCCAGAGAGTCCAAAGAGTCCAAAGAGTCCAAAGCAAACTACCGTGCATGCTGGAAG 1140
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Qy 1141 CTGAAGTTTAGATGAGACAGAAATGAGGAGACACCTGAGGCTGGTTTCTTTCATGCTC 1200
Db 1141 CTGAAGTTTAGATGAGACAGAAATGAGGAGACACCTGAGGCTGGTTTCTTTCATGCTC 1200
Qy 1201 CTTACCTGCCCCAGCTGGGAAATCAAAAGGGCCAAAGAACCAAGAAAGTCCACC 1260

Db 1201 CTTACCCCTGCCCCAGCTGGGAAATCAAAAGGGCCAAAGAACCAAAAGAAAGTCCACC 1260
Qy 1261 CTTGGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAG 1320
Db 1261 CTTGGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAG 1320
Qy 1321 AATGCCCTTCTCCTTATTGTAAACCCTGTCTGGATCCTATCCTCTACCTCCAAAAGCTTCC 1380
Db 1321 AATGCCCTTCTCCTTATTGTAAACCCTGTCTGGATCCTATCCTCTACCTCCAAAAGCTTCC 1380
Qy 1381 CACGGCCTTTCTAGCCTGGCTATGTCCCTAATAATATCCCACTGGGAGAAAGGAGTTTTC 1440
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Qy 1441 AAAGTGCAAGGACCTAAAAACATCTCATCAGTATCCAGTGGTAAAGGCCCTCCTGGCTGT 1500
Db 1441 AAAGTGCAAGGACCTAAAAACATCTCATCAGTATCCAGTATCCAGTGGTAAAGGCCCTCCTGGCTGT 1500
Qy 1501 CTGAGGCTAGGTGGGTTGAAAGCCAAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATT 1560
Db 1501 CTGAGGCTAGGTGGGTTGAAAGCCAAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATT 1560
Qy 1561 CCGCAGCTCAGACCCCTTTCTTCAGCTCTGAAAGAGAAACACGTATCCCACTGACATGTC 1620
Db 1561 CCGCAGCTCAGACCCCTTTCTTCAGCTCTGAAAGAGAAACACGTATCCCACTGACATGTC 1620
Qy 1621 CTTCTGAGCCCGGTAAGAGCAAAAAGAAATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGGA 1680
Db 1621 CTTCTGAGCCCGGTAAGAGCAAAAAGAAATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGGA 1680
Qy 1681 GATTCTCATAAATTGAGACCTAATCTCTGTAAAGCTAAAATAAAGAAATAGAACAGGCT 1740
Db 1681 GATTCTCATAAATTGAGACCTAATCTCTGTAAAGCTAAAATAAAGAAATAGAACAGGCT 1740
Qy 1741 GAGGATACGACAGTACACTGTGAGAGGGGACTGTAAACACAGACAGGCTCAAAGTGTTTT 1800
Db 1741 GAGGATACGACAGTACACTGTGAGAGGGGACTGTAAACACAGACAGGCTCAAAGTGTTTT 1800
Qy 1801 CTCTGAAACACATTGAGTTGGAATCACTGTTTAGAACACACACACTTACTTTTCTGGTCT 1860
Db 1801 CTCTGAAACACATTGAGTTGGAATCACTGTTTAGAACACACACACTTACTTTTCTGGTCT 1860
Qy 1861 CTACCCTGCTGATATTTTCTCTAGGAAATATACTTTTACAAGTAACAAAAATAAAAACT 1920
Db 1861 CTACCCTGCTGATATTTTCTCTAGGAAATATACTTTTACAAGTAACAAAAATAAAAACT 1920
Qy 1921 CTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGT 1980
Db 1921 CTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGT 1980
Qy 1981 AATTTGTTAAAAAGTAATAAAATTCACAAACATTTTAAAAAATAAAAAA 2029
Db 1981 AATTTGTTAAAAAGTAATAAAATTCACAAACATTTTAAAAAATAAAAAA 2029

RESULT 2

US-09-833-381-849
; Sequence 849, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 849
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-833-381-849

Query Match		98.8%;	Score 2005;	DB 9;	Length 2404;		
Best Local Similarity		99.7%;	Pred. No. 0;				
Matches 2019;		Conservative 0;	Mismatches 5;	Indels 1;	Gaps 1;		
QY	2	CTTGACAAAGTCAGAA-GCTTGAAAGCAGGGAATCCGGATGTCTCGGTTATGAAGTGGAG	60				
Db	8	CTTGACAAAGTCAGAAAGCGTTGAAAGCAGGGAATCCGGATGTCTCGGTTATGAAGTGGAG	67				
QY	61	CAGTGAGTGTGAGCCTCAACATAGTTCCAGAACTCTCCATCCGACTAGTTATTTAGCAT	120				
Db	68	CAGTGAGTGTGAGCCTCAACATAGTTCCAGAACTCTCCATCCGACTAGTTATTTAGCAT	127				
QY	121	CTGCCCTCTCATATCACAGTGGCCATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCA	180				
Db	128	CTGCCCTCTCATATCACAGTGGCCATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCA	187				
QY	181	CGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCCAGAGGCTCC	240				
Db	188	CGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCCAGAGGCTCC	247				
QY	241	TGGTCCAAAGGCTCTTTGCGTGCAGAAAGACTTTCCATCCAGGTGTCTATGCAGAAATTATGG	300				
Db	248	TGGTCCAAAGGCTCTTTGCGTGCAGAAAGACTTTCCATCCAGGTGTCTATGCAGAAATTATGG	307				
QY	301	GGATCACCCCTTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAAATTTACAGAAAGTAAAGGAGG	360				
Db	308	GGATCACCCCTTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAAATTTACAGAAAGTAAAGGAGG	367				
QY	361	CCTGTAGGCTGTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAG	420				
Db	368	CCTGTAGGCTGTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAG	427				
QY	421	CTAGCTTTGAACTTGCAGCTATGGCTGGTTGGAGATGGATTTCGTGGTCACTCTTAGGA	480				
Db	428	CTAGCTTTGAACTTGCAGCTATGGCTGGTTGGAGATGGATTTCGTGGTCACTCTTAGGA	487				
QY	481	TTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCTTGATTTGGAAAGTTCCAG	540				
Db	488	TTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCTTGATTTGGAAAGTTCCAG	547				
QY	541	TGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCA	600				
Db	548	TGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCA	607				
QY	601	TTCCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAA	660				
Db	608	TTCCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAA	667				
QY	661	CAGAAATTTATGTAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTG	720				
Db	668	CAGAAATTTATGTAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTG	727				
QY	721	CCCCTACTACTCTCCTGCTCCAGCTTCCACTTCTATTTCCACGGAGAAAAAATTGA	780				
Db	728	CCCCTACTACTCTCCTGCTCCAGCTTCCACTTCTATTTCCACGGAGAAAAAATTGA	787				
QY	781	TTTGTTGTACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAACTGAACCATTTG	840				
Db	788	TTTGTTGTACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAACTGAACCATTTG	847				
QY	841	TTGAAATAAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTC	900				
Db	848	TTGAAATAAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTC	907				
QY	901	TGCTAGTGTGCTCTCCTCTTCTTTGGTGTGCTGAGCTGGTCTTGGATTTTGCTATGTCA	960				
Db	908	TGCTAGTGTGCTCTCCTCTTCTTTGGTGTGCTGAGCTGGTCTTGGATTTTGCTATGTCA	967				
QY	961	AAAGGTATGTGAGGCTTCCCTTTTACAAACAAGAATCAGCAGAAAGGAAATGATCGAAA	1020				
Db	968	AAAGGTATGTGAGGCTTCCCTTTTACAAACAAGAATCAGCAGAAAGGAAATGATCGAAA	1027				

QY	1021	CCAAAGTAGTAAAGGAGAGAGGCCAAATGATAGCAACCCCTAATGAGGAATCAAAGAAA	1080
Db	1028	CCAAAGTAGTAAAGGAGAGAGGCCAAATGATAGCAACCCCTAATGAGGAATCAAAGAAA	1087
QY	1081	CTGATAAAAAACCCAGAAAGATCCAAGAGTCCAAGCAAAAACCTACCGTCCGATGCCTGGAAG	1140
Db	1088	CTGATAAAAAACCCAGAAAGATCCAAGAGTCCAAGCAAAAACCTACCGTCCGATGCCTGGAAG	1147
QY	1141	CTGAAGTTTATGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTC	1200
Db	1148	CTGAAGTTTATGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTC	1207
QY	1201	CTTACCCCTGCCCAGCTGGGGAATCAAAAGGGCCAAAGAACCAAGAAAGATCCACC	1260
Db	1208	CTTACCCCTGCCCAGCTGGGGAATCAAAAGGGCCAAAGAACCAAGAAAGATCCACC	1267
QY	1261	CTTGGTTCCCTAATCTGGAATCAGCTCAGGACTGSCATTTGGACTATGGAGTGCAACCAAGAG	1320
Db	1268	CTTGGTTCCCTAATCTGGAATCAGCTCAGGACTGSCATTTGGACTATGGAGTGCAACCAAGAG	1327
QY	1321	AATGCCCTTCTCCTTATTGTAACCCCTGTCTCGATCCTATCCTCCTACCTCCAAAAGCTTCC	1380
Db	1328	AATGCCCTTCTCCTTATTGTAACCCCTGTCTCGATCCTATCCTCCTACCTCCAAAAGCTTCC	1387
QY	1381	CACGGCCTTCTAGCCTGGCTATGTCTCTAATAATATCCCACCTGGGAGAAAGAGTTTTC	1440
Db	1388	CACGGCCTTCTAGCCTGGCTATGTCTCTAATAATATCCCACCTGGGAGAAAGAGTTTTC	1447
QY	1441	AAAGTGCAAGGACCTAAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCCTCCTGGCTGT	1500
Db	1448	AAAGTGCAAGGACCTAAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCCTCCTGGCTGT	1507
QY	1501	CTGAGGCTAGTGGGTTGAAAGCCAAAGGAGTCACTGAGACCAAGGCTTTCCTACTGATT	1560
Db	1508	CTGAGGCTAGTGGGTTGAAAGCCAAAGGAGTCACTGAGACCAAGGCTTTCCTACTGATT	1567
QY	1561	CCGCAGCTCAGACCCCTTCTTTCAGCTCTGAAAGAGAAACACGATCCCACTGACATGTC	1620
Db	1568	CCGCAGCTCAGACCCCTTCTTTCAGCTCTGAAAGAGAAACACGATCCCACTGACATGTC	1627
QY	1621	CTTCTGAGCCCGGTAAGAGCAAAAGAAATGCGAGAAAAAGTTTAGCCCTGAAAAGCCATGGA	1680
Db	1628	CTTCTGAGCCCGGTAAGAGCAAAAGAAATGCGAGAAAAAGTTTAGCCCTGAAAAGCCATGGA	1687
QY	1681	GATTCTCATAACTTGAGACCTAATCTCTGTAAAGCTAAAATAAGAAATAGAACCAAGGCT	1740
Db	1688	GATTCTCATAACTTGAGACCTAATCTCTGTAAAGCTAAAATAAGAAATAGAACCAAGGCT	1747
QY	1741	GAGGATACGACAGTACACTGTGAGCAGGACTGTAAAACACAGACAGGTCAAAAGTGTTTT	1800
Db	1748	GAGGATACGACAGTACACTGTGAGCAGGACTGTAAAACACAGACAGGTCAAAAGTGTTTT	1807
QY	1801	CTCTGAACACANTGAGTTGGAATCACTGTTAGAAACACACACACTTACTTTTCTGGTCT	1860
Db	1808	CTCTGAACACANTGAGTTGGAATCACTGTTAGAAACACACACACTTACTTTTCTGGTCT	1867
QY	1861	CTACCACTGCTGATATTTTCTCTAGGAAATATACCTTTTACAAGTAACAAAAATAAAACT	1920
Db	1868	CTACCACTGCTGATATTTTCTCTAGGAAATATACCTTTTACAAGTAACAAAAATAAAACT	1927
QY	1921	CTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTTAAGGAAGATTACTCAGT	1980
Db	1928	CTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTTAAGGAAGATTACTCAGT	1987
QY	1981	AATTTGTTAAAAAGTAATAAAATTCAACAAACATTTTAAAAAAA	2025
Db	1988	AATTTGTTAAAAAGTAATAAAATTCAACAAACATTTTGCTGAATA	2032

; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 853
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-853

Query Match		98.8%;	Score 2005;	DB 9;	Length 2404;
Best Local Similarity		99.7%;	Pred. No. 0;		
Matches 2019;		Conservative	0;	Mismatches	5; Indels 1; Gaps 1;
Qy	2	CTTGACAAGTCAGAA-GCTTGAAGCAGGGGAAATCCGGATGTCTCGGTATGAAGTGGAG	60		
Db	8	CTTGACAAGTCAGAACGCTTGAAGCAGGGGAAATCCGGATGTCTCGGTATGAAGTGGAG	67		
Qy	61	CAGTCAGTGTGAGCCTCAACATAGTTCAGAACTCTCCATCCGGAAGTATGAGCAT	120		
Db	68	CAGTCAGTGTGAGCCTCAACATAGTTCAGAACTCTCCATCCGGAAGTATGAGCAT	127		
Qy	121	CTGCCTCTCATATCACCAGTGGCCATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCA	180		
Db	128	CTGCCTCTCATATCACCAGTGGCCATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCA	187		
Qy	181	CGATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCATCTGGACCACGAGGCTCC	240		
Db	188	CGATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCATCTGGACCACGAGGCTCC	247		
Qy	241	TGGTCCAAGGCTCTTTGGCGTGCAAGAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGG	300		
Db	248	TGGTCCAAGGCTCTTTGGCGTGCAAGAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGG	307		
Qy	301	GGATCACCCCTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTCACAGAAGCTAAGGAGG	360		
Db	308	GGATCACCCCTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTCACAGAAGCTAAGGAGG	367		
Qy	361	CCCTGAGGCTGTGGGACTAAGTTTGGCCGGCAAGGACCAAGTGAACAGCCCTTGAAG	420		
Db	368	CCCTGAGGCTGTGGGACTAAGTTTGGCCGGCAAGGACCAAGTGAACAGCCCTTGAAG	427		
Qy	421	CTAGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCGTGATCTCTAGGA	480		
Db	428	CTAGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCGTGATCTCTAGGA	487		
Qy	481	TTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCCTGATTTGGAAGTTCCAG	540		
Db	488	TTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCCTGATTTGGAAGTTCCAG	547		
Qy	541	TGAGCCGACAGTTTGCAGCCTATTGTTACAACACTCATCTGATACTTGGACTAATCGTGCA	600		
Db	548	TGAGCCGACAGTTTGCAGCCTATTGTTACAACACTCATCTGATACTTGGACTAATCGTGCA	607		
Qy	601	TTCCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAA	660		
Db	608	TTCCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAA	667		
Qy	661	CAGAAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTG	720		
Db	668	CAGAAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTG	727		
Qy	721	CCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGA	780		
Db	728	CCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGA	787		

Qy	781	TTTGTGTCACAGAAAGTTTTTATGGAACCTAGCACCATGTCTACAGAAACTGAACCATTTG	840
Db	788	TTTGTGTCACAGAAAGTTTTTATGGAACCTAGCACCATGTCTACAGAAACTGAACCATTTG	847
Qy	841	TTGAAAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCACGGCTC	900
Db	848	TTGAAAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCACGGCTC	907
Qy	901	TGCTAGTGTGCTCTCCTCTTTTGGTGTGCTGAGCTGGTCTTGGATTTTGTCTATGTCA	960
Db	908	TGCTAGTGTGCTCTCCTCTTTTGGTGTGCTGAGCTGGTCTTGGATTTTGTCTATGTCA	967
Qy	961	AAAGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAAATGATCGAAA	1020
Db	968	AAAGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAAATGATCGAAA	1027
Qy	1021	CCAAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAA	1080
Db	1028	CCAAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAA	1087
Qy	1081	CTGATAAAAAACCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCCTGGAAG	1140
Db	1088	CTGATAAAAAACCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCCTGGAAG	1147
Qy	1141	CTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTC	1200
Db	1148	CTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTC	1207
Qy	1201	CTTACCCCTGCCCCAGCTGGGAAAAATCAAAAGGGCCAAAGAACCAAGAAAGTCCACC	1260
Db	1208	CTTACCCCTGCCCCAGCTGGGAAAAATCAAAAGGGCCAAAGAACCAAGAAAGTCCACC	1267
Qy	1261	CTTGGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAG	1320
Db	1268	CTTGGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAG	1327
Qy	1321	AATGCCCTTCTCCTTATTGTAACCCCTGTCTGGATCCTATCCTCCTACCTCCTAAAGCTTCC	1380
Db	1328	AATGCCCTTCTCCTTATTGTAACCCCTGTCTGGATCCTATCCTCCTACCTCCTAAAGCTTCC	1387
Qy	1381	CACGGCTTTCTAGCCTGGCTATGTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTCG	1440
Db	1388	CACGGCTTTCTAGCCTGGCTATGTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTCG	1447
Qy	1441	AAAGTGCAAGGACCTAAACATCTCATCAGTATCCAGTGTGTAATAAGGCTCCTGGCTGT	1500
Db	1448	AAAGTGCAAGGACCTAAACATCTCATCAGTATCCAGTGTGTAATAAGGCTCCTGGCTGT	1507
Qy	1501	CTGAGGCTAGGTGGTTGAAAGCCAAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATT	1560
Db	1508	CTGAGGCTAGGTGGTTGAAAGCCAAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATT	1567
Qy	1561	CCGAGCTCAGACCCCTTCTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTC	1620
Db	1568	CCGAGCTCAGACCCCTTCTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTC	1627
Qy	1621	CTTCTGAGCCCGGTAAGAGCAAAAGAATGGCAGAAAAAGTTTAGCCCCCTGAAAGCCATGGA	1680
Db	1628	CTTCTGAGCCCGGTAAGAGCAAAAGAATGGCAGAAAAAGTTTAGCCCCCTGAAAGCCATGGA	1687
Qy	1681	GATTCTCATAAATTGAGACCTTAATCTCTGTAAGCTAAAAATAAGAAAAATAGAACCAAGCT	1740
Db	1688	GATTCTCATAAATTGAGACCTTAATCTCTGTAAGCTAAAAATAAGAAAAATAGAACCAAGCT	1747
Qy	1741	GAGGATACGACAGTACACTGTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTT	1800
Db	1748	GAGGATACGACAGTACACTGTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTT	1807
Qy	1801	CTCTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACACTTACTTTTCTGGTCT	1860
Db	1808	CTCTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACACTTACTTTTCTGGTCT	1867
Qy	1861	CTACCACTGCTGATATTTTCTCTAGGAAATATACTTTTACAGTAACAAAAATAAAAACT	1920

Db 1868 CTACCACCTGCTGATATTTCTCTAGGAATATATCTTTACAAGTAACAAAATAAAAACT 1927

QY 1921 CTTATAAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGT 1980

Db 1928 CTTATAAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGT 1987

QY 1981 AATTTGTTTAAAAAGTAFAAAAATTCAACAAACATTTAAAAA 2025

Db 1988 AATTTGTTTAAAAAGTAFAAAAATTCAACAAACATTTGCTGAATA 2032

RESULT 4

US-09-909-320-200

; Sequence 200, Application US/09909320

; Patent No. US20020132240A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/909,320

; CURRENT FILING DATE: 2002-01-04

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29

; PRIOR APPLICATION NUMBER: PCT/US99/28313

; PRIOR FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: PCT/US99/28564

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/28565

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/30095

; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: PCT/US99/30911

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US99/30999

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US00/00219

; PRIOR FILING DATE: 2000-01-05

; NUMBER OF SEQ ID NOS: 423

; SEQ ID NO 200

; LENGTH: 2372

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-909-320-200

Query Match 98.3%; Score 1994; DB 9; Length 2372;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 24 AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGAGCAGTGAGTGTGAGCCTCAACATA 83

Db 1 AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGAGCAGTGAGTGTGAGCCTCAACATA 60

QY 84 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCCTCTCATATCACCAGTGGC 143

Db 61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCCTCTCATATCACCAGTGGC 120

QY 144 CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 203

Db 121 CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180

QY 204 GTGTTGTTCTCACTTCCATCTGGACCCAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 263

Db 181 GTGTTGTTCTCACTTCCATCTGGACCCAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240

QY 264 GAAAGAGCTTCCATCCAGGTGTCAATGCAGAAATATGGGGATCACCCCTTGTGAGCAAAAAG 323

Db 241 GAAAGAGCTTCCATCCAGGTGTCAATGCAGAAATATGGGGATCACCCCTTGTGAGCAAAAAG 300

QY 324 GCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCCCTGTAGGCTGCTGGGACTAAGT 383

Db 301 GCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCCCTGTAGGCTGCTGGGACTAAGT 360

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Db 421 GGCTGGGTTGGAGATGGATTCTGTTGTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGG 480

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Db 541 TGTTACAACCTCATCTGATACTTGGACTAACTCGTGCAATTCAGAAATTTATCACCACCAA 600

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Db 601 GATCCCATATTTCAACACTCAAACTGCAACACAAACAAGATTTATTGTCAGTGACAGT 660

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QY 744 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTGCAGAAAGTTTTTATG 803

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QY 804 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCATTTCAAG 863

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Qy 1224 ATCAAAAGGGCCAAAGAACCAAGAGAAAAGTCCACCCCTTGGTTCCTAACTGGAATCAGC 1283

Db 1201 ATCAAAAGGGCCAAAGAACCAAGAGAAAAGTCCACCCCTTGGTTCCTAACTGGAATCAGC 1260

Qy 1284 TCAGGACTGCCAATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1343

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Qy 1464 TCATCAGTATCCAGTGGTAAAAGGCCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC 1523

Db 1441 TCATCAGTATCCAGTGGTAAAAGGCCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC 1500

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Qy 1944 GAGTTACAGAAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 2003

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Db 1981 TTCAACAAACATTTGCTGAATA 2002

RESULT 5

US-09-909-088B-200
; Sequence 200, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,088B
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16

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; PRIOR FILING DATE: 1999-12-20									
; PRIOR APPLICATION NUMBER: PCT/US99/30999									
; PRIOR FILING DATE: 1999-12-20									
; PRIOR APPLICATION NUMBER: PCT/US00/00219									
; PRIOR FILING DATE: 2000-01-05									
; NUMBER OF SEQ ID NOS: 423									
; SEQ ID NO 200									
; LENGTH: 2372									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
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Query Match 98.3%; Score 1994; DB 9; Length 2372;									
Best Local Similarity 99.8%; Pred. No. 0;									
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;									
QY	24	AGCAGGGAATCCGGATGTC	CGGTTATGAAGTGGAGCAGT	GAGTGTGAGCCTCAACATA	83				
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QY	84	GTTCCAGAACTCTCCATCCG	ACTAGTTATTGAGCATCTGC	CTCTCATATCACCAGTGGC	143				
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QY	144	CATCTGAGGTGTTTCCCTGG	CTCTGAAGGGTAGGCACGAT	CGCCTCTCATATCAGCCTG	203				
Db	121	CATCTGAGGTGTTTCCCTGG	CTCTGAAGGGTAGGCACGAT	GGCCAGGTGCTTCAGCCTG	180				
QY	204	GTGTTGCTTCTCACTTCCAT	CTGGACCACGAGGCTCCTG	CTCCAAGGCTCTTTGCGTGCA	263				
Db	181	GTGTTGCTTCTCACTTCCAT	CTGGACCACGAGGCTCCTG	CTCCAAGGCTCTTTGCGTGCA	240				
QY	264	GAAGAGCTTTCCATCCAGGT	GTCAATGCAGAAATTATGG	GGATCACCCCTTGTGAGCAAAAAG	323				
Db	241	GAAGAGCTTTCCATCCAGGT	GTCAATGCAGAAATTATGG	GGATCACCCCTTGTGAGCAAAAAG	300				
QY	324	GCGAACCCAGCAGCTGAAT	TTACAGAAAGCTAAGGAGG	CGCTGTAGGCTGTGGGACTAAGT	383				
Db	301	GCGAACCCAGCAGCTGAAT	TTACAGAAAGCTAAGGAGG	CGCTGTAGGCTGTGGGACTAAGT	360				
QY	384	TTGGCCCGCAAGGACCAAG	TGAAACAGCCTTGAAAGT	AGCTTTGAAACTTGCAGCTAT	443				
Db	361	TTGGCCCGCAAGGACCAAG	TGAAACAGCCTTGAAAGT	AGCTTTGAAACTTGCAGCTAT	420				
QY	444	GGCTGGGTGGAGATGGATT	CGTGGTCATCTCTAGGATT	AGCCCAACCCCAAGTGGG	503				
Db	421	GGCTGGGTGGAGATGGATT	CGTGGTCATCTCTAGGATT	AGCCCAACCCCAAGTGGG	480				
QY	504	AAAAATGGGGTGGGTGTC	CTGATTTGGAAGGTTCCAG	TGAGCCGACAGTTTGCAGCCTAT	563				
Db	481	AAAAATGGGGTGGGTGTC	CTGATTTGGAAGGTTCCAG	TGAGCCGACAGTTTGCAGCCTAT	540				
QY	564	TGTTACAACCTCATCTGAT	CTTGGACTAACTCGTGCAT	TCCAGAAATTATCACCACCAAA	623				
Db	541	TGTTACAACCTCATCTGAT	CTTGGACTAACTCGTGCAT	TCCAGAAATTATCACCACCAAA	600				
QY	624	GATCCCATATTTCAACACT	CAAACTGCAACACAAACAG	AAATTTATTGTCAACAGT	683				
Db	601	GATCCCATATTTCAACACT	CAAACTGCAACACAAACAG	AAATTTATTGTCAAGT	660				
QY	684	ACCTACTCGGTGGCATCC	CTTACTCTACAATACCTG	CCCTACTACTCTCCTGCT	743				
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QY	804	GAAACTAGCACCATGTCT	ACAGAAACTGAACCATTT	TGTGAAAAATAAAGCAGAT	863				
Db	781	GAAACTAGCACCATGTCT	ACAGAAACTGAACCATTT	TGTGAAAAATAAAGCAGAT	840				

QY	864	AATGAAGCTGCTGGGTTT	TGAGGTTGTCCCCACGG	CTCTGCTAGTGTCTCTCT	923				
Db	841	AATGAAGCTGCTGGGTTT	TGAGGTTGTCCCCACGG	CTCTGCTAGTGTCTCTCT	900				
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Db	901	TTTGGTGTGCAGCTGGT	CTTTGGATTTTGCTATGT	CAAAAGGTATGTGAAGGC	960				
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QY	1104	AAGAGTCCAAGCAAAA	ACTACCGTGCATGCC	TGGAGCTGAAATTTAG	1163				
Db	1081	AAGAGTCCAAGCAAAA	ACTACCGTGCATGCC	TGGAGCTGAAATTTAG	1140				
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Db	1441	TCATCAGTATCCAG	TGTTAAAAAGGCCT	CTCCTGGCTGTCTG	1500				
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Db	1501	CAAGGAGTCACTG	AGACCAAGGCTTTCT	CTACTGATTCG	1560				
QY	1584	GCTCTGAAAAGAGA	AAACACGTATCCAC	CTGACATGTCCTTCT	1643				
Db	1561	GCTCTGAAAAGAGA	AAACACGTATCCAC	CTGACATGTCCTTCT	1620				
QY	1644	AGAATGGCAGAAA	AGTTTAGCCCCCTG	AAAGCCATGGAGATT	1703				
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Db	1801	CAC	TGTTTAGAACACAC	ACTTACTTTTTCTG	1860				
QY	1884	AGGAAATATAC	TTTTTACAAGTAA	CAAAAATAAAAACT	1943				
Db	1861	AGGAAATATAC	TTTTTACAAGTAA	CAAAAATAAAAACT	1920				
QY	1944	GAGTTACAGAAAT	GTATTACTAAGGA	AGATTACTCAGTA	2003				

Db 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTGTTAAAAAGTAATAAAA 1980
Qy 2004 TTCAACAAACATTTAAAAAAA 2025
Db 1981 TTCAACAAACATTTGCTGAATA 2002

RESULT 6
US-09-905-291A-200
; Sequence 200, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-905-291A-200

Query Match 98.3%; Score 1994; DB 9; Length 2372;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy 144 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCAGGTGCTTCAGCCTG 203
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Qy 744 CCAGTTCCACTTCTATTCACGGAGAAAAAATGATTTGTGTACAGAAATTTTATG 803
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QY 1824 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1883

Db 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1860

QY 1884 AGGAAATATACTTTTACAAGTAACAAAATAAAAACCTCTATAAATTTCTATTTTATCT 1943

Db 1861 AGGAAATATACTTTTACAAGTAACAAAATAAAAACCTCTATAAATTTCTATTTTATCT 1920

QY 1944 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 2003

Db 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980

QY 2004 TTCAACAAACATTTAAAAAAA 2025

Db 1981 TTCAACAAACATTTGCTGAATA 2002

RESULT 7

US-09-902-853-200

; Sequence 200, Application US/09902853

; Publication No. US20020192659A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/902,853

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: US/09/665,350

; PRIOR FILING DATE: 2000-09-18

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29

; PRIOR APPLICATION NUMBER: PCT/US99/28313

; PRIOR FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: PCT/US99/28564

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/28565

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/30095

; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: PCT/US99/30911

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US99/30999

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US00/00219									
; PRIOR FILING DATE: 2000-01-05									
; NUMBER OF SEQ ID NOS: 423									
; SEQ ID NO 200									
; LENGTH: 2372									
; TYPE: DNA									
; ORGANISM: Homo Sapien									
US-09-902-853-200									
Query Match 98.3%; Score 1994; DB 9; Length 2372;									
Best Local Similarity 99.8%; Pred. No. 0;									
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;									
Qy	24	AGCAGGGAATCCGGATGTC	CGGTTATGAAGTGGAGCAGT	GAGTGTGAGCCTCAACATA	83				
Db	1	AGCAGGGAATCCGGATGTC	CGGTTATGAAGTGGAGCAGT	GAGTGTGAGCCTCAACATA	60				
Qy	84	GTTCCAGAACTCTCCATCC	GGACTAGTTATTGAGCATCT	GCCTCTCATATCACCAGTGGC	143				
Db	61	GTTCCAGAACTCTCCATCC	GGACTAGTTATTGAGCATCT	GCCTCTCATATCACCAGTGGC	120				
Qy	144	CATCTGAGGTGTTCCCTGG	CTCTGAAGGGGTAGGCACG	ATGCGCCTTTCAGCCTG	203				
Db	121	CATCTGAGGTGTTCCCTGG	CTCTGAAGGGGTAGGCACG	ATGCGCCTTTCAGCCTG	180				
Qy	204	GTGTTGCTTCTCACTTCC	ATCTGGACACAGAGGCTC	TGGTCCAGGCTCTTTGCGTGCA	263				
Db	181	GTGTTGCTTCTCACTTCC	ATCTGGACACAGAGGCTC	TGGTCCAGGCTCTTTGCGTGCA	240				
Qy	264	GAAGAGCTTTCATCCAGG	TGTCATGCAGAATTATGG	GGATCACCTTGTGAGCAAAAAG	323				
Db	241	GAAGAGCTTTCATCCAGG	TGTCATGCAGAATTATGG	GGATCACCTTGTGAGCAAAAAG	300				
Qy	324	GCGAACACAGCAGCTGA	ATTTCACAGAAGCTAAGG	AGGCCTGTAGGCTGCTGGGACTAAGT	383				
Db	301	GCGAACACAGCAGCTGA	ATTTCACAGAAGCTAAGG	AGGCCTGTAGGCTGCTGGGACTAAGT	360				
Qy	384	TTGGCCCGCAAGGACCA	AGTTGAAACAGCCCTTGA	AAAGCTAGCTTTGAAAACCTTGACGCTAT	443				
Db	361	TTGGCCCGCAAGGACCA	AGTTGAAACAGCCCTTGA	AAAGCTAGCTTTGAAAACCTTGACGCTAT	420				
Qy	444	GGCTGGGTGGAGATGG	ATTCCGTGTCATCTCTAG	GATTAGCCAAACCCCAAGTGTGGG	503				
Db	421	GGCTGGGTGGAGATGG	ATTCCGTGTCATCTCTAG	GATTAGCCAAACCCCAAGTGTGGG	480				
Qy	504	AAAAATGGGTGGGTGTC	CTGATTGGAAAGGTTCC	AGTGAGCCGACAGTTTGCAGCCTAT	563				
Db	481	AAAAATGGGTGGGTGTC	CTGATTGGAAAGGTTCC	AGTGAGCCGACAGTTTGCAGCCTAT	540				
Qy	564	TGTTACAACTCATCTGA	TACTTGGACTAACTCGT	GCATCCAGAAATTATCACCACCCAAA	623				
Db	541	TGTTACAACTCATCTGA	TACTTGGACTAACTCGT	GCATCCAGAAATTATCACCACCCAAA	600				
Qy	624	GATCCCATATTCAACAC	TCAAACCTGCAACACAAA	CAACAGAAATTATTGTGACGACAGT	683				
Db	501	GATCCCATATTCAACAC	TCAAACCTGCAACACAAA	CAACAGAAATTATTGTGACGACAGT	660				
Qy	684	ACCTACTCGGTGGCATC	CCCTTACTCTACAATA	CCCTGCCCCCTACTACTCTCCTCGCT	743				
Db	661	ACCTACTCGGTGGCATC	CCCTTACTCTACAATA	CCCTGCCCCCTACTACTCTCCTCGCT	720				
Qy	744	CCAGTTCACACTTCTAT	TCCACGGAGAAAAAAT	TGATTTGTGTACAGAAAGTTTATTG	803				
Db	721	CCAGTTCACACTTCTAT	TCCACGGAGAAAAAAT	TGATTTGTGTACAGAAAGTTTATTG	780				
Qy	804	GAAACTAGCACCATGTCT	ACAGAACTGAACCATTT	TGTTGAAAAATAAAGCAGCATTTCAAG	863				
Db	781	GAAACTAGCACCATGTCT	ACAGAACTGAACCATTT	TGTTGAAAAATAAAGCAGCATTTCAAG	840				
Qy	864	AATGAAGCTGCTGGGTT	TGGAGGTGCCCCACGG	CTGCTAGTGTGCTCTCCTCTTC	923				
Db	841	AATGAAGCTGCTGGGTT	TGGAGGTGCCCCACGG	CTGCTAGTGTGCTCTCCTCTTC	900				

Qy	924	TTTGGTGTGCAGCTGGT	CTTGGATTTTGCTATGT	CAAAAGGTATGTGAAGGCCTTCCCT	983				
Db	901	TTTGGTGTGCAGCTGGT	CTTGGATTTTGCTATGT	CAAAAGGTATGTGAAGGCCTTCCCT	960				
Qy	984	TTTACAAAACAAGAAAT	CAGCAGAACGAAATGAT	CGAAACCAAAAGTAGTAAAGGAGGAGAAG	1043				
Db	961	TTTACAAAACAAGAAAT	CAGCAGAACGAAATGAT	CGAAACCAAAAGTAGTAAAGGAGGAGAAG	1020				
Qy	1044	GCCAATGATAGCAACCT	TAATGAGGAATCAAAGAA	AACTGATAAAAAACCCAGAGAGTCC	1103				
Db	1021	GCCAATGATAGCAACCT	TAATGAGGAATCAAAGAA	AACTGATAAAAAACCCAGAGAGTCC	1080				
Qy	1104	AAGAGTCCAAAGCAAAA	CTACCGTGCATGCTGGA	AGCTGAAAGTTAGATGAGACAGAAA	1163				
Db	1081	AAGAGTCCAAAGCAAAA	CTACCGTGCATGCTGGA	AGCTGAAAGTTAGATGAGACAGAAA	1140				
Qy	1164	TGAGGAGACACACCTG	AGGCTGTTCTTTCATG	CTCCTACCCCTGCCCCAGCTGGGAA	1223				
Db	1141	TGAGGAGACACACCTG	AGGCTGTTCTTTCATG	CTCCTACCCCTGCCCCAGCTGGGAA	1200				
Qy	1224	ATCAAAAGGGCCAAAGA	CCAAAGAAAGTCCAC	CCCTTGGTTCCTAACTGGAATCAGC	1283				
Db	1201	ATCAAAAGGGCCAAAGA	CCAAAGAAAGTCCAC	CCCTTGGTTCCTAACTGGAATCAGC	1260				
Qy	1284	TCAGGACTGCCATTGG	ACTATGGAGTGCACCAA	AGAGATGCCCTTCTCCTTATTGTAAC	1343				
Db	1261	TCAGGACTGCCATTGG	ACTATGGAGTGCACCAA	AGAGATGCCCTTCTCCTTATTGTAAC	1320				
Qy	1344	CCTGTCTGGATCCTAT	CCCTCCTACCTCCAA	AGCTTCCCACGGCTTTCTAGCCTGGCTAT	1403				
Db	1321	CCTGTCTGGATCCTAT	CCCTCCTACCTCCAA	AGCTTCCCACGGCTTTCTAGCCTGGCTAT	1380				
Qy	1404	GTCTTAATAATATCCC	ACTGGGAGAAAGGAG	TTTTGCAAAGTGAAGGACCTAAAAACATC	1463				
Db	1381	GTCTTAATAATATCCC	ACTGGGAGAAAGGAG	TTTTGCAAAGTGAAGGACCTAAAAACATC	1440				
Qy	1464	TCATCAGTATCCAGT	GGTAAAGGCCCTCCT	GGTGTCTGAGSCTAGGTGGTTGAAAGC	1523				
Db	1441	TCATCAGTATCCAGT	GGTAAAGGCCCTCCT	GGTGTCTGAGSCTAGGTGGTTGAAAGC	1500				
Qy	1524	CAAGGAGTCACTGAG	ACCAGGCTTCTCTACT	GATTTCCGACGCTCAGACCCCTTCTTCA	1583				
Db	1501	CAAGGAGTCACTGAG	ACCAGGCTTCTCTACT	GATTTCCGACGCTCAGACCCCTTCTTCA	1560				
Qy	1584	GCTCTGAAAGAGAA	ACACGTTATCCCAC	CTGACATGTCCTTCTGAGCCCCGTTAAGAGCAA	1643				
Db	1561	GCTCTGAAAGAGAA	ACACGTTATCCCAC	CTGACATGTCCTTCTGAGCCCCGTTAAGAGCAA	1620				
Qy	1644	AGAATGGCAGAAAAG	TTTAGCCCCCTGAA	AGCCATGGAGATTTCTATAACTTGAGACCTAA	1703				
Db	1621	AGAATGGCAGAAAAG	TTTAGCCCCCTGAA	AGCCATGGAGATTTCTATAACTTGAGACCTAA	1680				
Qy	1704	TCTCTGTAAGCTAAA	ATAAGAAATAGAA	CAAGGCTGAGGATACGACAGTACACTGTCA	1763				
Db	1681	TCTCTGTAAGCTAAA	ATAAGAAATAGAA	CAAGGCTGAGGATACGACAGTACACTGTCA	1740				
Qy	1764	GCAGGACTGTAAA	CACAGACAGGCTCA	AAAGTGTCTCTGAAACACATTTGAGTTGGAAT	1823				
Db	1741	GCAGGACTGTAAA	CACAGACAGGCTCA	AAAGTGTCTCTGAAACACATTTGAGTTGGAAT	1800				
Qy	1824	CACGTGTTAGAA	CACACACACTTACT	TTTTCTGGTCTCTACCACTGCTGATATTTCTCT	1883				
Db	1801	CACGTGTTAGAA	CACACACACTTACT	TTTTCTGGTCTCTACCACTGCTGATATTTCTCT	1860				
Qy	1884	AGGAAATATACTTTT	TACAAGTAAACAAA	ATAAAAACTCTATAAATTTCTATTTTATCT	1943				
Db	1861	AGGAAATATACTTTT	TACAAGTAAACAAA	ATAAAAACTCTATAAATTTCTATTTTATCT	1920				
Qy	1944	GAGTTACAGAAAAT	GATTACTAAGGAAGAT	TACTCAGTAATTTGTTTAAAAAGTAATAAAA	2003				
Db	1921	GAGTTACAGAAAAT	GATTACTAAGGAAGAT	TACTCAGTAATTTGTTTAAAAAGTAATAAAA	1980				
Qy	2004	TTCAACAAACATTTT	AAAAAAA	2025					

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Db      1981 TTCAACAAACATTTGCTGAATA 2002
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RESULT 8
US-09-907-824-200
; Sequence 200, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
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; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-907-824-200

Query Match      98.3%; Score 1994; DB 9; Length 2372;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      24 AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGAGCAGTGAGTGTGAGCCTCAACATA 83
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Db       1 AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGAGCAGTGAGTGTGAGCCTCAACATA 60

QY      84 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 143
      |||||||
Db       61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120

QY     144 CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 203
      |||||||
Db     121 CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180

QY     204 GTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAAGGCTCTTTGCGTGCA 263
      |||||||
Db     181 GTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAAGGCTCTTTGCGTGCA 240

QY     264 GAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGGATCACCCCTTGTCAGCAAAAAG 323
      |||||||
Db     241 GAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGGATCACCCCTTGTCAGCAAAAAG 300

QY     324 GCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCCCTGTAGGCTGCTGGGACTAAAGT 383
      |||||||
Db     301 GCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCCCTGTAGGCTGCTGGGACTAAAGT 360

QY     384 TTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 443
      |||||||
Db     361 TTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420

QY     444 GGCTGGGTTGGAGATGGATTGCTGGTTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGG 503
      |||||||
Db     421 GGCTGGGTTGGAGATGGATTGCTGGTTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGG 480

QY     504 AAAAATGGGGTGGGTGTCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 563
      |||||||
Db     481 AAAAATGGGGTGGGTGTCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540

QY     564 TGTTACAACTCATCTGATACCTTGGACTAATCGTGCAATTCAGAAATTTATCACCACCAA 623
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Db     541 TGTTACAACTCATCTGATACCTTGGACTAATCGTGCAATTCAGAAATTTATCACCACCAA 600

QY     624 GATCCCATATTCAACACTCAAACTGCAACACAAACAAAGAAATTTATTGTGAGTGACAGT 683
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Db     601 GATCCCATATTCAACACTCAAACTGCAACACAAACAAAGAAATTTATTGTGAGTGACAGT 660

QY     684 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTCCTCCTGCT 743
      |||||||
Db     661 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTCCTCCTGCT 720

QY     744 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTGTGTCAACAGAAATTTTATG 803
      |||||||
Db     721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTGTGTCAACAGAAATTTTATG 780

QY     804 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCATTCAG 863
      |||||||
Db     781 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCATTCAG 840

QY     864 AATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGTGCTCTCCTCTTC 923
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Db     841 AATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGTGCTCTCCTCTTC 900
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QY 924 TTTGGTGTGCAGCTGGTCTTGGATTTTGGCTATGTCAAAGGTATGTGAAGCCTTCCCT 983
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QY 984 TTTACAAACAAGAAATCAGCAGAAAGGAAATGATCGAAACCAAGTAGTAAAGGAGGAAG 1043
Db 961 TTTACAAACAAGAAATCAGCAGAAAGGAAATGATCGAAACCAAGTAGTAAAGGAGGAAG 1020

QY 1044 GCCAATGATAGCAACCCCTAATGAGGAATCAAAAGAAAACCTGATAAAAACCCAGAAGTCC 1103
Db 1021 GCCAATGATAGCAACCCCTAATGAGGAATCAAAAGAAAACCTGATAAAAACCCAGAAGTCC 1080

QY 1104 AAGAGTCCAAAGCAAAAACCTACCGTGCATGCTTCTTTCATGCTCCTTACCCCTGCCCAGCTGGGAA 1223
Db 1081 AAGAGTCCAAAGCAAAAACCTACCGTGCATGCTTCTTTCATGCTCCTTACCCCTGCCCAGCTGGGAA 1200

QY 1164 TGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCCTTACCCCTGCCCAGCTGGGAA 1223
Db 1141 TGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCCTTACCCCTGCCCAGCTGGGAA 1200

QY 1224 ATCAAAAGSGCCAAAAGAACCAAGAGAAAGTCCACCCCTTGGTTCTTAACCTGGAATCAGC 1283
Db 1201 ATCAAAAGSGCCAAAAGAACCAAGAGAAAGTCCACCCCTTGGTTCTTAACCTGGAATCAGC 1260

QY 1284 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAATGCCCTTCTCCTTATTGTAAC 1343
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QY 1344 CCTGTCTGGATCCTATCCTCCTACCTCGGAGAAAGTCCACCCCTTGGTTCTTAACCTGGAATC 1403
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QY 1404 GTCCTAAATAATATCCACTGGGAGAAAGGAGTTTTCGAAAAGTGCAGGACCTAAAACATC 1463
Db 1381 GTCCTAAATAATATCCACTGGGAGAAAGGAGTTTTCGAAAAGTGCAGGACCTAAAACATC 1440

QY 1464 TCATCAGTATCCAGTGGTAAAGGCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC 1523
Db 1441 TCATCAGTATCCAGTGGTAAAGGCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC 1500

QY 1524 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1583
Db 1501 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560

QY 1584 GCTCTGAAAGAGAAAACACGTATCCCACTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA 1643
Db 1561 GCTCTGAAAGAGAAAACACGTATCCCACTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA 1620

QY 1644 AGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1703
Db 1621 AGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680

QY 1704 TCTCTGAAAGCTAAAATAAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA 1763
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QY 1764 GCAGGACTGTAAACACAGACAGGGTCAAAGTGTCTTCTGAAACACATGAGTTGGAAT 1823
Db 1741 GCAGGACTGTAAACACAGACAGGGTCAAAGTGTCTTCTGAAACACATGAGTTGGAAT 1800

QY 1824 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACCTGATATTTTCTCT 1883
Db 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACCTGATATTTTCTCT 1860

QY 1884 AGGAAATATACTTTTACAAGTAACAAAATAAAACTCTTATAAATTTCTATTTTATCT 1943
Db 1861 AGGAAATATACTTTTACAAGTAACAAAATAAAACTCTTATAAATTTCTATTTTATCT 1920

QY 1944 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTTGTTTAAAAAGTAATAAA 2003
Db 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTTGTTTAAAAAGTAATAAA 1980

QY 2004 TTCAACAAACATTTAAAAAAA 2025

Db 1981 TTCAACAAACATTTGCTGAATA 2002

RESULT 9
US-09-907-841-200
; Sequence 200, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-841-200

Query Match 98.3%; Score 1994; DB 9; Length 2372;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 1 AGCAGGAAATCCGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60

QY 84 GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 143

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US-09-904-011-200

; Sequence 200, Application US/09904011

; Publication No. US20030003530A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

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Db 1981 TTCAACAAACATTTGCTGAATA 2002

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; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,011
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
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; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-011-200
Query Match 98.3%; Score 1994; DB 10; Length 2372;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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RESULT 11
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; Sequence 200, Application US/09906742
; Publication No. US20030023054a1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
Query Match 98.3%; Score 1994; DB 10; Length 2372;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 24 AGCAGGGAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 83
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; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
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; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-906-742-200

Db 1 AGCAGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60

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Qy 864 AATGAAGCTGCTGGGTTTGGAGGTGTCACAGGCTCTGCTAGTGCTTGTGCTCTCCTCTTC 923

Db 841 AATGAAGCTGCTGGGTTTGGAGGTGTCACAGGCTCTGCTAGTGCTTGTGCTCTCCTCTTC 900

Qy 924 TTTGGTGTGCAGCTGGTCTTGGAATTTTGCTATGTCAAAAGGTATGGAAGGCCTTCCCT 983

Db 901 TTTGGTGTGCAGCTGGTCTTGGAATTTTGCTATGTCAAAAGGTATGGAAGGCCTTCCCT 960

Qy 984 TTTACAACAAGAATCAGCAGAGGAAATGATCGAAACCAAGTAGTAAAGGAGGAAG 1043

Db 961 TTTACAACAAGAATCAGCAGAGGAAATGATCGAAACCAAGTAGTAAAGGAGGAAG 1020

Qy 1044 GCCAATGATACCAACCTTAATGAGGAATCAAGAAAACTGATAAAAAACCCAGAAGTCC 1103

Db 1021 GCCAATGATACCAACCTTAATGAGGAATCAAGAAAACTGATAAAAAACCCAGAAGTCC 1080

Qy 1104 AAGAGTCCAAGCAAAAACCTACCGTGCATGCCGTGGAAGCTGAAAGTTAGATGAGACAGAAA 1163

Db 1081 AAGAGTCCAAGCAAAAACCTACCGTGCATGCCGTGGAAGCTGAAAGTTAGATGAGACAGAAA 1140

Qy 1164 TGAGGAGACACACCTGAGGCTGGTTTCTTTTTCATGCTCCTTACCCTGCCCCAGCTGGGAA 1223

Db 1141 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCCTGCCCCAGCTGGGAA 1200

Qy 1224 ATCAAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACCTTGGTTCCCTAACTGGAATCAGC 1283

Db 1201 ATCAAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACCTTGGTTCCCTAACTGGAATCAGC 1260

Qy 1284 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1343

Db 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1320

Qy 1344 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCTTTCTAGCCTGGCTAT 1403

Db 1321 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCTTTCTAGCCTGGCTAT 1380

Qy 1404 GTCCTAATAATATCCCACCTGGGAGAAAGGAGTTTTTGCAAAGTGCAAGGACCTTAAACATC 1463

Db 1381 GTCCTAATAATATCCCACCTGGGAGAAAGGAGTTTTTGCAAAGTGCAAGGACCTTAAACATC 1440

Qy 1464 TCATCAGTATCCAGTGGTAAAGGCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAAGC 1523

Db 1441 TCATCAGTATCCAGTGGTAAAGGCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAAGC 1500

Qy 1524 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGANTCCGAGCTCAGACCCCTTCTTCA 1583

Db 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGANTCCGAGCTCAGACCCCTTCTTCA 1560

Qy 1584 GCTCTGAAAGAGAAACACGTCATCCACCTGACATGTCCTTCTGAGCCCGTAAAGACAA 1643

Db 1561 GCTCTGAAAGAGAAACACGTCATCCCACTGACATGTCCTTCTGAGCCCGTAAAGACAA 1620

Qy 1644 AGAATGGCAGAAAAAGTTTAGCCCCCTGAAAGCCATGGAGATTTCTCATAACTTGAGACCTAA 1703

Db 1621 AGAATGGCAGAAAAAGTTTAGCCCCCTGAAAGCCATGGAGATTTCTCATAACTTGAGACCTAA 1680

Qy 1704 TCTCTGTAAGCTAAAAATAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA 1763

Db 1681 TCTCTGTAAGCTAAAAATAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA 1740

Qy 1764 GCAGGACTGTAAACACAGACAGGCTCAAAAGTGTCTTCTGAAACACATTGAGTTGGAAT 1823

Db 1741 GCAGGACTGTAAACACAGACAGGCTCAAAAGTGTCTTCTGAAACACATTGAGTTGGAAT 1800

Qy 1824 CACTGTTAGAAACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1883

Db 1801 CACTGTTAGAAACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1860

Qy 1884 AGGAAATATACTTTTACAAGTAAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1943

Db 1861 AGGAAATATACTTTTACAAGTAAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1920

Qy 1944 GAGTTACAGAAATGATTACTAAGGAAAGATTACTCAGTAAATTTGTTAAAAAGTAATAAAA 2003

Db 1921 GAGTTACAGAAATGATTACTAAGGAAAGATTACTCAGTAAATTTGTTAAAAAGTAATAAAA 1980

Qy 2004 TTCAACAAACATTTAAAAAAA 2025

Db 1981 TTCAACAAACATTTGCTGAATA 2002

RESULT 12
US-09-906-838-200
; Sequence 200, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,838
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-906-838-200

Query Match 98.3%; Score 1994; DB 10; Length 2372;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 24 AGCAGGAAATCCGGATGTCCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 83
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Db 1 ACCAGGAAATCCGGATGTCCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60
QY 84 GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 143
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Db 61 GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
QY 144 CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCAGATGGCCAGGTGCTTCAGCCTG 203
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Db 121 CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCAGATGGCCAGGTGCTTCAGCCTG 180
QY 204 GTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 263
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Db 181 GTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240
QY 264 GAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGATCACCCCTTGTGAGCAAAAAG 323
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Db 241 GAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGATCACCCCTTGTGAGCAAAAAG 300
QY 324 GCGAACGACGAGCTGAATTTACAGAAAGCTAAGGAGGCTGTAGGCTGTGGGACTAAGT 383
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Db 301 GCGAACGACGAGCTGAATTTACAGAAAGCTAAGGAGGCTGTAGGCTGTGGGACTAAGT 360
QY 384 TTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGTAGCTTTGAAACTTGCAGCTAT 443
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Db 361 TTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGTAGCTTTGAAACTTGCAGCTAT 420
QY 444 GGCTGGGTTGGAGATGGATTCGTGGTCACTCTAGGANTAGCCCAACCCCAAGTGGG 503
Db 421 GGCTGGGTTGGAGATGGATTCGTGGTCACTCTAGGANTAGCCCAACCCCAAGTGGG 480
QY 504 AAAAAATGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 563
Db 481 AAAAAATGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540
QY 564 TGTTACAACTCATCTGATACTTGGACTAACTCGTGTGATTCAGAAATTATCACCACCAAA 623
Db 541 TGTTACAACTCATCTGATACTTGGACTAACTCGTGTGATTCAGAAATTATCACCACCAAA 600
QY 624 GATCCCATATTTCAACACTCAAACTGCAACACAAACAGAAATTTATTGTGAGTACAGT 683
Db 601 GATCCCATATTTCAACACTCAAACTGCAACACAAACAGAAATTTATTGTGAGTACAGT 660
QY 684 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTACTCCTCCTGCT 743
Db 661 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTACTCCTCCTGCT 720
QY 744 CCAGCTTCCACTTCTAATCCACGGAGAAAAAATGATTTGTGTACAGAAAGTTTATG 803
Db 721 CCAGCTTCCACTTCTAATCCACGGAGAAAAAATGATTTGTGTACAGAAAGTTTATG 780
QY 804 GAAACTAGCACCATGTCTACAGAAACTGAACCAATTTGTTGAAAAATAAGCAGCATTAAG 863
Db 781 GAAACTAGCACCATGTCTACAGAAACTGAACCAATTTGTTGAAAAATAAGCAGCATTAAG 840
QY 864 AATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGTGCTTCTCCTCTTC 923
Db 841 AATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGTGCTTCTCCTCTTC 900
QY 924 TTTGGTGTGCAGTGGTCTTTGGATTTTGTGCTATGTCAAAAGGTATGTGAAGGCTTCCCT 983
Db 901 TTTGGTGTGCAGTGGTCTTTGGATTTTGTGCTATGTCAAAAGGTATGTGAAGGCTTCCCT 960
QY 984 TTTACAAACAAGAAATCAGCAGAGGAATGATCGAAACCAAGTAGTAAAGGAGGAGAAG 1043
Db 961 TTTACAAACAAGAAATCAGCAGAGGAATGATCGAAACCAAGTAGTAAAGGAGGAGAAG 1020
QY 1044 GCCAATGATAGCAACCTTAATGAGGAATCAAGAAAACTGATAAAACCAGAAAGAGTCC 1103
Db 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAGAAAACTGATAAAACCAGAAAGAGTCC 1080
QY 1104 AAGAGTCCAAGCAAAAACTACCGTCCGATGCTTGAAGCTGAAAGTTTAGATGAGACAGAAA 1163
Db 1081 AAGAGTCCAAGCAAAAACTACCGTCCGATGCTTGAAGCTGAAAGTTTAGATGAGACAGAAA 1140

QY 1164 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCTGCCCCAGCTGGGAA 1223
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QY 1141 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCTGCCCCAGCTGGGAA 1200
Db |||||
QY 1224 ATCAAAAGGGCCAAAGAACCAAGAGAGAAAAGTCCACCCCTTGGTTCTCTAACTGGAATCAGC 1283
Db |||||
QY 1201 ATCAAAAGGGCCAAAGAACCAAGAGAGAAAAGTCCACCCCTTGGTTCTCTAACTGGAATCAGC 1260
Db |||||
QY 1284 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1343
Db |||||
QY 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1320
Db |||||
QY 1344 CCTGTCTGGATCCTATCCTCTACCTCCTCAAGCTTCCCACGGCCTTCTAGCCTGGCTAT 1403
Db |||||
QY 1321 CCTGTCTGGATCCTATCCTCTACCTCCTCAAGCTTCCCACGGCCTTCTAGCCTGGCTAT 1380
Db |||||
QY 1404 GTCCTAATAATATCCCACCTGGGAGAGAGAGTTTTGCAAAGTGCAGGACCTAAAAACATC 1463
Db |||||
QY 1381 GTCCTAATAATATCCCACCTGGGAGAGAGAGTTTTGCAAAGTGCAGGACCTAAAAACATC 1440
Db |||||
QY 1464 TCATCAGTATCCAGTGGTAAAAAGGCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC 1523
Db |||||
QY 1441 TCATCAGTATCCAGTGGTAAAAAGGCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC 1500
Db |||||
QY 1524 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTTTCTTCA 1583
Db |||||
QY 1501 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTTTCTTCA 1560
Db |||||
QY 1584 GCTCTGAAGAGAGAAACACGTATCCCACCTGACATGTCTTCTGAGCCGGTAAGAGCAAA 1643
Db |||||
QY 1561 GCTCTGAAGAGAGAAACACGTATCCCACCTGACATGTCTTCTGAGCCGGTAAGAGCAAA 1620
Db |||||
QY 1644 AGAATGGCAGAAAAGTTTAGCCCCCTGAAGCCCATGGAGATTCTCTATAACTTGAGACCTAA 1703
Db |||||
QY 1621 AGAATGGCAGAAAAGTTTAGCCCCCTGAAGCCCATGGAGATTCTCTATAACTTGAGACCTAA 1680
Db |||||
QY 1704 TCTCTGTAAGCTAAAAATAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTCA 1763
Db |||||
QY 1681 TCTCTGTAAGCTAAAAATAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTCA 1740
Db |||||
QY 1764 GCAGGGACTGTAAACACACAGACAGGGTCAAAGTGTCTCTGAAACATTTGAGTTGGAAT 1823
Db |||||
QY 1741 GCAGGGACTGTAAACACACAGACAGGGTCAAAGTGTCTCTGAAACATTTGAGTTGGAAT 1800
Db |||||
QY 1824 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1883
Db |||||
QY 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1860
Db |||||
QY 1884 AGGAAATATACTTTACAAGTAACAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1943
Db |||||
QY 1861 AGGAAATATACTTTACAAGTAACAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1920
Db |||||
QY 1944 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 2003
Db |||||
QY 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980
Db |||||
QY 2004 TTCAACAAACATTTAAAAAAA 2025
Db |||||
QY 1981 TTCAACAAACATTTGCTGAATA 2002
Db |||||

RESULT 13

US-09-907-613-200
; Sequence 200, Application US/09907613
; Publication No. US20030027145A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone

Query Match 98.3%; Score 1994; DB 10; Length 2372;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 24 AGCAGGGAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 83
Db 1 AGCAGGGAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60

; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,613
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-613-200

QY 84 GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 143
Db 61 GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
QY 144 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTCTTCAGCCTG 203
Db 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTCTTCAGCCTG 180
QY 204 GTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 263
Db 181 GTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240
QY 264 GAAAGAGCTTTCATCCAGTGTCTATGCAGAAATTATGGGATCACCCCTTGTCAGCAAAAAG 323
Db 241 GAAAGAGCTTTCATCCAGTGTCTATGCAGAAATTATGGGATCACCCCTTGTCAGCAAAAAG 300
QY 324 GCGAACCCAGCAGCTGAATTCACAGAAAGCTAAGGAGGCTGTAGGCTGTGGGACTAAAGT 383
Db 301 GCGAACCCAGCAGCTGAATTCACAGAAAGCTAAGGAGGCTGTAGGCTGTGGGACTAAAGT 360
QY 384 TTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 443
Db 361 TTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420
QY 444 GGCTGGGTTGGAGATGGATTCTGTTGGTCACTCTAGGATTAGCCCAACCCCAAGTGTGGG 503
Db 421 GGCTGGGTTGGAGATGGATTCTGTTGGTCACTCTAGGATTAGCCCAACCCCAAGTGTGGG 480
QY 504 AAAAATGGGGTGGGTGTCCTGATTTTGGAAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 563
Db 481 AAAAATGGGGTGGGTGTCCTGATTTTGGAAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540
QY 564 TGTTACAACTCATCTGATACTTGGACTAACTCGTGCAATCCAGAAATTATCACCACCAAA 623
Db 541 TGTTACAACTCATCTGATACTTGGACTAACTCGTGCAATCCAGAAATTATCACCACCAAA 600
QY 624 GATCCCATATTCACACTCAAACTGCAACACAAACACAGAAATTTATTGTCAAGTACAGT 683
Db 601 GATCCCATATTCACACTCAAACTGCAACACAAACACAGAAATTTATTGTCAAGTACAGT 660
QY 684 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCCCTACTACTCTCCTCTGCT 743
Db 661 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCCCTACTACTCTCCTCTGCT 720
QY 744 CCAGCTTCCACTTCTATTTCCACGGAGAAAAAATTGATTTGTGTCAAGAAATTTTATG 803
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QY 804 GAAACTAGCACCATGTCTACAGAACTGAACCAATTTGTTGTTGTTCAAGAAATTAAGCAGTCAAG 863
Db 781 GAAACTAGCACCATGTCTACAGAACTGAACCAATTTGTTGTTGTTCAAGAAATTAAGCAGTCAAG 840
QY 864 AATGAAGCTGCTGGGTTTGGAGGTGTCCCAAGGCTCTGCTAGTGTGCTCTCTCTCTTC 923
Db 841 AATGAAGCTGCTGGGTTTGGAGGTGTCCCAAGGCTCTGCTAGTGTGCTCTCTCTCTTC 900
QY 924 TTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAAAAAGGTATGTGAAGGCTTCCCT 983
Db 901 TTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAAAAAGGTATGTGAAGGCTTCCCT 960
QY 984 TTTACAAAACAAGATCAGCAGAGGAATGATCGAAACCAAAGTAGTAAGGAGGAGAA 1043
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QY 1104 AAGAGTCCAAAGCAAAACTACCGTGCAGTGCCTGGAAGCTGAAGTTTAGATGACACAGAAA 1163
Db 1081 AAGAGTCCAAAGCAAAACTACCGTGCAGTGCCTGGAAGCTGAAGTTTAGATGACACAGAAA 1140
QY 1164 TGAGGAGACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCTGCCCCAGCTGGGAA 1223

Db 1141 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCTGCCCCAGCTGGGAA 1200
QY 1224 ATCAAAAGGGCCAAAGAACCAAAAGAAAGTCCACCCCTTGTTCTTAACCTGGAATCAGC 1283
Db 1201 ATCAAAAGGGCCAAAGAACCAAAAGAAAGTCCACCCCTTGTTCTTAACCTGGAATCAGC 1260
QY 1284 TCAGGACTGCCATTTGGACTATGGAGTGCACCAAAAGAGAATGCCCTTCTCCTTATTGTAAC 1343
Db 1261 TCAGGACTGCCATTTGGACTATGGAGTGCACCAAAAGAGAATGCCCTTCTCCTTATTGTAAC 1320
QY 1344 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCTTTCTAGCCCTGGCTAT 1403
Db 1321 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCTTTCTAGCCCTGGCTAT 1380
QY 1404 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTTGCAAAAGTGCAAGGACCTAAAAATC 1463
Db 1381 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTTGCAAAAGTGCAAGGACCTAAAAATC 1440
QY 1464 TCATCAGTATCCAGTGTGTGTAAGGCTCCTGGTGTCTTGAGGCTAGGTGGGTGAAAAGC 1523
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QY 1524 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1583
Db 1501 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560
QY 1584 GCTCTGAAAGAGAAACACGATATCCCACCTGACATGTCTTCTGAGCCCGGTAAAGCAAA 1643
Db 1561 GCTCTGAAAGAGAAACACGATATCCCACCTGACATGTCTTCTGAGCCCGGTAAAGCAAA 1620
QY 1644 AGAATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1703
Db 1621 AGAATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680
QY 1704 TCTCTGTAAAGCTAAAAATAAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTCA 1763
Db 1681 TCTCTGTAAAGCTAAAAATAAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTCA 1740
QY 1764 GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAAT 1823
Db 1741 GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAAT 1800
QY 1824 CACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1883
Db 1801 CACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1860
QY 1884 AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1943
Db 1861 AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1920
QY 1944 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTTAAAAAGTAATAAAA 2003
Db 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTTAAAAAGTAATAAAA 1980
QY 2004 TTCAACAAACATTTAAAAAAA 2025
Db 1981 TTCAACAAACATTTGCTGAATA 2002

RESULT 14
US-09-907-942-200
; Sequence 200, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman

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; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,942
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-942-200

Query Match      98.3%; Score 1994; DB 10; Length 2372;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      24 AGCAGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 83
      |||||||
Db      1 AGCAGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60

QY      84 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 143
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Db      61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
QY      144 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 203
      |||||||
Db      121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180
QY      204 GTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAGGCTCTTTGCGTGCA 263
      |||||||
Db      181 GTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAGGCTCTTTGCGTGCA 240
QY      264 GAAGAGCTTTCATCCAGGTGTCAATTCACAGAAAGCTAAGGAGGCTGTAGGCTGTGAGCAAAAAG 323
      |||||||
Db      241 GAAGAGCTTTCATCCAGGTGTCAATTCACAGAAATTTATGGGGATCACCCCTGTGAGCAAAAAG 300
QY      324 GCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCTGTAGGCTGTGGGACTAAGT 383
      |||||||
Db      301 GCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCTGTAGGCTGTGGGACTAAGT 360
QY      384 TTGGCCGCAAGGACCAAGTTGAAACAGACCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 443
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Db      361 TTGGCCGCAAGGACCAAGTTGAAACAGACCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420
QY      444 GGCTGGGTTGGAGATGGATTTCGTGGTCACTCTCTAGGATTAGCCCAAAACCCCAAGTGTGG 503
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Db      421 GGCTGGGTTGGAGATGGATTTCGTGGTCACTCTCTAGGATTAGCCCAAAACCCCAAGTGTGG 480
QY      504 AAAATGGGGTGGGTGTCTGTGATTGGAAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 563
      |||||||
Db      481 AAAATGGGGTGGGTGTCTGTGATTGGAAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540
QY      564 TGTTACAACTCATCTGATCTTGGACTAACTCGTGCAATCCAGAAATTATCACCACCAA 623
      |||||||
Db      541 TGTTACAACTCATCTGATCTTGGACTAACTCGTGCAATCCAGAAATTATCACCACCAA 600
QY      624 GATCCCATATTCAACACTCAAACTGCAACACAAACAAACAGAAATTTATTGTGAGTACAGT 683
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Db      601 GATCCCATATTCAACACTCAAACTGCAACACAAACAAACAGAAATTTATTGTGAGTACAGT 660
QY      684 ACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCCCTTACTACTCTCCTCTGCT 743
      |||||||
Db      661 ACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCCCTTACTACTCTCCTCTGCT 720
QY      744 CCAGCTTCCACTTCTATTCCACCGAGAAAAAAATTTGATTGTGTGTCACAGAAAGTTTTTATG 803
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Db      721 CCAGCTTCCACTTCTATTCCACCGAGAAAAAAATTTGATTGTGTGTCACAGAAAGTTTTTATG 780
QY      804 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCATTTCAAG 863
      |||||||
Db      781 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCATTTCAAG 840
QY      864 AATGAAGCTGTGGGTTTGGAGGTGTCCTCACGGCTCTGTAGTGCTTCTCCTCTTC 923
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Db      841 AATGAAGCTGTGGGTTTGGAGGTGTCCTCACGGCTCTGTAGTGCTTCTCCTCTTC 900
QY      924 TTTGGTGTGAGCTGGTCTTGGATTTTGTATGTCAAAAGGTATGTGAAGGCTTCCCT 983
      |||||||
Db      901 TTTGGTGTGAGCTGGTCTTGGATTTTGTATGTCAAAAGGTATGTGAAGGCTTCCCT 960
QY      984 TTTACAAAACAAGAAATCAGCAGAAAGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAAG 1043
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Db      961 TTTACAAAACAAGAAATCAGCAGAAAGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAAG 1020
QY      1044 GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACTGATAAAAAACCCAGAGAGTCC 1103
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Db      1021 GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACTGATAAAAAACCCAGAGAGTCC 1080
QY      1104 AAGAGTCAAAGCAAAACTACCGTGCATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1163
      |||||||
Db      1081 AAGAGTCAAAGCAAAACTACCGTGCATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1140
QY      1164 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCCTGCCCCAGCTGGGGAA 1223
      |||||||
Db      1141 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCCTGCCCCAGCTGGGGAA 1200
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QY 1224 ATCAAAAGGGCCAAAGAACCAAAAGAAAGAAAGTCCACCCTGGTTCCTAACTGGAATCAGC 1283
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1201 ATCAAAAGGGCCAAAGAACCAAAAGAAAGAAAGTCCACCCTGGTTCCTAACTGGAATCAGC 1260
QY 1284 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAGATGCCCTTCTCCTTATTGTAAC 1343
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAGATGCCCTTCTCCTTATTGTAAC 1320
QY 1344 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCCTTTCTAGCCTGGCTAT 1403
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1321 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCCTTTCTAGCCTGGCTAT 1380
QY 1404 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTTGCAAAGTGCAAGGACCTAAACATC 1463
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1381 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTTGCAAAGTGCAAGGACCTAAACATC 1440
QY 1464 TCATCAGTATCCAGTGGTAAAGGCGCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC 1523
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1441 TCATCAGTATCCAGTGGTAAAGGCGCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC 1500
QY 1524 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGCAGCTCAGACCCCTTTCTTCA 1583
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1501 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGCAGCTCAGACCCCTTTCTTCA 1560
QY 1584 GCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCGTAAAGCAAA 1643
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1561 GCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCGTAAAGCAAA 1620
QY 1644 AGAATGGCAGAAAGTTTAGCCCTGAAAGCCATGGAGATTCCTATAACTTTGAGACCTAA 1703
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1621 AGAATGGCAGAAAGTTTAGCCCTGAAAGCCATGGAGATTCCTATAACTTTGAGACCTAA 1680
QY 1704 TCTCTGTAAGCTAAATAAAGAAATAGAACCAAGGCTGAGGATACGACAGTACACTGTCA 1763
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1681 TCTCTGTAAGCTAAATAAAGAAATAGAACCAAGGCTGAGGATACGACAGTACACTGTCA 1740
QY 1764 GCAGGGACTGTAACACACACACACTTACTTTTTCTGGTCTCTACCACCTGCTGATATTTCTCT 1823
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1741 GCAGGGACTGTAACACACACACAGGGTCAAAGTGTTTTCTCTGAACACATTTGAGTTGGAAT 1800
QY 1824 CACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACCTGCTGATATTTCTCT 1883
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1801 CACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACCTGCTGATATTTCTCT 1860
QY 1884 AGGAAATATACTTTTACAAGTAACAAATAAAACCTTTATAAATTTCTATTTTATCT 1943
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1861 AGGAAATATACTTTTACAAGTAACAAATAAAACCTTTATAAATTTCTATTTTATCT 1920
QY 1944 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAGTAATAAAA 2003
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAGTAATAAAA 1980
QY 2004 TTCAACAAACATTTTAAAAAAA 2025
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1981 TTCAACAAACATTTGCTGAATA 2002

RESULT 15
US-09-904-859-200
; Sequence 200, Application US/09904859
; Publication No. US20030036060A1
; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,859
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-859-200

Query Match 98.3%; Score 1994; DB 10; Length 2372;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 24 AGCAGGGAAATCCGATGTCTCGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 83
|||
Db 1 AGCAGGGAAATCCGATGTCTCGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60
QY 84 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 143
|||

Db	61	GTTCGAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC	120
Qy	144	CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTTCAGCCCTG	203
Db	121	CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTTCAGCCCTG	180
Qy	204	GTGTTGCTTCTCACTTCCATCTGGACCAAGAGGCTCCTGGTCCAAAGCTCTTTGCGTGCA	263
Db	181	GTGTTGCTTCTCACTTCCATCTGGACCAAGAGGCTCCTGGTCCAAAGCTCTTTGCGTGCA	240
Qy	264	GAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGATCACCTTGTGAGCAAAAAG	323
Db	241	GAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGATCACCTTGTGAGCAAAAAG	300
Qy	324	GCGAACCAAGAGCTGAATTTACAGAAAGCTAAAGGAGGCTGTAGGCTGCTGGACTAAGT	383
Db	301	GCGAACCAAGAGCTGAATTTACAGAAAGCTAAAGGAGGCTGTAGGCTGCTGGACTAAGT	360
Qy	384	TTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAAACCTTGCAGCTAT	443
Db	361	TTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAAACCTTGCAGCTAT	420
Qy	444	GGCTGGTGGAGATGGATTTCGTGGTCATCTCTAGGATTAGCCCCAAACCCCAAGTGTGGG	503
Db	421	GGCTGGTGGAGATGGATTTCGTGGTCATCTCTAGGATTAGCCCCAAACCCCAAGTGTGGG	480
Qy	504	AAAAATGGGTGGGTGTCCTGATTTGGNAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT	563
Db	481	AAAAATGGGTGGGTGTCCTGATTTGGNAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT	540
Qy	564	TGTTACAACTCATCTGATACTTGGACTAACTCGTGCAATCCAGAAATTATCACCACCCAAA	623
Db	541	TGTTACAACTCATCTGATACTTGGACTAACTCGTGCAATCCAGAAATTATCACCACCCAAA	600
Qy	624	GATCCCATATTCAACACTCAAACTGCAACACAAAACAACAGAAATTTATGTCAAGTACAGT	683
Db	601	GATCCCATATTCAACACTCAAACTGCAACACAAAACAACAGAAATTTATGTCAAGTACAGT	660
Qy	684	ACCTACTCGGTGGCATCCCTTACTCTPACAAATACCTGCCCTTACTACTCTCCTCGCT	743
Db	661	ACCTACTCGGTGGCATCCCTTACTCTPACAAATACCTGCCCTTACTACTCTCCTCGCT	720
Qy	744	CCAGCTTCCACTTCTATTCCACGGGAGAAAAAATTGATTTGTGTACAGAAAGTTTTTATG	803
Db	721	CCAGCTTCCACTTCTATTCCACGGGAGAAAAAATTGATTTGTGTACAGAAAGTTTTTATG	780
Qy	804	GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAATAAAGCAGCATTTCAAG	863
Db	781	GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAATAAAGCAGCATTTCAAG	840
Qy	864	AATGAAGCTGCTGGGTTTGGAGGTGTCCTTACTCTGCTGCTGCTGCTGCTGCTGCTGCT	923
Db	841	AATGAAGCTGCTGGGTTTGGAGGTGTCCTTACTCTGCTGCTGCTGCTGCTGCTGCTGCT	900
Qy	924	TTTGGTGTGAGCTGGTCTTGGATTTTGGATTTTGGATTTTGGATTTTGGATTTTGGATTT	983
Db	901	TTTGGTGTGAGCTGGTCTTGGATTTTGGATTTTGGATTTTGGATTTTGGATTTTGGATTT	960
Qy	984	TTTACAAAACAAGAATCAGCAGAAAGGAAATGATCGAAACCAAACTAGTAAAGGAGGAGAAG	1043
Db	961	TTTACAAAACAAGAATCAGCAGAAAGGAAATGATCGAAACCAAACTAGTAAAGGAGGAGAAG	1020
Qy	1044	GCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACTGATAAAAAACCCAGAGAGTCC	1103
Db	1021	GCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACTGATAAAAAACCCAGAGAGTCC	1080
Qy	1104	AAGAGTCCAAGCAAAAACCTACCGTGGATGCTGGAAGCTGAAGTTTAGATGAGACAGAAA	1163
Db	1081	AAGAGTCCAAGCAAAAACCTACCGTGGATGCTGGAAGCTGAAGTTTAGATGAGACAGAAA	1140
Qy	1164	TGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCCTTACCTTGCCTCCAGCTGGGGAA	1223
Db	1141	TGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCCTTACCTTGCCTCCAGCTGGGGAA	1200

Qy	1224	ATCAAAAAGGGCCAAAAGAACCAAAGAGAAAGTCCACCCCTTGGTTCTCTAACTGGAATCAGC	1283
Db	1201	ATCAAAAAGGGCCAAAAGAACCAAAGAGAAAGTCCACCCCTTGGTTCTCTAACTGGAATCAGC	1260
Qy	1284	TCAGGACTGCCATTGGACTATGGAGTGCCACCAAGAGAAATGCCCTTCTCTTATTGTAAC	1343
Db	1261	TCAGGACTGCCATTGGACTATGGAGTGCCACCAAGAGAAATGCCCTTCTCTTATTGTAAC	1320
Qy	1344	CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCCTTCTAGCCTGGCTAT	1403
Db	1321	CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCCTTCTAGCCTGGCTAT	1380
Qy	1404	GTCCTAATAATATCCCACCTGGGAGAAAGGAGTTTGTGCAAAGTGCAAGGACCTAAAAACATC	1463
Db	1381	GTCCTAATAATATCCCACCTGGGAGAAAGGAGTTTGTCAAAGTGCAAGGACCTAAAAACATC	1440
Qy	1464	TCATCAGTATCCAGTGGTAAAGGCTCCTGGCTGTCTGAGGTAGGTGGTTGAAAAGC	1523
Db	1441	TCATCAGTATCCAGTGGTAAAGGCTCCTGGCTGTCTGAGGTAGGTGGTTGAAAAGC	1500
Qy	1524	CAAGGACTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGTCCAGACCCCTTCTTCA	1583
Db	1501	CAAGGACTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGTCCAGACCCCTTCTTCA	1560
Qy	1584	GCTCTGAAAAGAGAAACACGTCATCCACCTGACATGTCTTCTGAGCCCGGTAAGAGCAAA	1643
Db	1561	GCTCTGAAAAGAGAAACACGTCATCCACCTGACATGTCTTCTGAGCCCGGTAAGAGCAAA	1620
Qy	1644	AGAATGGCAGAAAAAGTTTAGCCCTTGAAAAGCCATGGAGATTCTCATAACTTGAGACCTAA	1703
Db	1621	AGAATGGCAGAAAAAGTTTAGCCCTTGAAAAGCCATGGAGATTCTCATAACTTGAGACCTAA	1680
Qy	1704	TCTCTGTAAAGCTAAATAAAGAAATAGAACCAAGGCTGAGGATACGACAGTACACTGTCA	1763
Db	1681	TCTCTGTAAAGCTAAATAAAGAAATAGAACCAAGGCTGAGGATACGACAGTACACTGTCA	1740
Qy	1764	GCAGGACTGTAAACACAGACAGGGTCAAAGTGTCTTCTGAAACACATTGAGTTGGAAT	1823
Db	1741	GCAGGACTGTAAACACAGACAGGGTCAAAGTGTCTTCTGAAACACATTGAGTTGGAAT	1800
Qy	1824	CACGTGTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT	1883
Db	1801	CACGTGTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT	1860
Qy	1884	AGGAAATATACTTTTACAAAGTAAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT	1943
Db	1861	AGGAAATATACTTTTACAAAGTAAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT	1920
Qy	1944	GAGTTACAGAAATGATTACTTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA	2003
Db	1921	GAGTTACAGAAATGATTACTTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA	1980
Qy	2004	TTCAACAAACATTTTAAAAAAA 2025	
Db	1981	TTCAACAAACATTTTGTGAATA 2002	

Search completed: September 15, 2004, 14:11:36
Job time : 973 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 01:53:03 ; Search time 819 Seconds
(without alignments)
10524.535 Million cell updates/sec

Title: US-10-079-111-2
Perfect score: 2029
Sequence: 1 ccttgacaagtcagaagctt.....aaacatttaaaaaaaaaa 2029

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
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9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query		Description	
No.	Score	Match	Length	ID	
1	2029	100.0	2029	3	Aaz98172 Human sig
2	2029	100.0	2029	10	Ade71445 Human cDN
3	2027	99.9	2027	10	Ade71449 Human cDN
4	1994	98.3	2372	2	Aax52250 Protein P
5	1994	98.3	2372	3	Adc78520 Human PRO
6	1994	98.3	2372	4	Aaf72408 Human PRO
7	1994	98.3	2372	4	Aaf92060 Human PRO
8	1994	98.3	2372	6	Abs74380 Human cDN
9	1994	98.3	2372	6	Abl88087 Human PRO
10	1994	98.3	2372	6	Abl95576 Human ang
11	1994	98.3	2372	7	Aca59060 Human PRO
12	1994	98.3	2372	7	Aca58457 cDNA enco
13	1994	98.3	2372	7	Aca60164 Human cDN
14	1994	98.3	2372	7	Acd07564 Novel hum
15	1994	98.3	2372	7	Aca91166 Novel hum
16	1994	98.3	2372	7	Acd81543 Human cDN
17	1994	98.3	2372	7	Aca60365 Novel hum
18	1994	98.3	2372	7	Abx71612 Human cDN
19	1994	98.3	2372	7	Ach06944 Human sec
20	1994	98.3	2372	7	Aca58812 cDNA enco
21	1994	98.3	2372	7	Aca63988 cDNA enco
22	1994	98.3	2372	7	Aca91252 cDNA enco
23	1994	98.3	2372	7	Ac45151 Human sec

24	1994	98.3	2372	7	Abx96181 Human sec
25	1994	98.3	2372	7	ACA05502 cDNA enco
26	1994	98.3	2372	7	ACA93699 Human cDN
27	1994	98.3	2372	7	ACD20169 Human sec
28	1994	98.3	2372	7	ACA67273 cDNA enco
29	1994	98.3	2372	7	ACH66246 Novel hum
30	1994	98.3	2372	7	ACD02300 Novel hum
31	1994	98.3	2372	7	ACA89291 Novel hum
32	1994	98.3	2372	7	ACA68928 Novel hum
33	1994	98.3	2372	7	ACA54972 Novel hum
34	1994	98.3	2372	7	ACA98450 Human PRO
35	1994	98.3	2372	8	ACA63375 cDNA enco
36	1994	98.3	2372	8	ACD19807 Human sec
37	1994	98.3	2372	8	ADB29405 Human sec
38	1994	98.3	2372	8	ADB17062 Human cDN
39	1994	98.3	2372	8	ACH03578 Human sec
40	1994	98.3	2372	8	ADA18261 Human sec
41	1994	98.3	2372	8	ACD66954 Human cDN
42	1994	98.3	2372	8	ADA19867 Novel hum
43	1994	98.3	2372	8	ADB17250 Human cDN
44	1994	98.3	2372	8	ACD83115 Human PRO
45	1994	98.3	2372	8	ADA16236 Human sec

ALIGNMENTS

RESULT 1
AAZ98172

ID AAZ98172 standard; cDNA; 2029 BP.
XX
AC AAZ98172;
XX
DT 11-MAY-2000 (first entry)
XX
DE Human signal peptide containing protein HSP-64 cDNA SEQ ID NO:198.
XX
KW Human; signal peptide-containing protein; HSP; diagnosis; cancer;
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
KW reproductive disorder; developmental disorder; arteriosclerosis;
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW Parkinson's disease; Huntington's diseases; ovulatory defect;
KW muscular dystrophy; ss.
XX
OS Homo sapiens.
XX
PN WO200000610-A2.
XX
PD 06-JAN-2000. -
XX
PF 25-JUN-1999; 99WO-US014484.
XX
PR 26-JUN-1998; 98US-0090762P.
PR 31-JUL-1998; 98US-0094983P.
PR 01-OCT-1998; 98US-0102686P.
PR 11-DEC-1998; 98US-0112129P.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
PI Akerbloom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX
DR WPI; 2000-160673/14.
DR P-PSDB; AAY87287.
XX
PT New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
PT disease.
XX

PS Claim 9; Page 288-289; 327pp; English.

XX AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the

CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have

CC anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,

CC neuroprotective, cardiovascular and antiasthmatic activities, and can be

CC used in gene therapy. HSPPs can be used to treat or prevent disorders

CC associated with decreased activity or function of HSPP. Antagonists of

CC HSPP are used to treat or prevent disorders associated with increased

CC activity or function of HSPP. Such diseases include cell proliferation

CC (including cancer), inflammation, cardiovascular, neurological,

CC reproductive or developmental disorders, (e.g. arteriosclerosis,

CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,

CC asthma, Crohn's disease, microbial or other infections, congestive or

CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's

CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP

CC nucleic acids can be used for the recombinant production of HSPP, for

CC detecting HSPP in standard hybridisation and amplification assays (for

CC diagnosis and monitoring), in gene therapy, as antisense, triplex-forming

CC or ribozyme therapeutics, for detecting related sequences or genetic

CC variations, and for chromosomal mapping. HSPP are also used to raise

CC specific antibodies (Ab) and to screen for agonists and antagonists

CC (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP

CC -related diseases (in usual immunoassays), as therapeutic antagonists, in

CC competitive drug screens, and for purification of HSPP from natural

CC sources

XX

SQ Sequence 209 BP; 612 A; 463 C; 445 G; 509 T; 0 U; 0 Other;

Query Match 100.0%; Score 2029; DB 3; Length 2029;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2029; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTGACAAGTCAGAAGCTTGAAAGCAGGGGAAATCCGGATGTCGCGTTATGAAGTGGAG 60

Db |||||

QY 61 CAGTGAGTGTGAGCCTCAACATAGTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCAT 120

Db |||||

QY 61 CAGTGAGTGTGAGCCTCAACATAGTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCAT 120

QY 121 CTGCCCTCATATACACCAGTGGCCATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCA 180

Db |||||

QY 121 CTGCCCTCATATACACCAGTGGCCATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCA 180

QY 181 CGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCCAGGCTCC 240

Db |||||

QY 181 CGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCCAGGCTCC 240

QY 241 TGGTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGCATGCAGAATTATGG 300

Db |||||

QY 241 TGGTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGCATGCAGAATTATGG 300

QY 301 GGATCACCCCTTGTGAGCAAAAAGSGGAAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGG 360

Db |||||

QY 301 GGATCACCCCTTGTGAGCAAAAAGSGGAAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGG 360

QY 361 CCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAG 420

Db |||||

QY 361 CCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAG 420

QY 421 CTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATGGATTCGTTCTAGGA 480

Db |||||

QY 421 CTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTTCTAGGA 480

QY 481 TTAGCCAAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCCTGATTTGGAAGGTTCCAG 540

Db |||||

QY 481 TTAGCCAAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCCTGATTTGGAAGGTTCCAG 540

QY 541 TGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATCTGGACTAAGCTCGTGCA 600

Db |||||

QY 541 TGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATCTGGACTAAGCTCGTGCA 600

QY 601 TTCCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAAACTGCAACACAAACAA 660

Db |||||

QY 601 TTCCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCAAACTGCAACACAAACAA 660

QY 661 CAGAAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTG 720

Db |||||

QY 661 CAGAAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTG 720

QY 721 CCCCTACTACTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780

Db |||||

QY 721 CCCCTACTACTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780

QY 781 TTTGTGTACAGAAAGTTTTTATGGAACTAGCACCATGTCTACAGAACTGAACCATTTG 840

Db |||||

QY 781 TTTGTGTACAGAAAGTTTTTATGGAACTAGCACCATGTCTACAGAACTGAACCATTTG 840

QY 841 TTGAAAAATAAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGGAGTGTCCCCACGGCTC 900

Db |||||

QY 841 TTGAAAAATAAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGGAGTGTCCCCACGGCTC 900

QY 901 TGCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 960

Db |||||

QY 901 TGCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 960

QY 961 AAAGGTATGTGAAGGCCTTCCCCTTTTACAAACAAGAAATCAGCAGAAAGAAATGATCGAAA 1020

Db |||||

QY 961 AAAGGTATGTGAAGGCCTTCCCCTTTTACAAACAAGAAATCAGCAGAAAGAAATGATCGAAA 1020

QY 1021 CCAAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCTTAATGAGGAATCAAAGAAA 1080

Db |||||

QY 1021 CCAAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCTTAATGAGGAATCAAAGAAA 1080

QY 1081 CTGATAAAAAACCCAGAGAGTCCAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCTGGAAG 1140

Db |||||

QY 1081 CTGATAAAAAACCCAGAGAGTCCAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCTGGAAG 1140

QY 1141 CTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTC 1200

Db |||||

QY 1141 CTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTC 1200

QY 1201 CTTACCCCTGCCCCAGCTGGGGAATCAAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACC 1260

Db |||||

QY 1201 CTTACCCCTGCCCCAGCTGGGGAATCAAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACC 1260

QY 1261 CTTGGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTTGGAGTGCACCAAAGAG 1320

Db |||||

QY 1261 CTTGGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTTGGAGTGCACCAAAGAG 1320

QY 1321 AATGCCCTTCTCCTTATTGTAAACCTGTCTGGATCCTATCCTCTACCTCCAAGCTTCC 1380

Db |||||

QY 1321 AATGCCCTTCTCCTTATTGTAAACCTGTCTGGATCCTATCCTCTACCTCCAAGCTTCC 1380

QY 1381 CACGGCCTTTCTAGCCTGGTATGTCTTAATAATATCCACTGGGAGAAAGGAGTTTTCG 1440

Db |||||

QY 1381 CACGGCCTTTCTAGCCTGGTATGTCTTAATAATATCCACTGGGAGAAAGGAGTTTTCG 1440

QY 1441 AAAGTGCAAGGACCTAAAACATCTCATCAGTATCCAGTGTGTAATAAAGGCTTCTCTACTGAT 1500

Db |||||

QY 1441 AAAGTGCAAGGACCTAAAACATCTCATCAGTATCCAGTGTGTAATAAAGGCTTCTCTACTGAT 1500

QY 1501 CTGAGGCTAGGTGGGTGAAAGCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGAT 1560

Db |||||

QY 1501 CTGAGGCTAGGTGGGTGAAAGCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGAT 1560

QY 1561 CCGAGCTCAGACCCCTTTCTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTC 1620

Db |||||

QY 1561 CCGAGCTCAGACCCCTTTCTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTC 1620

QY 1621 CTTCTGAGCCCGGTAAAGAGCAAAAGAAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCATGGA 1680

Db |||||

QY 1621 CTTCTGAGCCCGGTAAAGAGCAAAAGAAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCATGGA 1680

QY 1681 GATTCTCATAACTTGAGACCTAAATCTCTGTAAAGCTAAAAATAAGAAATAGAACAAAGGCT 1740

Db 1681 GATTCTCATAACTTGAGACCCTAATCTCTGTAAAGCTAAATAAAGAAATAGAACAGGCT 1740
QY 1741 GAGGATACGACAGTACACTGTGACGAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTT 1800
Db 1741 GAGGATACGACAGTACACTGTGACGAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTT 1800
QY 1801 CTCTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACACTTACTTTTTCTGGTCT 1860
Db 1801 CTCTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACACTTACTTTTTCTGGTCT 1860
QY 1861 CTACCACTGCTGATATTTTCTCTAGGAAATATACTTTTACAAGTAAACAAAAATAAAAACT 1920
Db 1861 CTACCACTGCTGATATTTTCTCTAGGAAATATACTTTTACAAGTAAACAAAAATAAAAACT 1920
QY 1921 CTTATAAATTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGT 1980
Db 1921 CTTATAAATTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGT 1980
QY 1981 AATTGTGTTAAAAAGTAATAAAAAATTCACAAACATTTAAAAA 2029
Db 1981 AATTGTGTTAAAAAGTAATAAAAAATTCACAAACATTTAAAAA 2029

RESULT 2
ADE71445
ID ADE71445 standard; cDNA; 2029 BP.
XX
AC ADE71445;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human cDNA encoding PDEBC Incyte 3044710CB1.
XX
KW breast cancer; PDEBC; metastatic; human; ss; gene.
XX
OS Homo sapiens.

XX Key Location/Qualifiers
FH 183. .1151
FT /*tag= a
FT /product= "PDEBC"
XX
PN US2003124543-A1.
XX
PD 03-JUL-2003.
XX
PF 20-FEB-2002; 2002US-00079111.
XX
PR 15-JAN-1999; 99US-00232160.
XX (STUA/) STUART S G.
PA (STRE/) STREETER D G.
XX
PI Stuart SG, Streeter DG;
XX
DR WPI; 2004-009141/01.
XX P-PSDB; ADE71444.
PT A new cDNA encoding a protein differentially expressed in breast cancer
PT designated PCEBC is useful to stage, treat, and monitor progression or
PT treatment of breast cancer, particularly an invasive, metastatic stage of
PT the disease.
XX
PS Claim 2; SEQ ID NO 2; 31pp; English.
XX
CC The invention relates to an isolated cDNA encoding a protein that is
CC differentially expressed in breast cancer, designated PDEBC. The
CC invention is useful to diagnose breast cancer. The invention is also
CC useful to stage, treat, and monitor progression or treatment of breast
CC cancer, particularly an invasive, metastatic stage of the disease. The
CC present sequence represents cDNA encoding human PDEBC Incyte 3044710CB1.
CC Note: There are two sequences that have been assigned SEQ ID 2 in the

CC specification, the present sequence represents the sequence given in the
CC sequence listing.
XX
SQ Sequence 2029 BP; 612 A; 463 C; 445 G; 509 T; 0 U; 0 Other;
Query Match 100.0%; Score 2029; DB 10; Length 2029;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2029; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTTGACAAAGTCAGAAGCTTGAAAAGCAGGGAAATCCGGATGTCTCGTTATGAAGTGAG 60
Db 1 CCTTGACAAAGTCAGAAGCTTGAAAAGCAGGGAAATCCGGATGTCTCGTTATGAAGTGAG 60
QY 61 CAGTGAGTGTGAGCCCTCAACATAGTTCAGAACTCTCCATCCGACTAGTTATTGAGCAT 120
Db 61 CAGTGAGTGTGAGCCCTCAACATAGTTCAGAACTCTCCATCCGACTAGTTATTGAGCAT 120
QY 121 CTGCCTCTCATATCACCACTGGCCATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCA 180
Db 121 CTGCCTCTCATATCACCACTGGCCATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCA 180
QY 181 CGATGGCCAGGTGCTTCAGCCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCC 240
Db 181 CGATGGCCAGGTGCTTCAGCCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCC 240
QY 241 TGGTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGG 300
Db 241 TGGTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGG 300
QY 301 GGATCACCCCTTGAGCAAAAAGCGGAAACCCAGCAGCTGAATTTTCACAGAAGCTAAGGAGG 360
Db 301 GGATCACCCCTTGAGCAAAAAGCGGAAACCCAGCAGCTGAATTTTCACAGAAGCTAAGGAGG 360
QY 361 CCTGTAGGCTGCTGGACTAAGTTTGGCCGGAAGACCAAGTTGAAACAGCCTTGAAAG 420
Db 361 CCTGTAGGCTGCTGGACTAAGTTTGGCCGGAAGACCAAGTTGAAACAGCCTTGAAAG 420
QY 421 CTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGGTCACTCTTAGGA 480
Db 421 CTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGGTCACTCTTAGGA 480
QY 481 TTAGCCCAAACCCCAAAGTGTGGGAAAAATGGGTGGGTGTCCTGATTTGGAAGGTTCCAG 540
Db 481 TTAGCCCAAACCCCAAAGTGTGGGAAAAATGGGTGGGTGTCCTGATTTGGAAGGTTCCAG 540
QY 541 TGAGCCGACAGTTGCAGCCTATTGTTTACAACTCATCTGATACTTGGACTAACTCGTGCA 600
Db 541 TGAGCCGACAGTTGCAGCCTATTGTTTACAACTCATCTGATACTTGGACTAACTCGTGCA 600
QY 601 TTCCAGAAATTATCACCACCAAAGATCCCATATTTCAACACTCAAACCTGCAACACAAACAA 660
Db 601 TTCCAGAAATTATCACCACCAAAGATCCCATATTTCAACACTCAAACCTGCAACACAAACAA 660
QY 661 CAGAAATTTATTGTCACTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTG 720
Db 661 CAGAAATTTATTGTCACTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTG 720
QY 721 CCCCTACTACTCTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGA 780
Db 721 CCCCTACTACTCTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGA 780
QY 781 TTTGTGTCAACAGAAGTTTTTATGGAACTAGCACCATGTCTACAGAAACTGAACCATTTG 840
Db 781 TTTGTGTCAACAGAAGTTTTTATGGAACTAGCACCATGTCTACAGAAACTGAACCATTTG 840
QY 841 TTGAAAAATAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTC 900
Db 841 TTGAAAAATAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTC 900
QY 901 TGCTAGTGTGCTCTCCTCTTCTTTTGGTGCTGAGCTGGTCTTGGATTTTGCTATGTCA 960
Db 901 TGCTAGTGTGCTCTCCTCTTCTTTTGGTGCTGAGCTGGTCTTGGATTTTGCTATGTCA 960

QY 961 AAAGGTATGTGAAGGCCTTCCCTTTTACAAAACAAGAAATCAGCAGAGGAAATGATCGAAA 1020
|||
Db 961 AAAGGTATGTGAAGGCCTTCCCTTTTACAAAACAAGAAATCAGCAGAGGAAATGATCGAAA 1020
|||
QY 1021 CCAAAGTAGTAAAGGAGGAGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAA 1080
|||
Db 1021 CCAAAGTAGTAAAGGAGGAGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAA 1080
|||
QY 1081 CTGATAAAAACCCAGAAAGAGTCCAAGAGTCCAAGCAAAAACCTACCGTGCATGCCTGGAAG 1140
|||
Db 1081 CTGATAAAAACCCAGAAAGAGTCCAAGAGTCCAAGCAAAAACCTACCGTGCATGCCTGGAAG 1140
|||
QY 1141 CTGAAGTTTAGATGAGACAGAAAATGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTC 1200
|||
Db 1141 CTGAAGTTTAGATGAGACAGAAAATGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTC 1200
|||
QY 1201 CTTACCCCTGCCAGCTGGGGAATCAAAAAGGCCAAAGAACCAAGAAAGAAAGTCCACC 1260
|||
Db 1201 CTTACCCCTGCCAGCTGGGGAATCAAAAAGGCCAAAGAACCAAGAAAGAAAGTCCACC 1260
|||
QY 1261 CTTGGTTCCTAACTGGAATCAGCTCAGCACTGCCATTTGGACTATGGAGTGCACCAAGAG 1320
|||
Db 1261 CTTGGTTCCTAACTGGAATCAGCTCAGCACTGCCATTTGGACTATGGAGTGCACCAAGAG 1320
|||
QY 1321 AATGCCCTTCTCCTTATTGTAACCTGTCTCGATCCTATCCTCCTACCTCCAAAGCTTCC 1380
|||
Db 1321 AATGCCCTTCTCCTTATTGTAACCTGTCTCGATCCTATCCTCCTACCTCCAAAGCTTCC 1380
|||
QY 1381 CACGGCCTTTCTAGCCTGGCTATGTCCTTAATAATATCCCACTGGGAGAAAGGAGTTTTC 1440
|||
Db 1381 CACGGCCTTTCTAGCCTGGCTATGTCCTTAATAATATCCCACTGGGAGAAAGGAGTTTTC 1440
|||
QY 1441 AAAGTGCAAGGACCTAAACAATCTCATCAGTATCCAGTGGTAAAAAGCCCTCCTGGCTGT 1500
|||
Db 1441 AAAGTGCAAGGACCTAAACAATCTCATCAGTATCCAGTGGTAAAAAGCCCTCCTGGCTGT 1500
|||
QY 1501 CTGAGGCTAGTGGTTGAAAGCCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATT 1560
|||
Db 1501 CTGAGGCTAGTGGTTGAAAGCCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATT 1560
|||
QY 1561 CCGCAGCTCAGACCCCTTCTTCAGCTCTGAAAGAGAAAACACGTATCCCACCTGACATGTC 1620
|||
Db 1561 CCGCAGCTCAGACCCCTTCTTCAGCTCTGAAAGAGAAAACACGTATCCCACCTGACATGTC 1620
|||
QY 1621 CTTCTGAGCCCGGTAAGAGCAAAAGAAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGA 1680
|||
Db 1621 CTTCTGAGCCCGGTAAGAGCAAAAGAAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGA 1680
|||
QY 1681 GATTCTCATAACTTGAGACCTAATCTCTGTAAAGCTAAAAATAAGAAATAGAAACAAGGCT 1740
|||
Db 1681 GATTCTCATAACTTGAGACCTAATCTCTGTAAAGCTAAAAATAAGAAATAGAAACAAGGCT 1740
|||
QY 1741 GAGGATACGACAGTACACTGTGACGAGGACTGTAAACACAGACAGGCTCAAAGTGTTTT 1800
|||
Db 1741 GAGGATACGACAGTACACTGTGACGAGGACTGTAAACACAGACAGGCTCAAAGTGTTTT 1800
|||
QY 1801 CTCTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACACTTACTTTTCTGGTCT 1860
|||
Db 1801 CTCTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACACTTACTTTTCTGGTCT 1860
|||
QY 1861 CTACCACCTGCTGATATTTTCTCTAGGAAATATACTTTTACAAGTAACAAAAATAAAAACT 1920
|||
Db 1861 CTACCACCTGCTGATATTTTCTCTAGGAAATATACTTTTACAAGTAACAAAAATAAAAACT 1920
|||
QY 1921 CTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGT 1980
|||
Db 1921 CTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGT 1980
|||
QY 1981 AATTGTGTTTAAAAAGTAATAAAAATTCACAAACATTTAAAAAAAATAAAAA 2029
|||
Db 1981 AATTGTGTTTAAAAAGTAATAAAAATTCACAAACATTTAAAAAAAATAAAAA 2029
|||

RESULT 3
ADE71449
ID ADE71449 standard; cDNA; 2027 BP.
XX
AC ADE71449;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human cDNA encoding PDEBC #2.
XX
KW breast cancer; PDEBC; metastatic; human; ss; gene.
XX
OS Homo sapiens.
XX
PN US2003124543-A1.
XX
PD 03-JUL-2003.
XX
PF 20-FEB-2002; 2002US-00079111.
XX
PR 15-JAN-1999; 99US-00232160.
XX
PA (STUA/) STUART S G.
PA (STRE/) STREETER D G.
XX
PI Stuart SG, Streeter DG;
XX
DR WPI; 2004-009141/01.
DR P-PSDB; ADE71444.
XX
PT A new cDNA encoding a protein differentially expressed in breast cancer designated PCEBC is useful to stage, treat, and monitor progression or treatment of breast cancer, particularly an invasive, metastatic stage of the disease.
PS Claim 2; Fig 1; 3lpp; English.
XX
CC The invention relates to an isolated cDNA encoding a protein that is differentially expressed in breast cancer, designated PDEBC. The invention is useful to diagnose breast cancer. The invention is also useful to stage, treat, and monitor progression or treatment of breast cancer, particularly an invasive, metastatic stage of the disease. The present sequence represents cDNA encoding human PDEBC Incyte 3044710CB1.
CC Note: There are two sequences that have been assigned SEQ ID 2 in the specification, the present sequence represents the sequence given in figure 1.
XX
SQ Sequence 2027 BP; 612 A; 461 C; 445 G; 509 T; 0 U; 0 Other;

Query Match 99.9%; Score 2027; DB 10; Length 2027;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTGACAAGTCAGAAAGCTTGAAAGCAGGAAATCCGGATGTCTCGTTATGAAGTGGAGCA 62
|||
Db 1 TTGACAAGTCAGAAAGCTTGAAAGCAGGAAATCCGGATGTCTCGTTATGAAGTGGAGCA 60
|||
QY 63 GTGAGTGTGAGCCTCAACATAGTTCAGAACTCTCCATCCGACTAGTTATTGAGCATCT 122
|||
Db 61 GTGAGTGTGAGCCTCAACATAGTTCAGAACTCTCCATCCGACTAGTTATTGAGCATCT 120
|||
QY 123 GCCTCTCATATCACCAAGTGGCCATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACG 182
|||
Db 121 GCCTCTCATATCACCAAGTGGCCATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACG 180
|||
QY 183 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 242
|||
Db 181 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 240
|||
QY 243 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCTATGCAGAATTATGGGG 302
|||
Db 241 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCTATGCAGAATTATGGGG 300
|||

QY 303 ATCACCTTGTAGCAAAAAGGGAACCAAGCTGAATTTACAGAAAGCTAAAGGAGCC 362
Db |||||
301 ATCACCTTGTAGCAAAAAGGGAACCAAGCTGAATTTACAGAAAGCTAAAGGAGCC 360
QY 363 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 422
Db |||||
361 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 420
QY 423 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTGCTGGTCACTCTAGGATT 482
Db |||||
421 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTGCTGGTCACTCTAGGATT 480
QY 483 AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTGATTTGGAAAGTTCAGTG 542
Db |||||
481 AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTGATTTGGAAAGTTCAGTG 540
QY 543 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCAAT 602
Db |||||
541 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCAAT 600
QY 603 CCAGAAATTATCACCAACCAAGATCCCATATTTCAACACTCAAACCTGCAACACAAACA 662
Db |||||
601 CCAGAAATTATCACCAACCAAGATCCCATATTTCAACACTCAAACCTGCAACACAAACA 660
QY 663 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAACTACCTGCC 722
Db |||||
661 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAACTACCTGCC 720
QY 723 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 782
Db |||||
721 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 780
QY 783 TGTGTACAGAAAGTTTTATGGAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 842
Db |||||
781 TGTGTACAGAAAGTTTTATGGAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 840
QY 843 GAAATAAAGCAGCAATCAAGAAATGAAGCTGCTGGGTTGGAGGTGTCCTCCACGGCTCTG 902
Db |||||
841 GAAATAAAGCAGCAATCAAGAAATGAAGCTGCTGGGTTGGAGGTGTCCTCCACGGCTCTG 900
QY 903 CTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGAATTTTGTATGTCAA 962
Db |||||
901 CTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGAATTTTGTATGTCAA 960
QY 963 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAATGATCGAAACC 1022
Db |||||
961 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAATGATCGAAACC 1020
QY 1023 AAAGTAGTAAAGGAGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT 1082
Db |||||
1021 AAAGTAGTAAAGGAGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT 1080
QY 1083 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAAACCTACCGTGCATGCTGGAAGCT 1142
Db |||||
1081 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAAACCTACCGTGCATGCTGGAAGCT 1140
QY 1143 GAAGTTTAGATGACACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCT 1202
Db |||||
1141 GAAGTTTAGATGACACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCT 1200
QY 1203 TACCCTGCCCCAGCTGGGGAAATCAAAGGGCCAAAGAACCAAGAGAAAGTCCACCCCT 1262
Db |||||
1201 TACCCTGCCCCAGCTGGGGAAATCAAAGGGCCAAAGAACCAAGAGAAAGTCCACCCCT 1260
QY 1263 TGGTTCCTAACTGGAAATCAGCTCAGGACTGCCATTGGAACTATGGAGTGCACCAAGAGAA 1322
Db |||||
1261 TGGTTCCTAACTGGAAATCAGCTCAGGACTGCCATTGGAACTATGGAGTGCACCAAGAGAA 1320
QY 1323 TGCCCTTCTCCTTAATGTAAACCTGTCTGGATCCTATCCTACCTCCAAGCTTCCCA 1382
Db |||||
1321 TGCCCTTCTCCTTAATGTAAACCTGTCTGGATCCTATCCTACCTCCAAGCTTCCCA 1380
QY 1383 CGGCCTTTCTAGCCTGGCTATGTCTCTAATAATATCCCACTGGGAGAAAGGAGTTTGCAA 1442

Db |||||
1381 CGGCCTTTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTGCAA 1440
QY 1443 AGTGCAAGGACCTAAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCT 1502
Db |||||
1441 AGTGCAAGGACCTAAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCT 1500
QY 1503 GAGGCTAGGTGGGTTGAAAGCCAAAGGAGTCACTGAGACCAGGCTTTCTCTACTGATTCC 1562
Db |||||
1501 GAGGCTAGGTGGGTTGAAAGCCAAAGGAGTCACTGAGACCAGGCTTTCTCTACTGATTCC 1560
QY 1563 GCAGCTCAGACCCCTTTCTTCAGCTCTGAAAGAGAAACACGATATCCCACCTGACATGTCT 1622
Db |||||
1561 GCAGCTCAGACCCCTTTCTTCAGCTCTGAAAGAGAAACACGATATCCCACCTGACATGTCT 1620
QY 1623 TCTGAGCCCGGTAAGAGACAAAGAATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGGAGA 1682
Db |||||
1621 TCTGAGCCCGGTAAGAGACAAAGAATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGGAGA 1680
QY 1683 TTCTCATAACTTGAGACCTAATCTCTGTAAGCTAAAAATAAGAAATAAGAAACAGGCTGA 1742
Db |||||
1681 TTCTCATAACTTGAGACCTAATCTCTGTAAGCTAAAAATAAGAAATAAGAAACAGGCTGA 1740
QY 1743 GGATACGACAGTACACTGTGAGCAGGACTGTAAAAACACAGACAGGTCAAAAGTGTCTTCT 1802
Db |||||
1741 GGATACGACAGTACACTGTGAGCAGGACTGTAAACACAGACAGGTCAAAAGTGTCTTCT 1800
QY 1803 CTGAACACATTTGAGTTGGAATCACTGTTTAGAACACACACACTTACTTTTCTGGTCTCT 1862
Db |||||
1801 CTGAACACATTTGAGTTGGAATCACTGTTTAGAACACACACACTTACTTTTCTGGTCTCT 1860
QY 1863 ACCACTGCTGATATTTTCTCTAGGAAATATACTTTTACAAGTAACAAAAATAAAACTCT 1922
Db |||||
1861 ACCACTGCTGATATTTTCTCTAGGAAATATACTTTTACAAGTAACAAAAATAAAACTCT 1920
QY 1923 TATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAGATTACTCAGTAA 1982
Db |||||
1921 TATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAGATTACTCAGTAA 1980
QY 1983 TTTGTTTAAAAAGTAATAAAAATTCAACAACATTTAAAAAANAAAA 2029
Db |||||
1981 TTTGTTTAAAAAGTAATAAAAATTCAACAACATTTAAAAAANAAAA 2027

RESULT 4

AAx52250

ID AAX52250 standard; DNA; 2372 BP.

XX

AC AAX52250;

XX

DT 25-JUN-1999 (first entry) --

XX

DE Protein PRO263 cDNA clone DNA34431-1171.

XX

KW Secreted protein; transmembrane protein; human; enterocolitis;

KW Zollinger-Ellison syndrome; gastrointestinal ulceration;

KW congenital microvillus atrophy; skin disease; cell growth;

KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;

KW parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;

KW dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;

KW wound healing; tissue repair; ss.

XX

OS Homo sapiens.

XX

PN WO9914328-A2.

XX

PD 25-MAR-1999 --

XX

PF 16-SEP-1998; 98WO-US019330.

XX

PR 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059115P.

PR 17-SEP-1997; 97US-0059117P.

PR 17-SEP-1997; 97US-00591119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.

(GETH) GENENTECH INC.

Wood WI, Gurney AL, Goddard A, Pennica D, Chen J, Yuan J;

WPI; 1999-229533/19.
P-PSDB; AAY13379.

New isolated human genes and polypeptides used in, e.g. treatment of
gastrointestinal ulceration.

Claim 2; Fig 73; 320pp; English.

AAX52213-74 encode secreted and transmembrane human proteins, and are
obtained from cDNA libraries, prepared from fetal lung, fetal kidney,
fetal brain, fetal liver and fetal retina. The encoded polypeptides have
specific uses based on their homology to known polypeptides, e.g. PRO211
and PRO217 can be used for disorders associated with the preservation and
maintenance of gastrointestinal mucosa and the repair of acute and
chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome,
gastrointestinal ulceration and congenital microvillus atrophy), skin
diseases associated with abnormal keratinocyte differentiation (e.g.
psoriasis, epithelial cancers such as lung squamous cell carcinoma of the
vulva and gliomas), potent effects on cell growth and development,
diseases related to growth or survival of nerve cells including
Parkinson's disease, Alzheimer's disease, ALS, neuropathies or cancer.

CC PRO265 can be used as for fibromodulin, e.g. for reducing dermal
CC scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may
CC be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can
CC be used as an anti-thrombotic agent; PRO287 polypeptides and portions may
CC have therapeutic applications in wound healing and tissue repair; PRO317
CC can be used for treating problems of the kidney, uterus, endometrium,
CC blood vessels, or related tissue, e.g. in the heart of genital tract
XX

SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Query Match 98.3%; Score 1994; DB 2; Length 2372;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 24 AGCAGGGAAATCCGGATGTCGCGTTATGAAGTGGAGCAGTGAGTGTGAGCCCTCAACATA 83
Db |||||
1 AGCAGGGAAATCCGGATGTCGCGTTATGAAGTGGAGCAGTGAGTGTGAGCCCTCAACATA 60
QY 84 GTTCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 143
Db |||||
61 GTTCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
QY 144 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 203
Db |||||
121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180
QY 204 GTGTGCTTCTCATTCCATCTGGACCCAGAGGCTCCTGGTCCAAGGCTCTTTGGGTGCA 263
Db |||||
181 GTGTGCTTCTCATTCCATCTGGACCCAGAGGCTCCTGGTCCAAGGCTCTTTGGGTGCA 240
QY 264 GAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGATCACCCCTTGTGAGCAAAAAG 323
Db |||||
241 GAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGATCACCCCTTGTGAGCAAAAAG 300
QY 324 GCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCTGTAGGCTGTGGGACTAAGT 383
Db |||||
301 GCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCTGTAGGCTGTGGGACTAAGT 360
QY 384 TTGGCCGGCAAGGACCAAGTTGAAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 443
Db |||||
361 TTGGCCGGCAAGGACCAAGTTGAAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420
QY 444 GGCTGGGTTGGAGATGGATTGCTGGTTCATCTCTAGGATTAGCCCCAACCCCAAGTGTGG 503
Db |||||
421 GGCTGGGTTGGAGATGGATTGCTGGTTCATCTCTAGGATTAGCCCCAACCCCAAGTGTGG 480
QY 504 AAAAAATGGGGTGGGTGTCCTGATTGGAAGTTCCAGTGAGCCGACAGTTTGCGAGCCTAT 563
Db |||||
481 AAAAAATGGGGTGGGTGTCCTGATTGGAAGTTCCAGTGAGCCGACAGTTTGCGAGCCTAT 540
QY 564 TGTTACAACTCATCTGATCTGACTGGAATACTCGTGCATTCAGAAATATCACCACCAA 623
Db |||||
541 TGTTACAACTCATCTGATCTGACTGGAATACTCGTGCATTCAGAAATATCACCACCAA 600
QY 624 GATCCCATATTTCAACACTCAAACTGCAACACAAACACAGAAATTTATTGTGAGTGACAGT 683
Db |||||
601 GATCCCATATTTCAACACTCAAACTGCAACACAAACACAGAAATTTATTGTGAGTGACAGT 660
QY 684 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTCTCCTCTGCT 743
Db |||||
661 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTCTCCTCTGCT 720
QY 744 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTTGTTGTTCACAGAAAGTTTATG 803
Db |||||
721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTTGTTGTTCACAGAAAGTTTATG 780
QY 804 GAAACTAGCACCATTCTACAGAAACTGAACCATTTTGTGAAATAAAGCAGCATTTCAAG 863
Db |||||
781 GAAACTAGCACCATTCTACAGAAACTGAACCATTTTGTGAAATAAAGCAGCATTTCAAG 840
QY 864 AATGAAGCTGTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGTGCTCTCCTCTTC 923
Db |||||
841 AATGAAGCTGTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGTGCTCTCCTCTTC 900

QY	924	TTTGGTGTGCAGCTGGTCTTGGAATTTTGCTATGTCAAAGGTATGTGAAGGCCTTCCCT	983
Db	901	TTTTGGTGTGCAGCTGGTCTTGGAATTTTGCTATGTCAAAGGTATGTGAAGGCCTTCCCT	960
QY	984	TTTACAAACAAGAAATCAGCAAGAGAAATGATCGAAACCAAGTAGTAAAGGAGAGAA	1043
Db	961	TTTACAAACAAGAAATCAGCAAGAGAAATGATCGAAACCAAGTAGTAAAGGAGAGAA	1020
QY	1044	GCCAATGATAGCAACCCCTAATGAGGAATCAAGAAACTGATAAAAAACCCAGAGACTCC	1103
Db	1021	GCCAATGATAGCAACCCCTAATGAGGAATCAAGAAACTGATAAAAAACCCAGAGACTCC	1080
QY	1104	AAGAGTCCAAGCAAAACTACCGTCGATGCCCTGGAAGCTGAAAGTTTAGATGAGACAGAA	1163
Db	1081	AAGAGTCCAAGCAAAACTACCGTCGATGCCCTGGAAGCTGAAAGTTTAGATGAGACAGAA	1140
QY	1164	TGAGGAGACACACCTGAGCTGGTTCTTTCATGTCTCTTACCCCTGCCCCAGCTGGGAA	1223
Db	1141	TGAGGAGACACACCTGAGCTGGTTCTTTCATGTCTCTTACCCCTGCCCCAGCTGGGAA	1200
QY	1224	ATCAAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACCTTGGTTCCTAAGCTGGAATCAGC	1283
Db	1201	ATCAAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACCTTGGTTCCTAAGCTGGAATCAGC	1260
QY	1284	TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAATGCCCTTCTCCTTATTGTAAC	1343
Db	1261	TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAATGCCCTTCTCCTTATTGTAAC	1320
QY	1344	CCTGTCTGGATCCTATCCTCCTACCTCCTCAAAAGCTTCCACGGCCTTTCTAGCCCTGGCTAT	1403
Db	1321	CCTGTCTGGATCCTATCCTCCTACCTCCTCAAAAGCTTCCACGGCCTTTCTAGCCCTGGCTAT	1380
QY	1404	GTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAAAGTGCAGGACCTTAAACATC	1463
Db	1381	GTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAAAGTGCAGGACCTTAAACATC	1440
QY	1464	TCATCAGTATCCAGTGGTAAAAAAGGCCTCCTGGCTGTCTGAGGCTAGTGGGTGAAAGC	1523
Db	1441	TCATCAGTATCCAGTGGTAAAAAAGGCCTCCTGGCTGTCTGAGGCTAGTGGGTGAAAGC	1500
QY	1524	CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA	1583
Db	1501	CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA	1560
QY	1584	GCTCTGAAAGAGAAACAGTATCCACCTGACATGCTCTGAGCCCGTAAAGAGCAAA	1643
Db	1561	GCTCTGAAAGAGAAACAGTATCCACCTGACATGCTCTGAGCCCGTAAAGAGCAAA	1620
QY	1644	AGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA	1703
Db	1621	AGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA	1680
QY	1704	TCTCTGTAAGCTAAAATAAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTCA	1763
Db	1681	TCTCTGTAAGCTAAAATAAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTCA	1740
QY	1764	GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTCTCTGAAACACATTGAGTTGGAAT	1823
Db	1741	GCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTCTCTGAAACACATTGAGTTGGAAT	1800
QY	1824	CAGTGTTTAGAACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT	1883
Db	1801	CAGTGTTTAGAACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT	1860
QY	1884	AGGAAATATACTTTTACAAGTAACAAAAATAAAACTCTTATAAATTTCTATTTTATCT	1943
Db	1861	AGGAAATATACTTTTACAAGTAACAAAAATAAAACTCTTATAAATTTCTATTTTATCT	1920
QY	1944	GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTTAAAGTAATAAAA	2003
Db	1921	GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTTAAAGTAATAAAA	1980

QY	2004	TTCAACAAACATTTTAAAAAAA	2025
Db	1981	TTCAACAAACATTTGCTGAATA	2002
RESULT 5			
ADC78520			
ID	ADC78520	standard; cDNA; 2372 BP.	
XX	ADC78520;		
AC	AC		
XX	XX		
DT	01-JAN-2004	(first entry)	
XX	Human PRO263	cDNA.	
DE	DE		
XX	XX		
KW	KW	antiinflammatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;	
KW	KW	nootropic; neuroprotective; vasotropic; chemotaxic; angiogenic;	
KW	KW	neurotrophic; osteopathic; antiasthmatic; antiarthritic; antirheumatic;	
KW	KW	antiarteriosclerotic; cardiac; antidiabetic; cerebroprotective;	
KW	KW	thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;	
KW	KW	gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;	
KW	KW	Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;	
KW	KW	nerve repair; thrombosis; bone; cartilage formation; angiogenesis;	
KW	KW	asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;	
KW	KW	atherosclerosis; cardiac injury; infertility; premature aging; AIDS;	
KW	KW	diabetes; stroke; gene therapy; transgenic; PRO; human; ss; gene.	
XX	XX		
OS	OS	Homo sapiens.	
XX	XX		
PN	PN	WO200015796-A2.	
XX	XX		
PD	PD	23-MAR-2000.	
XX	XX		
PF	PF	15-SEP-1999; 99WO-US021090.	
XX	XX		
PR	PR	16-SEP-1998; 98WO-US019330.	
XX	XX		
PA	PA	(GETH) GENENTECH INC.	
XX	XX		
PI	PI	Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;	
PI	PI	Yuan J;	
XX	XX		
DR	DR	WPI; 2000-271434/23.	
DR	DR	P-PSDB; ADC78521.	
XX	XX		
PT	PT	Novel nucleic acids encoding secreted and transmembrane polypeptides with	
PT	PT	homology, e.g. to growth and cancer-associated antigens.	
XX	XX		
PS	PS	Claim 2; SEQ ID NO 200; 355pp; English.	
XX	XX		
CC	CC	The invention relates to a novel nucleic acid encoding a PRO polypeptide.	
CC	CC	The polypeptides and polynucleotides of the invention may be useful as	
CC	CC	research tools and as therapeutics for treating enterocolitis, Zollinger-	
CC	CC	Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,	
CC	CC	Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal	
CC	CC	scarring and wound healing, nerve repair, thrombosis, bone and/or	
CC	CC	cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple	
CC	CC	sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,	
CC	CC	infertility, premature aging, AIDS, diabetes complications and stroke.	
CC	CC	The molecules may also be utilised during gene therapy procedures and	
CC	CC	transgenic animal production. The current sequence is that of the human	
CC	CC	PRO cDNA of the invention.	
XX	XX		
SQ	SQ	Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;	

Query Match 98.3%; Score 1994; DB 3; Length 2372;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY	24	AGCAGGGAATCCGGATGTCTCGTTATGAAGTGAGCAGTGAGTGTGAGCCTCAACATA	83
Db	1	AGCAGGGAATCCGGATGTCTCGTTATGAAGTGAGCAGTGAGTGTGAGCCTCAACATA	60

QY 84 GTTCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 143
Db 61 GTTCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
QY 144 CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 203
Db 121 CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180
QY 204 GTGTTGCTTCTCACTTCCATCTGGACACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 263
Db 181 GTGTTGCTTCTCACTTCCATCTGGACACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240
QY 264 GAAGAGCTTCCATCCAGGTGTCATGCAGAAATTATGGGATCACCCCTTGTGAGCAAAAAG 323
Db 241 GAAGAGCTTCCATCCAGGTGTCATGCAGAAATTATGGGATCACCCCTTGTGAGCAAAAAG 300
QY 324 GCGAACAGCAGCTGAATTTACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGT 383
Db 301 GCGAACAGCAGCTGAATTTACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGT 360
QY 384 TTGGCCGCAAGGACCAAGTTGAAACAGACCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 443
Db 361 TTGGCCGCAAGGACCAAGTTGAAACAGACCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420
QY 444 GGCTGGGTGGAGATGGATTTCGTGGTTCATCTCTAGGATTAGCCCCAAACCCCAAGTGTGG 503
Db 421 GGCTGGGTGGAGATGGATTTCGTGGTTCATCTCTAGGATTAGCCCCAAACCCCAAGTGTGG 480
QY 504 AAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 563
Db 481 AAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540
QY 564 TGTTAAACTCATCTGATACTTGGACTPAACTCGTGCAATTCAGAAATTATCACCACCAA 623
Db 541 TGTTAAACTCATCTGATACTTGGACTPAACTCGTGCAATTCAGAAATTATCACCACCAA 600
QY 624 GATCCCATATTCAACACTCAAACCTGCAACACAAACAACAGAAATTATTGTGAGTACAGT 683
Db 601 GATCCCATATTCAACACTCAAACCTGCAACACAAACAACAGAAATTATTGTGAGTACAGT 660
QY 684 ACCTACTCGGTGGCATCCCTTTACTCTACAATACCTGCCCCCTACTACTCCTCCTGCT 743
Db 661 ACCTACTCGGTGGCATCCCTTTACTCTACAATACCTGCCCCCTACTACTCCTCCTGCT 720
QY 744 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAAGTTTTTATG 803
Db 721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAAGTTTTTATG 780
QY 804 GAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAATAAAGCAGCATTTCAAG 863
Db 781 GAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAATAAAGCAGCATTTCAAG 840
QY 864 AATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTGCTAGTGCTCTCCTCTTC 923
Db 841 AATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTGCTAGTGCTCTCCTCTTC 900
QY 924 TTTGTTGCTGCAGCTGGTCTTTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCCTTCCCT 983
Db 901 TTTGTTGCTGCAGCTGGTCTTTGGATTTTGCTATGTCAAAGGTATGTGAAGGCCTTCCCT 960
QY 984 TTTTACAAACAAGAAATCAGCAGAAAGGAAATGATCGAAACCAAAAGTAGTAAAGGAGAG 1043
Db 961 TTTTACAAACAAGAAATCAGCAGAAAGGAAATGATCGAAACCAAAAGTAGTAAAGGAGAG 1020
QY 1044 GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACTGATAAAAAACCCAGAAGTCC 1103
Db 1021 GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACTGATAAAAAACCCAGAAGTCC 1080
QY 1104 AAGAGTCCAAGCAAAAACCTACCGTGCATGCCTGGAAAGCTGAAGTTTAGATGAGACAGAA 1163
Db 1081 AAGAGTCCAAGCAAAAACCTACCGTGCATGCCTGGAAAGCTGAAGTTTAGATGAGACAGAA 1140
QY 1164 TGAGGAGACACCTGAGGCTGGTTTCTTTCATGCTCCTTACCTGCCCCCAGCTGGGGA 1223

Db 1141 TGAGGAGACACACCTGAGGCTGGTTCTTTTCATGTCCTTACCTGCCCCAGCTGGGAA 1200
QY 1224 ATCAAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACCCTTGTTCTTAACTGGAATCAGC 1283
Db 1201 ATCAAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACCCTTGTTCTTAACTGGAATCAGC 1260
QY 1284 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1343
Db 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1320
QY 1344 CCTGTCTGGATCCTATCCTCCTACCTCCAAGCTTCCCACGGCCTTCTAGCCTGGCTAT 1403
Db 1321 CCTGTCTGGATCCTATCCTCCTACCTCCAAGCTTCCCACGGCCTTCTAGCCTGGCTAT 1380
QY 1404 GTCCTAAATAATATCCCACTGGGAGAAAGGAGTTTGTGCAAGTGCAGGACCTTAAACATC 1463
Db 1381 GTCCTAAATAATATCCCACTGGGAGAAAGGAGTTTGTGCAAGTGCAGGACCTTAAACATC 1440
QY 1464 TCATCAGTATCCAGTGGTAAAGGCCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC 1523
Db 1441 TCATCAGTATCCAGTGGTAAAGGCCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC 1500
QY 1524 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGGAGCTCAGACCCCTTCTTTCA 1583
Db 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGGCAGCTCAGACCCCTTCTTTCA 1560
QY 1584 GCTCTGAAAGAGAAAACACGTATCCACACCTGACATGTCTCTGAGCCCCGGTAAGAGCAA 1643
Db 1561 GCTCTGAAAGAGAAAACACGTATCCACACCTGACATGTCTCTGAGCCCCGGTAAGAGCAA 1620
QY 1644 AGAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1703
Db 1621 AGAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680
QY 1704 TCTCTGTAAGCTAAAATAAAGAAATAGAACCAAGGCTGAGGATACGACAGTACACTGTCA 1763
Db 1681 TCTCTGTAAGCTAAAATAAAGAAATAGAACCAAGGCTGAGGATACGACAGTACACTGTCA 1740
QY 1764 GCAGGACTGTAAACACACAGACAGGTCAAAAGTGTCTCTGAAACACATTGAGTTGGAAT 1823
Db 1741 GCAGGACTGTAAACACACAGACAGGTCAAAAGTGTCTCTGAAACACATTGAGTTGGAAT 1800
QY 1824 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1883
Db 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1860
QY 1884 AGGAATATACTTTTACAAGTAAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1943
Db 1861 AGGAATATACTTTTACAAGTAAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1920
QY 1944 GAGTTACAGAAATGATTACTTAAGGAAGATTACTCAGTAATTTGTTAAAAAGTAATAAA 2003
Db 1921 GAGTTACAGAAATGATTACTTAAGGAAGATTACTCAGTAATTTGTTAAAAAGTAATAAA 1980
QY 2004 TTCAACAAACATTTTAAAAAAA 2025
Db 1981 TTCAACAAACATTTGCTGAATA 2002

RESULT 6

AAF72408

ID AAF72408 standard; cdna; 2372 bp.

XX

AC AAF72408;

XX

DT 24-APR-2001 (first entry)

XX

DE Human PRO263 cdna.

XX

KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;

antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;

antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;

QY 1224 ATCAAAAGGGCCAAAGAACCAAGAAGAAAGTCCACCCTTGGTTCCTAACTGGAATCAGC 1283
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1201 ATCAAAAGGGCCAAAGAACCAAGAAGAAAGTCCACCCTTGGTTCCTAACTGGAATCAGC 1260
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1284 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAATGCCCTTCTCCTTATTGTTAAC 1343
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAATGCCCTTCTCCTTATTGTTAAC 1320
QY 1344 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCTTTCTAGCCTGGCTAT 1403
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1321 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCTTTCTAGCCTGGCTAT 1380
QY 1404 GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAAAGTGCAAGGACCTAAAAACATC 1463
Db GTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAAAGTGCAAGGACCTAAAAACATC 1440
QY 1464 TCATCAGTATCCAGTGGTAAAGGCTCCTCGGTGTCTGAGGCTAGGTGGTTGAAAGC 1523
Db TCATCAGTATCCAGTGGTAAAGGCTCCTCGGTGTCTGAGGCTAGGTGGTTGAAAGC 1500
QY 1524 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1583
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560
QY 1584 GCTCTGAAAGAGAAACACGATATCCCACTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA 1643
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1561 GCTCTGAAAGAGAAACACGATATCCCACTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA 1620
QY 1644 AGAATGGCAGAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1703
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1621 AGAATGGCAGAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680
QY 1704 TCTCTGTAAGCTAAAAATAAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA 1763
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1681 TCTCTGTAAGCTAAAAATAAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA 1740
QY 1764 GCAGGAGCTGTAAACACAGACAGGGTCAAAAGTGTCTTCTGAAACACATTGAGTTGGAAT 1823
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1741 GCAGGAGCTGTAAACACAGACAGGGTCAAAAGTGTCTTCTGAAACACATTGAGTTGGAAT 1800
QY 1824 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1883
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1860
QY 1884 AGGAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1943
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1861 AGGAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1920
QY 1944 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAA 2003
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2004 TTCAACAAACATTTAAAAAAA 2025
Db |||||||||||||||||||||
QY 1981 TTCAACAAACATTTGCTGAATA 2002

RESULT 7
AAF92060
ID AAF92060 standard; cDNA; 2372 BP.
XX
AC AAF92060;

15-MAY-2001 (first entry)

Human PRO263 cDNA.

Human; PRO protein; mapping; ss.

Homo sapiens.

XX WO200116318-A2.

XX

PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US023328.
XX
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 07-DEC-1999; 99US-0169495P.
PR 09-DEC-1999; 99US-0170262P.
PR 11-JAN-2000; 2000US-0175481P.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 03-MAR-2000; 2000US-0187202P.
PR 21-MAR-2000; 2000US-0191007P.
PR 30-MAR-2000; 2000WO-US008439.
PR 25-APR-2000; 2000US-0199397P.
PR 22-MAY-2000; 2000WO-US014042.
PR 05-JUN-2000; 2000US-0209832P.
XX
(GETH) GENENTECH INC.
PA
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX WPI; 2001-183260/18.
DR P-PSDB; AAB87528.
XX
PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT biology, including use as hybridization probes, and in chromosome and
PT gene mapping.
XX
PS Claim 2; Fig 5; 278pp; English.
XX
CC The present sequence is the coding sequence for a human PRO polypeptide
CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
CC antagonists or anti-PRO antibodies are useful for preparation of a
CC medicament useful in the treatment of a condition which is responsive to
CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
CC protein may also be employed as molecular weight markers for protein
CC electrophoresis. The PRO coding sequence has applications in molecular
CC biology, including use as hybridisation probes, and in chromosome and
CC gene mapping
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Query Match 98.3%; Score 1994; DB 4; Length 2372;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 24 AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTAGCCCTCAACATA 83
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 84 GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 143
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
QY 144 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 203
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180
QY 204 GTGTTGCTTCTCACTTCCATCTCGACACGAGGCTCCTGTGCCAAGGCTCTTTGCGTGCA 263
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 181 GTGTTGCTTCTCACTTCCATCTCGACACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240
QY 264 GAAGAGCTTTCCATCCAGGTGTCTATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAG 323
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 241 GAAGAGCTTTCCATCCAGGTGTCTATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAG 300
QY 324 GCGAACCCAGCAGCTGAATTTTCAGAAAGCTAAGGAGGCCCTGTAGGCTGCTGGGACTAAGT 383
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 301 GCGAACCCAGCAGCTGAATTTTCAGAAAGCTAAGGAGGCCCTGTAGGCTGCTGGGACTAAGT 360

PR	10-JUN-1998;	98US-0088740P;
PR	10-JUN-1998;	98US-0088811P;
PR	10-JUN-1998;	98US-0088824P;
PR	10-JUN-1998;	98US-0088825P;
PR	11-JUN-1998;	98US-0088863P;
PR	12-JUN-1998;	98US-0089105P;
PR	16-JUN-1998;	98US-0089514P;
PR	17-JUN-1998;	98US-0089653P;
PR	19-JUN-1998;	98US-0089952P;
PR	22-JUN-1998;	98US-0090246P;
PR	24-JUN-1998;	98US-0090444P;
PR	25-JUN-1998;	98US-0090688P;
PR	25-JUN-1998;	98US-0090686P;
PR	26-JUN-1998;	98US-0090862P;
PR	02-JUL-1998;	98US-0091628P;
PR	10-AUG-1998;	98US-0096012P;
PR	17-AUG-1998;	98US-0096757P;
PR	18-AUG-1998;	98US-0096949P;
PR	18-AUG-1998;	98US-0096959P;
PR	26-AUG-1998;	98US-0097954P;
PR	26-AUG-1998;	98US-0097971P;
PR	26-AUG-1998;	98US-0097979P;
PR	01-SEP-1998;	98US-0098749P;
PR	10-SEP-1998;	98US-0099741P;
PR	10-SEP-1998;	98US-0099763P;
PR	10-SEP-1998;	98US-0099792P;
PR	10-SEP-1998;	98US-0099812P;
PR	10-SEP-1998;	98US-0099815P;
PR	16-SEP-1998;	98US-0100627P;
PR	16-SEP-1998;	98US-0100662P;
PR	16-SEP-1998;	98WO-US019330;
PR	17-SEP-1998;	98US-0100683P;
PR	17-SEP-1998;	98US-0100684P;
PR	17-SEP-1998;	98US-0100930P;
PR	22-SEP-1998;	98US-0101279P;
PR	23-SEP-1998;	98US-0101475P;
PR	24-SEP-1998;	98US-0101738P;
PR	24-SEP-1998;	98US-0101743P;
PR	24-SEP-1998;	98US-0101916P;
PR	30-SEP-1998;	98US-0102570P;
PR	06-OCT-1998;	98US-0103449P;
PR	08-MAR-1999;	99WO-US005028;
PR	14-MAY-1999;	99WO-US010733;
PR	02-JUN-1999;	99WO-US012252;
PR	01-SEP-1999;	99WO-US020111;
PR	15-SEP-1999;	99WO-US021090;
PR	15-SEP-1999;	99WO-US021194;
PR	22-DEC-1999;	99WO-US030720;
PR	18-FEB-2000;	2000WO-US004341;
PR	18-FEB-2000;	2000WO-US004342;
PR	22-FEB-2000;	2000WO-US004414;
PR	01-MAR-2000;	2000WO-US005601;
PR	30-MAR-2000;	2000WO-US008439;
PR	22-MAY-2000;	2000WO-US014042;
PR	02-JUN-2000;	2000WO-US015264;
PR	23-AUG-2000;	2000WO-US023522;
PR	24-AUG-2000;	2000WO-US023328;
PR	10-NOV-2000;	2000WO-US030873;
PR	01-DEC-2000;	2000WO-US032378;
PR	20-DEC-2000;	2000WO-US034956;
PR	28-FEB-2001;	2001WO-US006520;
PR	01-MAR-2001;	2001WO-US006666;
PR	30-MAY-2001;	2001WO-US017443;
PR	01-JUN-2001;	2001WO-US017800;
PR	20-JUN-2001;	2001WO-US019692;
PR	29-JUN-2001;	2001WO-US021066;
PR	09-JUL-2001;	2001WO-US021735;
XX		
PA	(GETH) GENENTECH INC.	

WPI; 2002-731348/79.
P-PSDB; ABG95853.

New isolated secreted and transmembrane PRO polypeptide useful for modulating biological activity of a cell, or for treating sports-related joint problems, osteoarthritis or rheumatoid arthritis.

Claim 2; Fig 5; 399pp; English.

The invention relates to an isolated secreted and transmembrane PRO polypeptide having 80 % sequence identity to a sequence appearing as ABG95851-ABG95934 or their associated signal peptide, or a sequence of an extracellular domain of the proteins with their associated signal peptide or lacking its associated signal peptide. Also included are the nucleic acids encoding the proteins, vectors, host cells, fusion proteins and antibodies which specifically bind to the proteins. The proteins are useful for detecting a polypeptide designated as A, B, C or D in a sample suspected of containing an A, B, C or D polypeptide, by contacting the sample with a polypeptide designated as E, F, G, H or I (or vice versa) and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide conjugate in the sample, where the formation of the conjugate is indicative of the presence of an A, B, C or D polypeptide in the sample, where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with a detectable label or is attached to a solid support. The proteins are useful for linking a bioactive molecule to a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive molecule is a toxin, a radiolabel or an antibody. The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies against them are useful for modulating a biological activity of a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H, or I. The cell is killed. The proteins are useful for identifying agonists or antagonists, for the preparation of a medicament useful in the treatment of a condition which is responsive to the proteins, as molecular weight markers for protein electrophoresis purposes, and as therapeutic agents for treating sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis. Nucleic acids encoding the proteins are useful as hybridisation probes, in chromosome and gene mapping, in the generation of anti-sense RNA and DNA, for the preparation of the proteins, to generate transgenic or knockout animals which are useful in the development and screening of therapeutic useful reagents, for chromosome identification, and in gene therapy. The antibody is useful as a therapeutic agent, in a diagnostic assay and for affinity purification of the protein from recombinant cell culture natural sources. The present sequence encodes a novel secreted or transmembrane protein of the invention

PF 20-JUN-2001; 2001WO-US019692.
XX 23-JUN-2000; 2000US-0213637P.
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000US-0222695P.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-090516/12.
DR P-PSDB; ABB84832.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 2; Fig 31; 565pp; English.
XX
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC antiangiogenic, hypotensive, vulnery and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The PRO polynucleotides have applications in molecular biology,
CC including use as hybridisation probes, and in chromosome and gene
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC exemplification of the present invention
xx
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Query Match 98.3%; Score 1994; DB 6; Length 2372;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY	24	AGCAGGGAATCCGGATGTC	CGGTATGAAGTGAGCAGTGAGCCTCAACATA	83
Db	1	AGCAGGGAATCCGGATGTC	CGGTATGAAGTGAGCAGTGAGCCTCAACATA	60
QY	84	GTTCAGAACTCTCCATCCG	ACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC	143
Db	61	GTTCAGAACTCTCCATCCG	ACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC	120
QY	144	CATCTGAGGTGTTTCCCT	TGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG	203
Db	121	CATCTGAGGTGTTTCCCT	TGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG	180
QY	204	GTGTTGCTTCTCACTTCC	ATCTGGACCAAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA	263
Db	181	GTGTTGCTTCTCACTTCC	ATCTGGACCAAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA	240
QY	264	GAAGAGCTTTCATCCAG	GTGTCAGAAATTATGGGGATCACCTTGTGAGCAAAAAG	323
Db	241	GAAGAGCTTTCATCCAG	GTGTCAGAAATTATGGGGATCACCTTGTGAGCAAAAAG	300
QY	324	GCGAACCAAGCTGAATTT	CACAGAAGCTAAGGAGGCCTGTAGGTGCTGGGACTAAGT	383
Db	301	GCGAACCAAGCTGAATTT	CACAGAAGCTAAGGAGGCCTGTAGGTGCTGGGACTAAGT	360
QY	384	TTGGCCGCAAGGACCAAG	TTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT	443
Db	361	TTGGCCGCAAGGACCAAG	TTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT	420
QY	444	GGCTGGGTTGGAGATGG	ATTCGTGTCATCTCTAGGATTAGCCCAAAACCCCAAGTGGG	503
Db	421	GGCTGGGTTGGAGATGG	ATTCGTGTCATCTCTAGGATTAGCCCAAAACCCCAAGTGGG	480
QY	504	AAAAATGGGGTGGGTGTC	CTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT	563
Db	481	AAAAATGGGGTGGGTGTC	CTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT	540
QY	564	TGTTACAACTCATCTGAT	ACTTGGACTAACTCGTGATTCAGAAATTATCACCACCAA	623
Db	541	TGTTACAACTCATCTGAT	ACTTGGACTAACTCGTGATTCAGAAATTATCACCACCAA	600
QY	624	GATCCATATTTCAACACT	CAAACTGCAACACAAACAGAAATTTATGTGAGTGACAGT	683
Db	601	GATCCATATTTCAACACT	CAAACTGCAACACAAACAGAAATTTATGTGAGTGACAGT	660
QY	684	ACCTACTCGGTGGCATCC	CCCTTACTCTACAATACCTGCCCTACTACTCTCCTGCT	743
Db	661	ACCTACTCGGTGGCATCC	CCCTTACTCTACAATACCTGCCCTACTACTCTCCTGCT	720
QY	744	CCAGCTTCCACTTCTATT	CCACGGAGAAAAAATTGATTTGTGCACAGAAATTTTATG	803
Db	721	CCAGCTTCCACTTCTATT	CCACGGAGAAAAAATTGATTTGTGCACAGAAATTTTATG	780
QY	804	GAACCTAGCACCATTGTC	TACAGAACTGAACCATTTGTTGAAAAATAAGCAGCATTTCAAG	863
Db	781	GAACCTAGCACCATTGTC	TACAGAACTGAACCATTTGTTGAAAAATAAGCAGCATTTCAAG	840
QY	864	AATGAAGCTGCTGGGTTT	GGAGGTGTCCTCCACGGCTCTGCTAGTGCTTCTCCTCTTC	923
Db	841	AATGAAGCTGCTGGGTTT	GGAGGTGTCCTCCACGGCTCTGCTAGTGCTTCTCCTCTTC	900
QY	924	TTTGGTGCTGCAGTGGT	CTTGGATTTGCTATGTCAAAAGGTATGTGAAGGCCTTCCCT	983
Db	901	TTTGGTGCTGCAGTGGT	CTTGGATTTGCTATGTCAAAAGGTATGTGAAGGCCTTCCCT	960
QY	984	TTTACAAAACAAGAATC	AGCAGAGGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAAG	1043
Db	961	TTTACAAAACAAGAATC	AGCAGAGGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAAG	1020
QY	1044	GCCATGATAGCAACCTT	ATAGGAATCAAAGAAAACTGATAAAAAACCCAGAGAGTCC	1103
Db	1021	GCCATGATAGCAACCTT	ATAGGAATCAAAGAAAACTGATAAAAAACCCAGAGAGTCC	1080

QY 1104 AAGAGTCCAAAGCAAAACTACCGTGCATGCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1163
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1081 AAGAGTCCAAAGCAAAACTACCGTGCATGCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1140
QY 1164 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCCTGCCCCAGCTGGGGAA 1223
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1141 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCCTGCCCCAGCTGGGGAA 1200
QY 1224 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCCTTGTTCTCTAACTGGAATCAGC 1283
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1201 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCCTTGTTCTCTAACTGGAATCAGC 1260
QY 1284 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1343
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1320
QY 1344 CCTGCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCTTCTAGCCTGGCTAT 1403
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1321 CCTGCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCTTCTAGCCTGGCTAT 1380
QY 1404 GTCCTAATAATATCCCACCTGGAGAGAAAGGAGTTTGTCAAAGTGCAGGACCTTAAACATC 1463
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1381 GTCCTAATAATATCCCACCTGGAGAGAAAGGAGTTTGTCAAAGTGCAGGACCTTAAACATC 1440
QY 1464 TCATCAGTATCCAGTGGTAAAGAGCCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC 1523
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1441 TCATCAGTATCCAGTGGTAAAGAGCCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGC 1500
QY 1524 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1583
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560
QY 1584 GCTCTGAAAGAGAAACACGTATCCCACTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA 1643
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1561 GCTCTGAAAGAGAAACACGTATCCCACTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA 1620
QY 1644 AGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTATAACTTGAGACCTAA 1703
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1621 AGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTATAACTTGAGACCTAA 1680
QY 1704 TCTCTGTAAGCTAAATAAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTCA 1763
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1681 TCTCTGTAAGCTAAATAAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTCA 1740
QY 1764 GCAGGACTGTAAACACACAGAGGTCAAAGTGTCTCTGAAACACATTGAGTTGGAAT 1823
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1741 GCAGGACTGTAAACACACAGAGGTCAAAGTGTCTCTGAAACACATTGAGTTGGAAT 1800
QY 1824 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACCTGCTGATATTTCTCT 1883
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACCTGCTGATATTTCTCT 1860
QY 1884 AGGAAATATACTTTTACAGTAACAAAAATAAAACTCTTATAAATTTCTATTTTATCT 1943
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1861 AGGAAATATACTTTTACAGTAACAAAAATAAAACTCTTATAAATTTCTATTTTATCT 1920
QY 1944 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 2003
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980
QY 2004 TTCAACAAACATTTAAAAAAA 2025
Db ||||||||||||||| |||
1981 TTCAACAAACATTTGCTGAATA 2002

RESULT 10
ABL95576
ID ABL95576 standard; cDNA; 2372 BP.
XX
AC ABL95576;
XX
DT 19-JUL-2002 (first entry)
XX

DE Human angiogenesis related cDNA PRO263 SEQ ID NO: 31.
XX
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
KW antiarteriosclerotic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US021735.
XX
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
XX
(GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-171999/22.

QY 1884 AGGAATATACCTTTTACAAGTAACAAAAATAAAAACTCTTATAAAATTTCTATTTTATCT 1943
|||||
Db 1861 AGGAATATACCTTTTACAAGTAACAAAAATAAAAACTCTTATAAAATTTCTATTTTATCT 1920
QY 1944 GAGTTACAGAAATGATTACTTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 2003
|||||
Db 1921 GAGTTACAGAAATGATTACTTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980
QY 2004 TTCAACAAACATTTAAAAAAA 2025
|||||
Db 1981 TTCAACAAACATTTGCTGAATA 2002

RESULT 11
ACA59060
ID ACA59060 standard; cDNA; 2372 BP.
XX
AC ACA59060;
XX
DT 16-JUN-2003 (first entry)
XX
DE Human PRO polynucleotide #36.
XX
KW Human; PRO; gene; ss; secreted polypeptide; transmembrane polypeptide;
KW pathological disorder; cardiac insufficiency disorder; protein secretion;
KW pancreas; diabetes; gastrointestinal mucosa; mucosal lesion; psoriasis;
KW skin disease; keratinocyte differentiation; epithelial cancer; tumour;
KW lung squamous cell carcinoma; epidermoid carcinoma; vulva; glioma;
KW cytosstatic; cardiant; endocrine; antidiabetic; gastrointestinal;
KW antiulcer; dermatological; vulnery.
XX
OS Homo sapiens.
XX
PN US2002146709-A1.
XX
PD 10-OCT-2002.
XX
PF 18-JUL-2001; 2001US-00909088.
XX
PR 17-SEP-1997; 97US-00591113P.
PR 17-SEP-1997; 97US-00591115P.
PR 17-SEP-1997; 97US-00591117P.
PR 17-SEP-1997; 97US-00591119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.

PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-328338/31.
DR P-PSDB; ABU71625.
XX
PT Isolated nucleic acid useful for e.g., treating pathological disorders
XX encodes a secreted or transmembrane protein.
PS Claim 2; Fig 73; 473pp; English.
XX
CC The invention relates to human PRO polypeptides (secreted or
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC PRO polypeptides and polynucleotides can be used in treating pathological
CC disorders and tumours, in therapeutic treatment of cardiac insufficiency
CC disorders and in therapeutic treatment of disorders involving protein
CC secretion by the pancreas, including diabetes. They can also be used in
CC treating disorders associated with the preservation and maintenance of
CC gastrointestinal mucosa and the repair of acute and chronic mucosal
CC lesions, and skin diseases associated with abnormal keratinocyte
CC differentiation (e.g., psoriasis, epithelial cancers such as lung

CC squamous cell carcinoma, epidermoid carcinoma of the vulva and gliomas).
CC The sequences can be used as molecular markers for protein
CC electrophoresis purposes and can be utilised in protein-protein binding
CC assays, biochemical screening assays, immunoassays and cell-based assays.
CC This sequence represents a human PRO polynucleotide of the invention
xx
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Query Match 98.3%; Score 1994; DB 7; Length 2372;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 24 AGCAGGAAATCCGGATGTTCTCGGTTATGAAGTGGAGCAGTGAAGTGTGAGCCTCAACATA 83
Db 1 AGCAGGAAATCCGGATGTTCTCGGTTATGAAGTGGAGCAGTGAAGTGTGAGCCTCAACATA 60

QY 84 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 143
Db 61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120

QY 144 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCAGGTGCTTTCAGCCTG 203
Db 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCAGGTGCTTTCAGCCTG 180

QY 204 GTGTTGCTTCTCACTTCCATCTGGACCAAGGCTCCTGGTCCAAAGCTCTTTGCGTGCA 263
Db 181 GTGTTGCTTCTCACTTCCATCTGGACCAAGGCTCCTGGTCCAAAGCTCTTTGCGTGCA 240

QY 264 GAAGAGCTTTCATCCAGGTGTATGCAGAAATTATGGGATCACCTTGTGAGCAAAAAG 323
Db 241 GAAGAGCTTTCATCCAGGTGTATGCAGAAATTATGGGATCACCTTGTGAGCAAAAAG 300

QY 324 GCGAACCAAGCAGCTGAATTTACAGAAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGT 383
Db 301 GCGAACCAAGCAGCTGAATTTACAGAAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGT 360

QY 384 TTGGCCGCAAGGACCAAGTTGAAACAGGCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 443
Db 361 TTGGCCGCAAGGACCAAGTTGAAACAGGCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420

QY 444 GGCTGGGTTGGAGATGGATTTCGTGGTCACTCTAGGATTAGCCCCAAACCCCAAGTGTGG 503
Db 421 GGCTGGGTTGGAGATGGATTTCGTGGTCACTCTAGGATTAGCCCCAAACCCCAAGTGTGG 480

QY 504 AAAATGGGTGGGTGTCCTGATTTTGGNAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 563
Db 481 AAAATGGGTGGGTGTCCTGATTTTGGNAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540

QY 564 TGTTACAACTCATCTGATACTTGGACTAACTCGTGCATTTCCAGAAATTATCACCACCAA 623
Db 541 TGTTACAACTCATCTGATACTTGGACTAACTCGTGCATTTCCAGAAATTATCACCACCAA 600

QY 624 GATCCCATATTCAACTCAAACTGCAACACAAAACAAACAGAAATTATGTGAGTGCAGT 683
Db 601 GATCCCATATTCAACTCAAACTGCAACACAAAACAAACAGAAATTATGTGAGTGCAGT 660

QY 684 ACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCCCTACTACTACTCCTCTGCT 743
Db 661 ACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCCCTACTACTACTCCTCTGCT 720

QY 744 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAAGTTTATTG 803
Db 721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAAGTTTATTG 780

QY 804 GAAACTAGCAACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCATTCAG 863
Db 781 GAAACTAGCAACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCATTCAG 840

QY 864 AATGAAGCTGCTGGGTTGGAGGTGTCCCACGGCTCTGCTAGTGTGCTCTCCTCTTC 923
Db 841 AATGAAGCTGCTGGGTTGGAGGTGTCCCACGGCTCTGCTAGTGTGCTCTCCTCTTC 900

QY 924 TTTGGTGTGCAGCTGGTCTTGGATTTTGGTATGTCAAAGGTATGTGAAGGCCTTCCCT 983

Db 901 TTTGGTGTGCAGCTGGTCTTGGATTTTGGTATGTCAAAAGGTATGTGAAGCCTTCCCT 960

QY 984 TTTACAAAACAAGAAATCAGCAGAAGAAATGATCGAAACCAGAAAGTAGTAAGGAGGAGAAG 1043
Db 961 TTTACAAAACAAGAAATCAGCAGAAGAAATGATCGAAACCAGAAAGTAGTAAGGAGGAGAAG 1020

QY 1044 GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACTGATAAAAAACCAGAAAGAGTCC 1103
Db 1021 GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACTGATAAAAAACCAGAAAGAGTCC 1080

QY 1104 AAGAGTCCAAAGCAAAACTACCGTGCATGCCCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1163
Db 1081 AAGAGTCCAAAGCAAAACTACCGTGCATGCCCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1140

QY 1164 TGAGGAGACACACCTGAGGCTGTTTCTTTCATGCTCCTTACCTGCCCCAGCTGGGGAA 1223
Db 1141 TGAGGAGACACACCTGAGGCTGTTTCTTTCATGCTCCTTACCTGCCCCAGCTGGGGAA 1200

QY 1224 ATCAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACCCCTTGGTTCTTAACCTGGAATCAGC 1283
Db 1201 ATCAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACCCCTTGGTTCTTAACCTGGAATCAGC 1260

QY 1284 TCAGGACTGCCATTGGACTATGAGGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1343
Db 1261 TCAGGACTGCCATTGGACTATGAGGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1320

QY 1344 CCTGTCTGGATCCTATCCTCCTACCTCAAAGCTTCCCACGGCCTTCTAGCCTGGCTAT 1403
Db 1321 CCTGTCTGGATCCTATCCTCCTACCTCAAAGCTTCCCACGGCCTTCTAGCCTGGCTAT 1380

QY 1404 GTCCTAATAATATCCCACCTGGGAGAAAGGAGTTTGTCAAAGTGCAAGGACCTAAAAACATC 1463
Db 1381 GTCCTAATAATATCCCACCTGGGAGAAAGGAGTTTGTCAAAGTGCAAGGACCTAAAAACATC 1440

QY 1464 TCATCAGTATCCAGTGGTAAAGGSCCTCCTGGTGTCTGAGGCTAGGTGGTTGAAAGC 1523
Db 1441 TCATCAGTATCCAGTGGTAAAGGSCCTCCTGGTGTCTGAGGCTAGGTGGTTGAAAGC 1500

QY 1524 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCCGCAGCTCAGACCCCTTCTTCA 1583
Db 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCCGCAGCTCAGACCCCTTCTTCA 1560

QY 1584 GCTCTGAAAGAGAAACACGTATCCACCTGACATGTCTTCTGAGCCCGGTAAGAGCAAA 1643
Db 1561 GCTCTGAAAGAGAAACACGTATCCACCTGACATGTCTTCTGAGCCCGGTAAGAGCAAA 1620

QY 1644 AGAATGGCAGAAAAAGTTTAGCCCTTGAAAAGCCATGGAGATTCTCAFAACTTGAGACCTAA 1703
Db 1621 AGAATGGCAGAAAAAGTTTAGCCCTTGAAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680

QY 1704 TCTCTGTAAGCTAAAATAAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA 1763
Db 1681 TCTCTGTAAGCTAAAATAAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA 1740

QY 1764 GCAGGGACTGTAAACACAGACAGGGTCAAAAGTGTTTTCTCTGAACACATTTGAGTTGGAAT 1823
Db 1741 GCAGGGACTGTAAACACAGACAGGGTCAAAAGTGTTTTCTCTGAACACATTTGAGTTGGAAT 1800

QY 1824 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1883
Db 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1860

QY 1884 AGGAAATATACTTTTACAAGTAAACAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1943
Db 1861 AGGAAATATACTTTTACAAGTAAACAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1920

QY 1944 GAGTTACAGAAATGATTACTAAGGAGATTACTCAGTAATTTGTTAAAAAGTAATAAAA 2003
Db 1921 GAGTTACAGAAATGATTACTAAGGAGATTACTCAGTAATTTGTTAAAAAGTAATAAAA 1980

QY 2004 TTCAACAAACATTTAAAAAAA 2025
|||||

Db 1981 TTCAACAACATTTGCTGAATA 2002

RESULT 12

ACA58457

ID ACA58457 standard; cDNA; 2372 BP.

XX

AC ACA58457;

XX

DT 10-JUN-2003 (first entry)

XX

DE cDNA encoding human PRO polypeptide #36.

XX

KW Human; secreted and transmembrane protein; PRO polypeptide; cancer;

KW Alzheimer's disease; ischaemia; cytostatic; nootropic; vasotropic;

KW neuroprotective; gene; ss.

XX

OS Homo sapiens.

XX

PN US2002192659-A1.

XX

PD 19-DEC-2002.

XX

PF 10-JUL-2001; 2001US-00902853.

XX

PR 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059115P.

PR 17-SEP-1997; 97US-0059117P.

PR 17-SEP-1997; 97US-0059119P.

PR 17-SEP-1997; 97US-0059121P.

PR 17-SEP-1997; 97US-0059122P.

PR 17-SEP-1997; 97US-0059184P.

PR 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 15-OCT-1997; 97US-0062125P.

PR 17-OCT-1997; 97US-0062285P.

PR 17-OCT-1997; 97US-0062287P.

PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0062814P.

PR 24-OCT-1997; 97US-0062816P.

PR 24-OCT-1997; 97US-0063045P.

PR 24-OCT-1997; 97US-0063120P.

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PR 24-OCT-1997; 97US-0063128P.

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PR 27-OCT-1997; 97US-0063329P.

PR 28-OCT-1997; 97US-0063541P.

PR 28-OCT-1997; 97US-0063542P.

PR 28-OCT-1997; 97US-0063544P.

PR 28-OCT-1997; 97US-0063549P.

PR 28-OCT-1997; 97US-0063550P.

PR 28-OCT-1997; 97US-0063564P.

PR 29-OCT-1997; 97US-0063435P.

PR 29-OCT-1997; 97US-0063704P.

PR 29-OCT-1997; 97US-0063732P.

PR 29-OCT-1997; 97US-0063734P.

PR 29-OCT-1997; 97US-0063735P.

PR 29-OCT-1997; 97US-0063738P.

PR 29-OCT-1997; 97US-0064215P.

PR 31-OCT-1997; 97US-0063870P.

PR 31-OCT-1997; 97US-0064103P.

PR 03-NOV-1997; 97US-0064248P.

PR 07-NOV-1997; 97US-0064809P.

PR 12-NOV-1997; 97US-0065186P.

PR 17-NOV-1997; 97US-0065846P.

PR 18-NOV-1997; 97US-0065693P.

PR 21-NOV-1997; 97US-0066120P.

PR 21-NOV-1997; 97US-0066364P.

PR 24-NOV-1997; 97US-0066453P.

PR 24-NOV-1997; 97US-0066466P.

PR 24-NOV-1997; 97US-0066511P.

PR 24-NOV-1997; 97US-0066770P.

PR 24-NOV-1997; 97US-0066772P.

PR 10-SEP-1998; 98WO-US018824.

PR 14-SEP-1998; 98WO-US019177.

PR 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98WO-US019437.

PR 01-DEC-1998; 98WO-US025108.

PR 08-SEP-1999; 99WO-US020594.

PR 13-SEP-1999; 99WO-US020944.

PR 15-SEP-1999; 99WO-US021090.

PR 15-SEP-1999; 99WO-US021547.

PR 05-OCT-1999; 99WO-US023089.

PR 29-NOV-1999; 99WO-US028214.

PR 30-NOV-1999; 99WO-US028313.

PR 01-DEC-1999; 99WO-US028301.

PR 02-DEC-1999; 99WO-US028564.

PR 02-DEC-1999; 99WO-US028565.

PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.

PR 20-DEC-1999; 99WO-US030999.

PR 05-JAN-2000; 2000WO-US000219.

PR 11-FEB-2000; 2000WO-US003565.

PR 22-FEB-2000; 2000WO-US004414.

PR 24-FEB-2000; 2000WO-US005004.

PR 02-MAR-2000; 2000WO-US005841.

PR 20-MAR-2000; 2000WO-US007377.

PR 30-MAR-2000; 2000WO-US008439.

PR 22-MAY-2000; 2000WO-US014042.

PR 02-JUN-2000; 2000WO-US015264.

PR 28-JUL-2000; 2000WO-US020710.

PR 24-AUG-2000; 2000WO-US023328.

PR 18-SEP-2000; 2000US-00665350.

XX

PA (GETH) GENENTECH INC.

XX

PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;

PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;

PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;

PI Williams PM, Wood WI;

XX

DR WPI; 2003-361832/34.

DR P-PSDB; ABU71480.

XX

PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or

PT PRO1868, useful in molecular biology, chromosome and gene mapping, in

PT generating antisense RNA and DNA, and in gene therapy.

XX

PS Claim 2; Fig 73; 474pp; English.

XX

CC The present invention relates to the isolation of novel human secreted

CC and transmembrane proteins (PRO polypeptides), and the polynucleotide

CC sequences encoding them. The polynucleotide sequences are useful in

CC molecular biology, as hybridisation probes, in chromosome and gene

CC mapping, in generating antisense RNA and DNA, and in gene therapy. The

CC polynucleotide sequences may also be used in preparing PRO polypeptides

CC by recombinant techniques, and in generating either transgenic animals or

CC knock-out animals which, in turn, are useful in the development and

CC screening of therapeutically useful reagents. The PRO polypeptides or

CC their antibodies are useful in preparing a medicament for treating a

CC condition responsive to the polypeptide or antibody, such as cancer,

CC Alzheimer's disease or ischaemia, and in various diagnostic assays. The

CC present sequence encodes a human PRO polypeptide of the invention

XX

SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Query Match 98.3%; Score 1994; DB 7; Length 2372;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 24 AGCAGGGAATCCGGATGTCTCGTTATGAAGTGAGCAGTGAGTGTGAGCCTCAACATA 83

Db 1 AGCAGGGAATCCGGATGTCTCGTTATGAAGTGAGCAGTGAGTGTGAGCCTCAACATA 60

QY 84 GTTCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 143
Db |||||
61 GTTCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
QY 144 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTTCAGCCTG 203
Db |||||
121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTTCAGCCTG 180
QY 204 GTGTTGCTTCTCACTTCCATCTGGACCAAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 263
Db |||||
181 GTGTTGCTTCTCACTTCCATCTGGACCAAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240
QY 264 GAAGAGCTTTCATCCAGGTGTCTGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAG 323
Db |||||
241 GAAGAGCTTTCATCCAGGTGTCTGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAG 300
QY 324 GCGAACCAAGCAGCTGAAATTTACAGAAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGT 383
Db |||||
301 GCGAACCAAGCAGCTGAAATTTACAGAAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGT 360
QY 384 TTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 443
Db |||||
361 TTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420
QY 444 GGCTGGGTTGGAGATGGATTTCGTGGTTCATCTCTAGGATTAGCCCCAAACCCCAAGTGTGGG 503
Db |||||
421 GGCTGGGTTGGAGATGGATTTCGTGGTTCATCTCTAGGATTAGCCCCAAACCCCAAGTGTGGG 480
QY 504 AAAAATGGGGTGGGTGTCCTGATTGGAAGGTTCCAGTGAGCGGACAGTTTGCAGCCTAT 563
Db |||||
481 AAAAATGGGGTGGGTGTCCTGATTGGAAGGTTCCAGTGAGCGGACAGTTTGCAGCCTAT 540
QY 564 TGTTACAACTCATCTGATACCTTGGAATACTCGTGCAATCCAGAAATTATGTGAGTACAGT 623
Db |||||
541 TGTTACAACTCATCTGATACCTTGGAATACTCGTGCAATCCAGAAATTATCACCACCAA 600
QY 624 GATCCCATATTCAACACTCAACTGCAACACAAACACAGAAATTATTGTGAGTACAGT 683
Db |||||
601 GATCCCATATTCAACACTCAACTGCAACACAAACACAGAAATTATTGTGAGTACAGT 660
QY 684 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCCCTACTACTCCTCCTGCT 743
Db |||||
561 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCCCTACTACTCCTCCTGCT 720
QY 744 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTGTGTGCAGAAAGTTTATTATG 803
Db |||||
721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTGTGTGCAGAAAGTTTATTATG 780
QY 804 GAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAATAAAGCAGCATTCAG 863
Db |||||
781 GAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAATAAAGCAGCATTCAG 840
QY 864 AATGAAGCTGCTGGGTTTGAGGTGTCCTCCACGGCTCTGCTAGTCTCTCCTCTTC 923
Db |||||
841 AATGAAGCTGCTGGGTTTGAGGTGTCCTCCACGGCTCTGCTAGTCTCTCCTCTTC 900
QY 924 TTTGGTGTGCAGCTGGTCTTGGATTGTGATTTGCTATGTCAAAGGSPATGTGAAGGCTTCCCT 983
Db |||||
901 TTTGGTGTGCAGCTGGTCTTGGATTGTGATTTGCTATGTCAAAGGTATGTGAAGGCTTCCCT 960
QY 984 TTTACAAAACAAGATCAGCAGAGGAAATGATCGAAACCAAGATAGTAAAGGAGGAGAG 1043
Db |||||
961 TTTACAAAACAAGATCAGCAGAGGAAATGATCGAAACCAAGATAGTAAAGGAGGAGAG 1020
QY 1044 GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACCTGATAAAAAACCCAGAGAGTCC 1103
Db |||||
1021 GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACCTGATAAAAAACCCAGAGAGTCC 1080
QY 1104 AAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAGCTGAAGTTAGATGAGACAGAAA 1163
Db |||||
1081 AAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAGCTGAAGTTAGATGAGACAGAAA 1140
QY 1164 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCTTACCTTACCTGCCCCAGCTGGGGAA 1223

Db |||||
1141 TGAGGAGACACACCTGAGGCTGGTTCTTTTCATGTCCTTACCCTGCCCCAGCTGGGGAA 1200
QY 1224 ATCAAAAGGGCCAAAGAACCCAAAGAAAGAGTCCACCCCTTGFTTCTAACTGGAATCAGC 1283
Db |||||
1201 ATCAAAAGGGCCAAAGAACCCAAAGAAAGAGTCCACCCCTTGTTCTTAACTGGAATCAGC 1260
QY 1284 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAAC 1343
Db |||||
1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAAC 1320
QY 1344 CCTGTCTGGATCCTATCCTCCTACCTCCAAGCTTCCCACGGCCTTTCTAGCCTGGCTAT 1403
Db |||||
1321 CCTGTCTGGATCCTATCCTCCTACCTCCAAGCTTCCCACGGCCTTTCTAGCCTGGCTAT 1380
QY 1404 GTCCTAAATAATATCCCACCTGGGAGAAAGGAGTTTGTGCAAGTGCAAAGGACCTAAACATC 1463
Db |||||
1381 GTCCTAAATAATATCCCACCTGGGAGAAAGGAGTTTGTCAAGTGCAAAGGACCTAAACATC 1440
QY 1464 TCATCAGTATCCAGTGGTAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAAGC 1523
Db |||||
1441 TCATCAGTATCCAGTGGTAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAAGC 1500
QY 1524 CAAGGAGTCACTGAGACCAAGGCTTTCTACTGATTCGGCAGCTCAGACCCCTTCTTCA 1583
Db |||||
1501 CAAGGAGTCACTGAGACCAAGGCTTTCTACTGATTCGGCAGCTCAGACCCCTTCTTCA 1560
QY 1584 GCTCTGAAAGAGAAACACGATATCCACCTGACATGTCCTTCTGAGCCCCGGTAAGAGCAAA 1643
Db |||||
1561 GCTCTGAAAGAGAAACACGATATCCACCTGACATGTCCTTCTGAGCCCCGGTAAGAGCAAA 1620
QY 1644 AGAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCCATGGAGATTCTCATAACTTGAGACCCTAA 1703
Db |||||
1621 AGAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCCATGGAGATTCTCATAACTTGAGACCCTAA 1680
QY 1704 TCTCTGTAAGCTAAAATAAAGAAATAGAACCAAGGCTGAGGATACGACAGTACACTGTCA 1763
Db |||||
1681 TCTCTGTAAGCTAAAATAAAGAAATAGAACCAAGGCTGAGGATACGACAGTACACTGTCA 1740
QY 1764 GCAGGACTGTAAACACAGACAGGGGTCAAAGTGTTCCTCTGAAACACATTGAGTTGGAAT 1823
Db |||||
1741 GCAGGACTGTAAACACAGACAGGGGTCAAAGTGTTCCTCTGAAACACATTGAGTTGGAAT 1800
QY 1824 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACACTGCTGATATTTCTCT 1883
Db |||||
1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACACTGCTGATATTTCTCT 1860
QY 1884 AGGAAATATACTTTTACAGTAACAAAAATAAAAACTCTATAAAATTTCTATTTTATCT 1943
Db |||||
1861 AGGAAATATACTTTTACAGTAACAAAAATAAAAACTCTATAAAATTTCTATTTTATCT 1920
QY 1944 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 2003
Db |||||
1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980
QY 2004 TTCAACAAACATTTTAAAAAAA 2025
Db |||||
1981 TTCAACAAACATTTGCTGAATA 2002

RESULT 13

ACA60164

ID ACA60164 standard; cDNA; 2372 BP.

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AC ACA60164;

XX

DT 12-JUN-2003 (first entry)

XX

DE Human cDNA for secreted/transmembrane protein PRO263.

XX

KW Human; ss; gene; secreted protein; transmembrane protein; PRO;

XX

gene therapy; chromosome identification; chromosome marker.

OS	Homo sapiens.		
XX	US2003003530-A1.		
PN			
XX			
PD	02-JAN-2003.		
XX			
PF	11-JUL-2001; 2001US-00904011.	PR	20-DEC-1999; 99WO-US030911.
XX		PR	20-DEC-1999; 99WO-US030999.
PR	17-SEP-1997; 97US-0059113P.	PR	05-JAN-2000; 2000WO-US000219.
PR	17-SEP-1997; 97US-0059115P.	PR	11-FEB-2000; 2000WO-US003565.
PR	17-SEP-1997; 97US-0059117P.	PR	22-FEB-2000; 2000WO-US004414.
PR	17-SEP-1997; 97US-0059119P.	PR	24-FEB-2000; 2000WO-US005004.
PR	17-SEP-1997; 97US-0059121P.	PR	02-MAR-2000; 2000WO-US005841.
PR	17-SEP-1997; 97US-0059122P.	PR	20-MAR-2000; 2000WO-US007377.
PR	17-SEP-1997; 97US-0059184P.	PR	30-MAR-2000; 2000WO-US008439.
PR	18-SEP-1997; 97US-0059263P.	PR	22-MAY-2000; 2000WO-US014042.
PR	18-SEP-1997; 97US-0059266P.	PR	02-JUN-2000; 2000WO-US015264.
PR	15-OCT-1997; 97US-0062125P.	PR	28-JUL-2000; 2000WO-US020710.
PR	17-OCT-1997; 97US-0062285P.	PR	24-AUG-2000; 2000WO-US023328.
PR	17-OCT-1997; 97US-0062287P.	PR	18-SEP-2000; 2000US-00665350.
PR	21-OCT-1997; 97US-0063486P.	XX	
PR	24-OCT-1997; 97US-0062814P.	PA	(GETH) GENENTECH INC.
PR	24-OCT-1997; 97US-0062816P.	XX	
PR	24-OCT-1997; 97US-0063045P.	PI	Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PR	24-OCT-1997; 97US-0063120P.	PI	Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PR	24-OCT-1997; 97US-0063121P.	PI	Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PR	24-OCT-1997; 97US-0063127P.	PI	Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PR	24-OCT-1997; 97US-0063128P.	PI	Williams PM, Wood WI;
PR	27-OCT-1997; 97US-0063327P.	XX	
PR	27-OCT-1997; 97US-0063329P.	DR	WPI; 2003-329602/31.
PR	28-OCT-1997; 97US-0063541P.	DR	P-PSDB; ABU71926.
PR	28-OCT-1997; 97US-0063542P.	XX	
PR	28-OCT-1997; 97US-0063544P.	CC	New transmembrane polypeptides and nucleic acids encoding the
PR	28-OCT-1997; 97US-0063549P.	CC	polypeptides, useful in gene therapy, in chromosome identification, as
PR	28-OCT-1997; 97US-0063550P.	CC	chromosome markers, in generating probes and in tissue typing.
PR	28-OCT-1997; 97US-0063564P.	CC	
PR	29-OCT-1997; 97US-0063435P.	CC	Claim 2; Fig 73; 484pp; English.
PR	29-OCT-1997; 97US-0063704P.	CC	
PR	29-OCT-1997; 97US-0063732P.	CC	The invention relates to an isolated nucleic acid with at least 80%
PR	29-OCT-1997; 97US-0063734P.	CC	nucleic acid sequence identity to a nucleotide sequence encoding one of
PR	29-OCT-1997; 97US-0063735P.	CC	61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a
PR	29-OCT-1997; 97US-0063738P.	CC	PRO protein extracellular domain. Also included are a vector comprising
PR	29-OCT-1997; 97US-0064215P.	CC	the PRO nucleic acid, a host cell comprising the vector, producing a PRO
PR	31-OCT-1997; 97US-0063870P.	CC	polypeptide (by culturing the host cell for the expression of the PRO
PR	31-OCT-1997; 97US-0064103P.	CC	polypeptide, and recovering the PRO polypeptide from the cell culture),
PR	03-NOV-1997; 97US-0064248P.	CC	an isolated PRO polypeptide (having at least 80% sequence identity to: (
PR	07-NOV-1997; 97US-0064809P.	CC	a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino
PR	12-NOV-1997; 97US-0065186P.	CC	acid sequence encoded by a nucleic acid molecule deposited with an ATCC
PR	17-NOV-1997; 97US-0065846P.	CC	number (detailed in the specification); or (c) an extracellular domain of
PR	18-NOV-1997; 97US-0065693P.	CC	a PRO polypeptide or to a PRO polypeptide lacking its associated signal
PR	21-NOV-1997; 97US-0066120P.	CC	peptide), a chimaeric molecule comprising a PRO polypeptide of fused to a
PR	21-NOV-1997; 97US-0066364P.	CC	heterologous amino acid sequence, an anti-PRO antibody, detecting a
PR	24-NOV-1997; 97US-0066453P.	CC	PRO245 or PRO1868 in a sample suspected of containing the polypeptide,
PR	24-NOV-1997; 97US-0066456P.	CC	linking a bioactive molecule to a cell expressing a PRO245 or PRO1868 and
PR	24-NOV-1997; 97US-0066511P.	CC	modulating at least one biological activity of a cell expressing a PRO245
PR	24-NOV-1997; 97US-0066770P.	CC	or PRO1868. Nucleic acids which encode PRO can be used to generate either
PR	24-NOV-1997; 97US-0066772P.	CC	transgenic animals or knock-out animals which may be used in the
PR	10-SEP-1998; 98WO-US018824.	CC	development and screening of therapeutically useful reagents. The nucleic
PR	14-SEP-1998; 98WO-US019177.	CC	acids may also be used in gene therapy, in chromosome identification, as
PR	16-SEP-1998; 98WO-US019330.	CC	useful as molecular markers for protein electrophoresis, and the isolated
PR	17-SEP-1998; 98WO-US019437.	CC	nucleic acids may be used for recombinantly expressing those markers. The
PR	01-DEC-1998; 98WO-US025108.	CC	PRO polypeptides and nucleic acids may also be used in tissue typing.
PR	08-SEP-1999; 99WO-US020594.	CC	Anti-PRO antibodies are useful in diagnostic assays for PRO, and in
PR	13-SEP-1999; 99WO-US020944.	CC	affinity purification of PRO from recombinant cell culture or natural
PR	15-SEP-1999; 99WO-US021090.	XX	sources. The present sequence encodes a PRO protein
PR	15-SEP-1999; 99WO-US021547.	SQ	Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
PR	05-OCT-1999; 99WO-US023089.		
PR	29-NOV-1999; 99WO-US028214.		
PR	30-NOV-1999; 99WO-US028313.		
PR	01-DEC-1999; 99WO-US028301.		
PR	02-DEC-1999; 99WO-US028564.		
PR	02-DEC-1999; 99WO-US028565.		
PR	16-DEC-1999; 99WO-US030095.		
<hr/>			
QY	24 AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA	83	
Dd	1 AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA	60	
QY	84 GTTCCAGAACTCTCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC	143	
<hr/>			
Query Match		98.3%;	Score 1994; DB 7; Length 2372;
Best Local Similarity		99.8%;	Pred. No. 0;
Matches 1997;		Conservative	0; Mismatches 5; Indels 0; Gaps 0;

Db 61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120
QY 144 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCCTG 203
Db 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCCTG 180
QY 204 GTGTTGCTTCTCACTTCCATCTGGACCAACAGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 263
Db 181 GTGTTGCTTCTCACTTCCATCTGGACCAACAGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240
QY 264 GAAGAGTTCATCCAGGTGTCATGCAGAAATTATGGGATCACCTTGTGAGCAAAAAG 323
Db 241 GAAGAGTTCATCCAGGTGTCATGCAGAAATTATGGGATCACCTTGTGAGCAAAAAG 300
QY 324 GCGAACAGCAGCTGAATTTACAGAAAGCTAAGGAGGCCCTGTAGGCTGCTGGACTAAGT 383
Db 301 GCGAACAGCAGCTGAATTTACAGAAAGCTAAGGAGGCCCTGTAGGCTGCTGGACTAAGT 360
QY 384 TTGGCCGCAAGGACCAAGTTGAAACAGACCTTGAAAGCTAGCTTTGAAAACCTTGACGCTAT 443
Db 361 TTGGCCGCAAGGACCAAGTTGAAACAGACCTTGAAAGCTAGCTTTGAAAACCTTGACGCTAT 420
QY 444 GGCTGGGTTGGAGATGGATTTCGTGGTTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGG 503
Db 421 GGCTGGGTTGGAGATGGATTTCGTGGTTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGG 480
QY 504 AAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 563
Db 481 AAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540
QY 564 TGTTAAACTCATCTGATACCTTGGAATAACTCGTGCAATCCAGAAATTATCACCACCAA 623
Db 541 TGTTAAACTCATCTGATACCTTGGAATAACTCGTGCAATCCAGAAATTATCACCACCAA 600
QY 624 GATCCCATATTCAACACTCAAACCTGCAACACAAACAGAAATTTATGTGAGTACAGT 683
Db 601 GATCCCATATTCAACACTCAAACCTGCAACACAAACAGAAATTTATGTGAGTACAGT 660
QY 684 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCCCTACTACTCTCCTGCT 743
Db 661 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCCCTACTACTCTCCTGCT 720
QY 744 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTGCACAGAAAGTTTATG 803
Db 721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTGCACAGAAAGTTTATG 780
QY 804 GAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAATAAAGCAGCATTTCAAG 863
Db 781 GAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAATAAAGCAGCATTTCAAG 840
QY 864 AATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTGCTAGTGTGCTCTCCTCTTC 923
Db 841 AATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTGCTAGTGTGCTCTCCTCTTC 900
QY 924 TTTGCTGCTGCAGCTGGTCTTGGAATTTTGCTATGTCAAAAGGTATGTGAAGGCTTCCCT 983
Db 901 TTTGCTGCTGCAGCTGGTCTTGGAATTTTGCTATGTCAAAAGGTATGTGAAGGCTTCCCT 960
QY 984 TTTACAAACAAGAATCAGCAGAGGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAG 1043
Db 961 TTTACAAACAAGAATCAGCAGAGGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAG 1020
QY 1044 GCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAAACTGATAAAAAACCCAGAAGTCC 1103
Db 1021 GCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAAACTGATAAAAAACCCAGAAGTCC 1080
QY 1104 AAGAGTCCAAGCAAAACTACCGTGCATGCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1163
Db 1081 AAGAGTCCAAGCAAAACTACCGTGCATGCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1140
QY 1164 TGAGGAGACACACTGAGGCTGGTTTCTTCATGCTCCTTACCTGCTCCCGAGCTGGGGAA 1223
Db 1141 TGAGGAGACACACTGAGGCTGGTTTCTTCATGCTCCTTACCTGCTCCCGAGCTGGGGAA 1200

QY 1224 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCCCTGGTTCCTAAACTGGAATCAGC 1283
Db 1201 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCCCTGGTTCCTAAACTGGAATCAGC 1260
QY 1284 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1343
Db 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1320
QY 1344 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCCTTCTAGCCTGGCTAT 1403
Db 1321 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCCTTCTAGCCTGGCTAT 1380
QY 1404 GTCCTAATAATATCCCACTGGGAGAAAAGGAGTTTTTGCAAAGTGCAAAGACCTAAACATC 1463
Db 1381 GTCCTAATAATATCCCACTGGGAGAAAAGGAGTTTTTGCAAAGTGCAAAGACCTAAACATC 1440
QY 1464 TCATCAGTATCCAGTGGTAAAAAGGCCCTCCTGGCTGTCTGAGGTAGGTGGTTGAAAGC 1523
Db 1441 TCATCAGTATCCAGTGGTAAAAAGGCCCTCCTGGCTGTCTGAGGTAGGTGGTTGAAAGC 1500
QY 1524 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGTCCAGACCCCTTCTTCA 1583
Db 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTTCCGCGAGTCCAGACCCCTTCTTCA 1560
QY 1584 GCTCTGAAAAGAGAAACACGTCATCCACACCTGACATGTCCTTCTGAGCCCCGGTAAGAGCAA 1643
Db 1561 GCTCTGAAAAGAGAAACACGTCATCCACACCTGACATGTCCTTCTGAGCCCCGGTAAGAGCAA 1620
QY 1644 AGAATGCGAGAAAAGTTTTAGCCCCCTGAAAAGCCATGGAGATTTCTCATAACTTGAGACCTAA 1703
Db 1621 AGAATGCGAGAAAAGTTTTAGCCCCCTGAAAAGCCATGGAGATTTCTATAACTTGAGACCTAA 1680
QY 1704 TCTCTGTAAAGCTAAATAAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACTGTCA 1763
Db 1681 TCTCTGTAAAGCTAAATAAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACTGTCA 1740
QY 1764 GCAGGACTGTAAACACACAGACAGGTCAAAAGTGTCTCTGAAACACATTGAGTTGGAAT 1823
Db 1741 GCAGGACTGTAAACACACAGACAGGTCAAAAGTGTCTCTGAAACACATTGAGTTGGAAT 1800
QY 1824 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1883
Db 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1860
QY 1884 AGGAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1943
Db 1861 AGGAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1920
QY 1944 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 2003
Db 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980
QY 2004 TTCAACAAACATTTTAAAAAAA 2025
Db 1981 TTCAACAAACATTTGCTGAATA 2002

RESULT 14
ACD07564
ID ACD07564 standard; cDNA; 2372 BP.
XX
AC ACD07564;
XX
DT 07-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO263 cDNA.
KW Human; secreted and transmembrane protein; PRO; pharmaceutical;
KW diagnostic; biosensor; bioreactor; Parkinson's disease;
KW Alzheimer's disease; inflammation; nephritis; wound healing;
KW nerve repair; collateral blood vessel formation; cancer;
KW colorectal cancer; haemorrhage; rheumatoid arthritis; diabetes;

KW cirrhosis; fibrosis; restenosis; dermal fibrotic condition; keloid;
KW scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis;
KW infertility; gene therapy; gene; ss.

XX Homo sapiens.

PN US2002197671-A1.

XX 26-DEC-2002.

PF 17-JUL-2001; 2001US-00907824.

XX 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059115P.

PR 17-SEP-1997; 97US-0059117P.

PR 17-SEP-1997; 97US-0059119P.

PR 17-SEP-1997; 97US-0059121P.

PR 17-SEP-1997; 97US-0059122P.

PR 17-SEP-1997; 97US-0059184P.

PR 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 15-OCT-1997; 97US-0062125P.

PR 17-OCT-1997; 97US-0062285P.

PR 17-OCT-1997; 97US-0062287P.

PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0062814P.

PR 24-OCT-1997; 97US-0062816P.

PR 24-OCT-1997; 97US-0063045P.

PR 24-OCT-1997; 97US-0063120P.

PR 24-OCT-1997; 97US-0063121P.

PR 24-OCT-1997; 97US-0063127P.

PR 24-OCT-1997; 97US-0063128P.

PR 27-OCT-1997; 97US-0063327P.

PR 27-OCT-1997; 97US-0063329P.

PR 28-OCT-1997; 97US-0063541P.

PR 28-OCT-1997; 97US-0063542P.

PR 28-OCT-1997; 97US-0063544P.

PR 28-OCT-1997; 97US-0063549P.

PR 28-OCT-1997; 97US-0063550P.

PR 28-OCT-1997; 97US-0063564P.

PR 29-OCT-1997; 97US-0063435P.

PR 29-OCT-1997; 97US-0063704P.

PR 29-OCT-1997; 97US-0063732P.

PR 29-OCT-1997; 97US-0063734P.

PR 29-OCT-1997; 97US-0063735P.

PR 29-OCT-1997; 97US-0063738P.

PR 31-OCT-1997; 97US-0063870P.

PR 31-OCT-1997; 97US-0064103P.

PR 03-NOV-1997; 97US-0064248P.

PR 07-NOV-1997; 97US-0064809P.

PR 12-NOV-1997; 97US-0065186P.

PR 17-NOV-1997; 97US-0065846P.

PR 18-NOV-1997; 97US-0065693P.

PR 21-NOV-1997; 97US-0066120P.

PR 21-NOV-1997; 97US-0066364P.

PR 24-NOV-1997; 97US-0066453P.

PR 24-NOV-1997; 97US-0066466P.

PR 24-NOV-1997; 97US-0066511P.

PR 24-NOV-1997; 97US-0066770P.

PR 24-NOV-1997; 97US-0066772P.

PR 10-SEP-1998; 98WO-US018824.

PR 14-SEP-1998; 98WO-US019177.

PR 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98WO-US019437.

PR 01-DEC-1998; 98WO-US025108.

PR 08-SEP-1999; 99WO-US020594.

PR 13-SEP-1999; 99WO-US020944.

PR 15-SEP-1999; 99WO-US021090.

PR 15-SEP-1999; 99WO-US021547.

PR 05-OCT-1999; 99WO-US023089.

PR 29-NOV-1999; 99WO-US028214.

PR 30-NOV-1999; 99WO-US028313.

PR 01-DEC-1999; 99WO-US028301.

PR 02-DEC-1999; 99WO-US028564.

PR 02-DEC-1999; 99WO-US028565.

PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.

PR 20-DEC-1999; 99WO-US030999.

PR 05-JAN-2000; 2000WO-US000219.

PR 11-FEB-2000; 2000WO-US003565.

PR 22-FEB-2000; 2000WO-US004414.

PR 24-FEB-2000; 2000WO-US005004.

PR 02-MAR-2000; 2000WO-US005841.

PR 20-MAR-2000; 2000WO-US007377.

PR 30-MAR-2000; 2000WO-US008439.

PR 22-MAY-2000; 2000WO-US014042.

PR 02-JUN-2000; 2000WO-US015264.

PR 28-JUL-2000; 2000WO-US020710.

PR 24-AUG-2000; 2000WO-US023328.

PR 18-SEP-2000; 2000US-00665350.

XX (GETH) GENENTECH INC.

PA Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;

XX Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;

PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;

PI Williams PM, Wood WI;

XX WPI; 2003-370793/35.

DR P-PSDB; ABO01809.

DR XX

XX

PT New genes and secreted and transmembrane polypeptides (e.g. PRO245 or

PT PRO335), useful for treating or diagnosing e.g. Alzheimer's disease,

PT cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia

PT or strokes.

XX Claim 2; Fig 73; 482pp; English.

XX

CC The invention describes a new isolated nucleic acid molecule comprising

CC the full length coding sequence of the DNA deposited with the American

CC Type Culture Collection (e.g. ATCC Deposit No. 209258) , or a sequence

CC with at least 80% identity to a DNA encoding a PRO polypeptide comprising

CC any of 61 sequences having 164-1119 amino acids fully defined in the

CC specification. The PRO polypeptides or polynucleotides are useful as

CC pharmaceuticals, diagnostics, biosensors or bioreactors. These are

CC particularly useful for detecting or treating e.g. Parkinson's disease,

CC Alzheimer's disease, inflammations, nephritis, wound healing, nerve

CC repair, collateral blood vessel formation, cancers (e.g. colorectal

CC cancer), haemorrhage (or reduce risk for haemorrhage), rheumatoid

CC arthritis, diabetes, cirrhosis of the liver, fibrosis of the lungs,

CC restenosis, dermal fibrotic conditions (e.g. keloids or scarring),

CC ischaemia, strokes, hypertension, heart attacks, atherosclerosis, or

CC infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep,

CC pigs, goats, or rabbits) The PRO polypeptides are useful as targets for

CC therapeutic intervention in these diseases, and diagnostic determination

CC of the presence of these diseases. The PRO polypeptides are also useful

CC as molecular weight markers, or for chromosome identification. The PRO

CC genes are useful as hybridisation probes, or for screening libraries of

CC human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene

CC therapy, particularly for replacing a defective gene. This sequence

CC encodes a novel human secreted and transmembrane PRO polypeptide

XX Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

SQ

Query Match 98.3%; Score 1994; DB 7; Length 2372;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 24 AGCAGGGAAATCCGGATGTCCTCGGTTATGAACTGGAGCAGTGAGTGTGAGCCTCAACATA 83

|||||

Db 1 AGCAGGGAAATCCGGATGTCCTCGGTTATGAACTGGAGCAGTGAGTGTGAGCCTCAACATA 60

|||||

QY 84 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 143

|||||

Db 61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120

QY 144 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 203

Db 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180

QY 204 GTGTTGCTTCTCACTTCCATCTGGACCAAGAGGCTCCTGGTCCAAAGGCTCTTTGCGTGCA 263

Db 181 GTGTTGCTTCTCACTTCCATCTGGACCAAGAGGCTCCTGGTCCAAAGGCTCTTTGCGTGCA 240

QY 264 GAAGAGCTTTCCATCCAGGTGTATGCAGAAATTATGGGATCACCCCTGTGAGCAAAAAG 323

Db 241 GAAGAGCTTTCCATCCAGGTGTATGCAGAAATTATGGGATCACCCCTGTGAGCAAAAAG 300

QY 324 GCGAACCCAGCAGCTGAATTTACAGAAAGCTAAAGGAGGCCTGTAGGCTGCTGGACTAAGT 383

Db 301 GCGAACCCAGCAGCTGAATTTACAGAAAGCTAAAGGAGGCCTGTAGGCTGCTGGACTAAGT 360

QY 384 TTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 443

Db 361 TTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420

QY 444 GGCTGGGTTGGAGATGGATTTCGTGGTCACTCTAGGATTAGCCCCAAACCCCAAGTGTGGG 503

Db 421 GGCTGGGTTGGAGATGGATTTCGTGGTCACTCTAGGATTAGCCCCAAACCCCAAGTGTGGG 480

QY 504 AAAAATGGGTGGGTGTCCTGATTTTGGAAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 563

Db 481 AAAAATGGGTGGGTGTCCTGATTTTGGAAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540

QY 564 TGTTACAACTCATCTGATACTTTGGACTAACTCGTGCAATCCAGAAATTATCACCACCAAA 623

Db 541 TGTTACAACTCATCTGATACTTTGGACTAACTCGTGCAATCCAGAAATTATCACCACCAAA 600

QY 624 GATCCCAATTAACACTCAAACTGCAACAAAACAAGAAATTTATTTGTCAGTGACAGT 683

Db 601 GATCCCAATTAACACTCAAACTGCAACAAAACAAGAAATTTATTTGTCAGTGACAGT 660

QY 684 ACCTACTCGTGGCATCCCCTTACTCTACAATACCTGCCCTACTACTACTCCTCCTGCT 743

Db 661 ACCTACTCGTGGCATCCCCTTACTCTACAATACCTGCCCTACTACTACTCCTCCTGCT 720

QY 744 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTGTCACAGAAAGTTTTTATG 803

Db 721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTGTCACAGAAAGTTTTTATG 780

QY 804 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAATAAAGCAGCATTTCAAG 863

Db 781 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAATAAAGCAGCATTTCAAG 840

QY 864 AATGAAGCTGCTGGGTTTGGAGGTGCCCCACGGCTCTGCTAGTGCTGCTCCTCTTC 923

Db 841 AATGAAGCTGCTGGGTTTGGAGGTGCCCCACGGCTCTGCTAGTGCTGCTCCTCTTC 900

QY 924 TTTGGTGTGCAGCTGGTCTTGGAATTTTGCTATGTCAAAAGGTATGTGAAGGCCTTCCCT 983

Db 901 TTTGGTGTGCAGCTGGTCTTGGAATTTTGCTATGTCAAAAGGTATGTGAAGGCCTTCCCT 960

QY 984 TTTTACAAACAAGAATCAGCAGAAAGGAAATGATCGAAACCAAACTAGTAAAGGAGGAGAAG 1043

Db 961 TTTTACAAACAAGAATCAGCAGAAAGGAAATGATCGAAACCAAACTAGTAAAGGAGGAGAAG 1020

QY 1044 GCCAATGATAGCAACCCCTAATGAGGAATCAAAAGAAAACCTGATAAAAACCCAGAAGATCC 1103

Db 1021 GCCAATGATAGCAACCCCTAATGAGGAATCAAAAGAAAACCTGATAAAAACCCAGAAGATCC 1080

QY 1104 AAGAGTCCAAGCAAAAACCTACCGTGCATGCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1163

Db 1081 AAGAGTCCAAGCAAAAACCTACCGTGCATGCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1140

QY 1164 TGAGGAGACACCTGAGGCTGGTTTCTTCATGCTCCTTACCCTGCCCCAGCTGGGAA 1223

Db 1141 TGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCCTTACCCTGCCCCAGCTGGGGAA 1200

QY 1224 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCCTTGGTTCCTAAACTGGAATCAGC 1283

Db 1201 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCCTTGGTTCCTAAACTGGAATCAGC 1260

QY 1284 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1343

Db 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAAC 1320

QY 1344 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCTTCTAGCCTGGCTAT 1403

Db 1321 CCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCTTCTAGCCTGGCTAT 1380

QY 1404 GTCCTAATAATATCCCACCTGGGAGAAAGGAGTTTGTCAAAGTGCAAGGACCTAAAACATC 1463

Db 1381 GTCCTAATAATATCCCACCTGGGAGAAAGGAGTTTGTCAAAGTGCAAGGACCTAAAACATC 1440

QY 1464 TCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGTGTGAAAGC 1523

Db 1441 TCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGTGTGAAAGC 1500

QY 1524 CAAGGAGTCACTGAGACCAGGCTTCTCTACTGATTCCGCAGCTCAGACCCCTTCTTTCA 1583

Db 1501 CAAGGAGTCACTGAGACCAGGCTTCTCTACTGATTCCGCAGCTCAGACCCCTTCTTTCA 1560

QY 1584 GCTCTGAAAGAGAAAACACGTATCCCACTGACATGTCTCTGAGCCCGTAAAGAGCAAA 1643

Db 1561 GCTCTGAAAGAGAAAACACGTATCCCACTGACATGTCTCTGAGCCCGTAAAGAGCAAA 1620

QY 1644 AGAATGCGAGAAAAGTTTAGCCCTCGAAAGCCCATGGAGATTCTCATAACTTGAGACCTAA 1703

Db 1621 AGAATGCGAGAAAAGTTTAGCCCTCGAAAGCCCATGGAGATTCTCATAACTTGAGACCTAA 1680

QY 1704 TCTCTGTAAAGCTAAAATAAAGAAATAGAACCAAGGCTGAGGATACGACAGTACACTGTCA 1763

Db 1681 TCTCTGTAAAGCTAAAATAAAGAAATAGAACCAAGGCTGAGGATACGACAGTACACTGTCA 1740

QY 1764 GCAGGACTGTAAACACACAGACAGGTCAAAAGTGTCTCTGAAACACATTTGGAAT 1823

Db 1741 GCAGGACTGTAAACACACAGACAGGTCAAAAGTGTCTCTGAAACACATTTGGAAT 1800

QY 1824 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1883

Db 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1860

QY 1884 AGGAAATATACTTTTACAAGTAAACAAAATAAAAACCTCTTATAAATTTCTATTTTATCT 1943

Db 1861 AGGAAATATACTTTTACAAGTAAACAAAATAAAAACCTCTTATAAATTTCTATTTTATCT 1920

QY 1944 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 2003

Db 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980

QY 2004 TTCAACAAACATTTTAAAAAAA 2025

Db 1981 TTCAACAAACATTTGCTGAATA 2002

RESULT 15
ACA91166
ID ACA91166 standard; cDNA; 2372 BP.
XX
AC ACA91166;
XX
DT 11-JUL-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO263 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; antibody therapy;
XX
KW pharmaceutical; diagnostic; biosensor; bioreactor; gene; ss.
OS Homo sapiens.
XX

Db	1561		GCTCTGAAAGAGAGAAAACACG	TATCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAA	1620
Qy	1644		AGAATGGCAGAGAAAAGTTTAGCC	CCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA	1703
Db	1621		AGAATGGCAGAGAAAAGTTTAGCC	CCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA	1680
Qy	1704		TCTCTGTAAAGCTAAAAATAAGAA	ATAAGAAAGGCTGAGGATACGACAGTACACTGTCA	1763
Db	1681		TCTCTGTAAAGCTAAAAATAAGAA	ATAAGAAAGGCTGAGGATACGACAGTACACTGTCA	1740
Qy	1764		GCAGGGACTGTAAACACAGACAG	ACAGGGTCAAAGTGTCTCTGAAACACATTGAGTTGGAAT	1823
Db	1741		GCAGGGACTGTAAACACAGACAG	ACAGGGTCAAAGTGTCTCTGAAACACATTGAGTTGGAAT	1800
Qy	1824		CACTGTTTAGAACACACACACACT	TACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT	1883
Db	1801		CACTGTTTAGAACACACACACACT	TACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT	1860
Qy	1884		AGGAAATATACTTTTACAAGTAA	CAAAATAAAAACTCTTATAAATTCTATTTTATCT	1943
Db	1861		AGGAAATATACTTTTACAAGTAA	CAAAATAAAAACTCTTATAAATTCTATTTTATCT	1920
Qy	1944		GAGTTACAGAAATGATTACTAAG	GAGATTACTCAGTAATTTGTTAAAAAGTAATAAAA	2003
Db	1921		GAGTTACAGAAATGATTACTAAG	GAGATTACTCAGTAATTTGTTAAAAAGTAATAAAA	1980
Qy	2004		TTCAACAACACATTAAAAAAA		2025
Db	1981		TTCAACAACACATTGCTGAATA		2002

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 13, 2004, 09:54:56 ; Search time 217 Seconds
(without alignments)
5283.769 Million cell updates/sec

Title: US-10-079-111-2
Perfect score: 3604
Sequence: 1 ccttgacaagtcagaagctt.....aacattttaaaaaaaaaa 2029

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 3172214

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_p/US10079111/runat_13092004_102125_1809/app_query.fasta_1.2183
-DB=A_Geneseq_29Jan04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pt0 -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10079111@CGN_1_1_308@runat_13092004_102125_1809 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		SUMMARIES	
Result No.	Score	Query Match	Description
1	1772	49.2	344 4 ABB11979 Human PRO
2	1657	46.0	322 2 AAY13379 Amino aci
3	1657	46.0	322 3 AAY87287 Human sig
4	1657	46.0	322 3 ADC78521 Human PRO
5	1657	46.0	322 4 AAB80247 Human PRO
6	1657	46.0	322 4 AAB87528 Human PRO
7	1657	46.0	322 4 AAB88391 Human mem
8	1657	46.0	322 5 ABG95853 Human sec
9	1657	46.0	322 5 ABB84832 Human PRO
10	1657	46.0	322 5 ABB95438 Human ang

11	1657	46.0	322 6 ABU71625	Abu71625 Human PRO
12	1657	46.0	322 6 ABU71480	Abu71480 Human PRO
13	1657	46.0	322 6 ABU71926	Abu71926 Human sec
14	1657	46.0	322 6 ABO01809	Abo01809 Novel hum
15	1657	46.0	322 6 ABU90878	Abu90878 Novel hum
16	1657	46.0	322 6 ABO33937	Abo33937 Human sec
17	1657	46.0	322 6 ABU71954	Abu71954 Novel hum
18	1657	46.0	322 6 ABU54382	Abu54382 Human sec
19	1657	46.0	322 6 ABO47397	Abo47397 Human sec
20	1657	46.0	322 6 ABU71508	Abu71508 Human sec
21	1657	46.0	322 6 ABU72289	Abu72289 Human PRO
22	1657	46.0	322 6 ABU90962	Abu90962 Human PRO
23	1657	46.0	322 6 ABO27283	Abo27283 Human sec
24	1657	46.0	322 6 ABU64534	Abu64534 Human sec
25	1657	46.0	322 6 ABU67380	Abu67380 Human sec
26	1657	46.0	322 6 ABU92478	Abu92478 Human sec
27	1657	46.0	322 6 ABO14900	Abo14900 Human sec
28	1657	46.0	322 6 ABU81148	Abu81148 Human sec
29	1657	46.0	322 6 ABO53263	Abo53263 Novel hum
30	1657	46.0	322 6 ABU98265	Abu98265 Novel hum
31	1657	46.0	322 6 ABU89270	Abu89270 Novel hum
32	1657	46.0	322 6 ABU82477	Abu82477 Novel hum
33	1657	46.0	322 6 ABU69657	Abu69657 Novel hum
34	1657	46.0	322 6 ABU96441	Abu96441 Human PRO
35	1657	46.0	322 6 ABU72111	Abu72111 Human PRO
36	1657	46.0	322 6 ABO14839	Abo14839 Human sec
37	1657	46.0	322 6 ADB29406	Adb29406 Human sec
38	1657	46.0	322 6 ADB17063	Adb17063 Human tra
39	1657	46.0	322 6 ABO44241	Abo44241 Human sec
40	1657	46.0	322 6 ADA18262	Ada18262 Human sec
41	1657	46.0	322 6 ABO32791	Abo32791 Human sec
42	1657	46.0	322 6 ADA19868	Ada19868 Novel hum
43	1657	46.0	322 6 ADB17251	Adb17251 Human tra
44	1657	46.0	322 6 ABO34851	Abo34851 Human PRO
45	1657	46.0	322 6 ADA16237	Ada16237 Human sec

ALIGNMENTS

RESULT 1
ABB11979
ID ABB11979 standard; peptide; 344 AA.
XX
AC ABB11979;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human PRO263 homologue, SEQ ID NO:2349.
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnery; antiulcer.

OS	Homo sapiens.
XX	
PN	WO200157188-A2.
XX	
PD	09-AUG-2001.
XX	
PF	05-FEB-2001; 2001WO-US003800.
XX	
PR	03-FEB-2000; 2000US-00496914.
PR	27-APR-2000; 2000US-00560875.

XX (HYSE-) HYSEQ INC.
PA
XX
PI Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-457740/49.
DR N-PSDB; ABA09223.
DR
XX
PT Human proteins and DNA encoding sequences useful for preventing, treating
PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
PT and cancer.
XX
PS Claim 20; Page 291; 1963pp; English.
PS
XX
CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a novel human
CC polypeptide of the invention
XX
SQ Sequence 344 AA;

Alignment Scores:
Pred. No.: 3.95e-175 Length: 344
Score: 1772.00 Matches: 343
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.71% Mismatches: 0
Query Match: 49.17% Indels: 0
DB: 4 Gaps: 0

US-10-079-111-2 (1-2029) x ABB11979 (1-344)

QY 117 GCATCTGCTCTCATATCACCAGTGGCCATCTGAGGTGTTCCCTGGCTCTGAAGGGTA 176
Db 1 AlaSerAlaSerHisIleThrSerGlyHisLeuArgCysPheProGlySerGluGlyVal 20

QY 177 GGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGG 236
Db 21 GlyThrMetAlaArgCysPheSerLeuValLeuLeuThrSerIleTyrThrArg 40

QY 237 CTCCTGGTCCAAAGGCTCTTTGGGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATT 296

Db 41 LeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIle 60
QY 297 ATGGGGATCACCCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAGAAAGCTAAG 356
Db 61 MetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLys 80
QY 357 GAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCCGCAAGGACCAAGTTGAAAACAGCCTTG 416
Db 81 GluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeu 100
QY 417 AAAGCTAGCTTTGAAACTTGACGCTATGGCTGGGTGGAGATGGATTCGTGGTCACTCTCT 476
Db 101 LysAlaSerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSer 120
QY 477 AGGATTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTCTCTGATTTGGAAGGTT 536
Db 121 ArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValIleThrLysVal 140
QY 537 CCAGTGAGCCGACAGTTTGCAGCCTATTGTGTACAACTCATCTGATACTGGACTAACTCG 596
Db 141 ProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSer 160
QY 597 TGCATTCCAGAAAATTATCACCAACCACCAAGATCCCATATTCAACACTCAAACTGCAACAAA 656
Db 161 CysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGln 180
QY 657 ACAACAGAAATTTATTGTTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTTACATA 716
Db 181 ThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIle 200
QY 717 CCTGCCCCCTACTACTCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAAA 776
Db 201 ProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLys 220
QY 777 TTGATTTGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCA 836
Db 221 LeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPro 240
QY 837 TTTGTTGAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGAGGTTGTCCTCCACG 896
Db 241 PheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThr 260
QY 897 GCTCTGCTAGTGTGCTCTCCTCTCTCTTTTGGTGTGCTGAGTGGTCTTGGATTCTTGCTAT 956
Db 261 AlaLeuLeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyr 280
QY 957 GTCAAAAGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAATGATC 1016
Db 281 ValLysArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIle 300
QY 1017 GAAACCAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAAG 1076
Db 301 GluThrLysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLys 320
QY 1077 AAAACTGATAAAACCCAGAGAGTCCAGAGTCCAGCAAACTACCGTGGATGCCTG 1136
Db 321 LysThrAspLysAsnProGluGluSerLysSerProSerLysThrThrMetArgCysLeu 340
QY 1137 GAAGCTGAAGTT 1148
Db 341 GluAlaGluVal 344

RESULT 2
AAV13379
ID AAY13379 standard; protein; 322 AA.
XX
AC AAV13379;
XX
DT 25-JUN-1999 (first entry)
XX
DE Amino acid sequence of protein PRO263.
XX

KW Secreted protein; transmembrane protein; human; enterocolitis;
KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
KW congenital microvillus atrophy; skin disease; cell growth;
KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;
KW dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;
KW wound healing; tissue repair.

XX Homo sapiens.

PN WO9914328-A2.

XX 25-MAR-1999.

PF 16-SEP-1998; 98WO-US019330.

XX 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059115P.

PR 17-SEP-1997; 97US-0059117P.

PR 17-SEP-1997; 97US-0059119P.

PR 17-SEP-1997; 97US-0059121P.

PR 17-SEP-1997; 97US-0059122P.

PR 17-SEP-1997; 97US-0059184P.

PR 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 15-OCT-1997; 97US-0062125P.

PR 17-OCT-1997; 97US-0062285P.

PR 17-OCT-1997; 97US-0062287P.

PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0062814P.

PR 24-OCT-1997; 97US-0062816P.

PR 24-OCT-1997; 97US-0063045P.

PR 24-OCT-1997; 97US-0063120P.

PR 24-OCT-1997; 97US-0063121P.

PR 24-OCT-1997; 97US-0063127P.

PR 24-OCT-1997; 97US-0063128P.

PR 27-OCT-1997; 97US-0063327P.

PR 27-OCT-1997; 97US-0063329P.

PR 28-OCT-1997; 97US-0063541P.

PR 28-OCT-1997; 97US-0063542P.

PR 28-OCT-1997; 97US-0063544P.

PR 28-OCT-1997; 97US-0063549P.

PR 28-OCT-1997; 97US-0063550P.

PR 28-OCT-1997; 97US-0063564P.

PR 29-OCT-1997; 97US-0063435P.

PR 29-OCT-1997; 97US-0063704P.

PR 29-OCT-1997; 97US-0063732P.

PR 29-OCT-1997; 97US-0063734P.

PR 29-OCT-1997; 97US-0063735P.

PR 29-OCT-1997; 97US-0063738P.

PR 29-OCT-1997; 97US-0064215P.

PR 31-OCT-1997; 97US-0063870P.

PR 31-OCT-1997; 97US-0064103P.

PR 03-NOV-1997; 97US-0064248P.

PR 07-NOV-1997; 97US-0064809P.

PR 12-NOV-1997; 97US-0065186P.

PR 17-NOV-1997; 97US-0065846P.

PR 18-NOV-1997; 97US-0065693P.

PR 21-NOV-1997; 97US-0066120P.

PR 21-NOV-1997; 97US-0066364P.

PR 24-NOV-1997; 97US-0066453P.

PR 24-NOV-1997; 97US-0066466P.

PR 24-NOV-1997; 97US-0066511P.

PR 24-NOV-1997; 97US-0066770P.

PR 24-NOV-1997; 97US-0066772P.

PR 25-NOV-1997; 97US-0066840P.

XX (GETH) GENENTECH INC.

PA Wood WI, Gurney AL, Goddard A, Pennica D, Chen J, Yuan J;

XX WPI; 1999-229533/19.

DR N-PSDB; AAX52250.

XX

PT New isolated human genes and polypeptides used in, e.g. treatment of gastrointestinal ulceration.

PT gastrointestinal ulceration.

XX Claim 12; Fig 74; 320pp; English.

PS AAY13344-403 represent secreted and transmembrane human proteins. The

CC cDNA sequences are obtained from cDNA libraries, prepared from fetal

CC lung, fetal kidney, fetal brain, fetal liver and fetal retina. The

CC encoded polypeptides have specific uses based on their homology to known

CC polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated

CC with the preservation and maintenance of gastrointestinal mucosa and the

CC repair of acute and chronic mucosal lesions (e.g. enterocolitis,

CC Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital

CC microvillus atrophy), skin diseases associated with abnormal keratinocyte

CC differentiation (e.g. psoriasis, epithelial cancers such as lung squamous

CC cell carcinoma of the vulva and gliomas), potent effects on cell growth

CC and development, diseases related to growth or survival of nerve cells

CC including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or

CC cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal

CC scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may

CC be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can

CC be used as an anti-thrombotic agent; PRO287 polypeptides and portions may

CC have therapeutic applications in wound healing and tissue repair; PRO317

CC can be used for treating problems of the kidney, uterus, endometrium,

CC blood vessels, or related tissue, e.g. in the heart of genital tract

XX

SQ Sequence 322 AA;

Alignment Scores:

Pred. No.: 3.74e-163 Length: 322

Score: 1657.00 Matches: 322

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 45.98% Indels: 0

DB: 2 Gaps: 0

US-10-079-111-2 (1-2029) x AAY13379 (1-322)

QY 183 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCATTCTCCATCTGGACCACGAGGCTCCTG 242

Db 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20

QY 243 GTCCAAGGCTCTTTGCGTGCAGAGAGCTTTCCATCCAGGTGTCATGCAGAAATATGGGG 302

Db 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

QY 303 ATCACCCCTTGTGAGCAAAAAGCGCAACCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 362

Db 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60

QY 363 TGTAGGCTGTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 422

Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

QY 423 AGCTTTGAAACTTGACGCTATGGCTGGTGGGTGGGTGCTCTGATTGGAGGTTCCAGT 482

Db 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

QY 483 AGCCCAAACCCCAAGTGTGGAAAAAATGGGTGGGTGCTCTGATTGGAGGTTCCAGTG 542

Db 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

QY 543 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATCTTGGACTAACTCGTGCATT 602

Db 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

QY 603 CCAGAAATTATCACCAAAAGATCCCATATTCAACTCAAACTGCAACACAAACAACA 662

Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

QY 663 GAATTTATTGTCAGTGACAGTAGCTACTCTCGGTGGCATCCCCTTACTCTACAATACCTGCC 722

Db

QY 603 CCAGAAATTATCACCAAAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 662
Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
QY 663 GAAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAAATACCTGCC 722
Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
QY 723 CCTACTACTCCTCCTCGTCCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT 782
Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
QY 783 TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCAATTTGTT 842
Db 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
QY 843 GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCAACGGCTCTG 902
Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
QY 903 CTAGTGCTTGCTCTCCTCTCTTTGGTGCTGCAGCTGGTCTTTGGATTTTGCTATGTCAAA 962
Db 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
QY 963 AGGTATGTGAAGGCCTTCCCTTTTACAAAACAAGAAATCAGCAGAGGAAATGATCGAAACC 1022
Db 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
QY 1023 AAAGTAGTAAAGGAGGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACT 1082
Db 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
QY 1083 GATAAAAACCCAGAGAGTCCAAAGAGTCCAAAGCAAAACTACCGTGCGATGCCCTGGAAGCT 1142
Db 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
QY 1143 GAAGTT 1148
Db 321 GluVal 322
RESULT 4
ADC78521
ID ADC78521 standard; protein; 322 AA.
XX AC ADC78521;
XX 01-JAN-2004 (first entry)
XX DE Human PRO263 protein.
XX antiinflammatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;
KW nootropic; neuroprotective; vasotropic; chemotactic; angiogenic;
KW neurotrophic; osteopathic; antiasthmatic; antiarthritic; antirheumatic;
KW antiarteriosclerotic; cardiant; antidiabetic; cerebroprotective;
KW thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;
KW gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;
KW Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;
KW nerve repair; thrombosis; bone; cartilage formation; angiogenesis;
KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;
KW atherosclerosis; cardiac injury; infertility; premature aging; AIDS;
KW diabetes; stroke; gene therapy; transgenic; PRO; human.
XX OS Homo sapiens.
XX WO200015796-A2.
XX PD 23-MAR-2000.
XX PF 15-SEP-1999; 99WO-US021090.
XX PR 16-SEP-1998; 98WO-US019330.
XX

PA (GETH) GENENTECH INC.
XX Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;
PI Yuan J;
XX WPI; 2000-271434/23.
DR N-PSDB; ADC78520.
XX Novel nucleic acids encoding secreted and transmembrane polypeptides with
PT homology, e.g. to growth and cancer-associated antigens.
XX Claim 12; SEQ ID NO 201; 355pp; English.
XX The invention relates to a novel nucleic acid encoding a PRO polypeptide.
CC The polypeptides and polynucleotides of the invention may be useful as
CC research tools and as therapeutics for treating enterocolitis, Zollinger-
CC Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,
CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies, bone and/or
CC scarring and wound healing, nerve repair, thrombosis, bone and/or
CC cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple
CC sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,
CC infertility, premature aging, AIDS, diabetes complications and stroke.
CC The molecules may also be utilised during gene therapy procedures and
CC transgenic animal production. The current sequence is that of the human
CC PRO protein of the invention.
XX SQ Sequence 322 AA;
Alignment Scores:
Pred. No.: 3.74e-163 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0
DB: 3 Gaps: 0
US-10-079-111-2 (1-2029) x ADC78521 (1-322)
QY 183 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 242
Db 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
QY 243 GTCCAAGGCTCTTTGGCTGCAGAAGAGCTTTCATCCAGGTGTCATGCAGAATTATGGGG 302
Db 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
QY 303 ATCACCCCTTGTGAGCAAAAAGCGGAACCCAGCAGCTGAATTTACAGAAGCTAAGAGGCC 362
Db 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
QY 363 TGTAGGCTGCTGGGACTAAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 422
Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
QY 423 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGGTGCATCTCTAGGATT 482
Db 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
QY 483 AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTTTGGAAGGTTCCAGTG 542
Db 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
QY 543 AGCCGACAGTTTGAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCAATT 602
Db 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
QY 603 CCAGAAATTATCACCAAAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 662
Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
QY 663 GAAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAAATACCTGCC 722
Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

QY 723 CCTACTACTCCTCCTGCTCCAGCTTCACCTTCACTTCCACGGAGAAAAAATTGATT 782
Db |||||||
181 ProThrThrProProAlaProAlaSerThrSerIleProArgLysLysLeuIle 200

QY 783 TGTGTACAGAAAGTTTTTATGGAACCTAGCACCATGTCTACAGAAACTGAACCATTTGTT 842
Db |||||||
201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220

QY 843 GAAATAAAGCAGCATTCAAGAATGAAGCTGTGGTGGTTTGGAGGTGTCCCCACGGCTCTG 902
Db |||||||
221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240

QY 903 CTAGTGCTTGCTCCTCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAA 962
Db |||||||
241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260

QY 963 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAAGGAAATGATCGAAACC 1022
Db |||||||
261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280

QY 1023 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCTAATGAGGAATCAAGAAGAACT 1082
Db |||||||
281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300

QY 1083 GATAAAACCCAGAAAGAGTCCAAAGAGTCCAAGAGCAAAACTACCGTGCATGCCTGGAAGCT 1142
Db |||||||
301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320

QY 1143 GAAGTT 1148
Db ||||||
321 GluVal 322

RESULT 5
AAB80247

ID AAB80247 standard; protein; 322 AA.

XX AAB80247;

DT 24-APR-2001 (first entry)

XX Human PRO263 protein.

KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW ischaemia; inflammation.

XX Homo sapiens.

OS WO200104311-A1.

PD 18-JAN-2001.

XX 22-FEB-2000; 2000WO-US004414.

PR 07-JUL-1999; 99US-0143048P.

PR 26-JUL-1999; 99US-0145698P.

PR 28-JUL-1999; 99US-0146222P.

PR 08-SEP-1999; 99WO-US020594.

PR 13-SEP-1999; 99WO-US020944.

PR 15-SEP-1999; 99WO-US021090.

PR 15-SEP-1999; 99WO-US021547.

PR 05-OCT-1999; 99WO-US023089.

PR 29-NOV-1999; 99WO-US028214.

PR 30-NOV-1999; 99WO-US028313.

PR 02-DEC-1999; 99WO-US028564.

PR 02-DEC-1999; 99WO-US028565.

PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.

PR 20-DEC-1999; 99WO-US030999.

PR 05-JAN-2000; 2000WO-US000219.
XX (GETH) GENENTECH INC.

PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tunas D;
PI Williams PM, Wood WI;
XX WPI; 2001-081051/09.
DR N-PSDB; AAF72408.

XX Sixty one nucleic acids encoding PRO polypeptides which are useful in the
PT treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
PT cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
PT disease).

XX Claim 1; Fig 74; 393pp; English.

XX The present sequence is one of sixty one novel secreted and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful for treating skin
CC diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
CC gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
CC diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
CC cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
CC ischaemias such as coronary ischaemia, atherosclerosis), inflammatory
CC disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
CC infertility, AIDS and diabetes and retinal disorders such as retinitis
CC pigmentosum. The PRO nucleic acids have applications in molecular
CC biology, including use as hybridization probes, and in chromosome and
CC gene mapping

XX Sequence 322 AA;

Alignment Scores:

Pred. No.: 3.74e-163 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0
DB: 4 Gaps: 0

US-10-079-111-2 (1-2029) x AAB80247 (1-322)

QY 183 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 242
Db |||||||
1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu 20

QY 243 GTCCAAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG 302
Db |||||||
21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

QY 303 ATCACCCTTGTGAGCAAAAAGGCGAAACCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 362
Db |||||||
41 IleThrLeuValSerLysLysAlaAsnGlnLysLeuAsnPheThrGluAlaLysGluAla 60

QY 363 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTCAGACCTTGAAAGCT 422
Db |||||||
61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

QY 423 AGCTTTGAAACTTGACGCTATGGCTGGGTTGGAGATGGATTCGTGGTTCATCTCTAGGATT 482
Db |||||||
81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

QY 483 AGCCCAAACCCCAAGTGTGGGAAAAAATGGGGTGGTGTCTCTGATTTTGAAGGTTCCAGTG 542
Db |||||||
101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

QY 543 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACCTGGACTTAACCTCGTGCATT 602
Db |||||||
121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrThrTrpThrAsnSerCysIle 140

QY 603 CCAGAAATTATCACCAAAAGATCCCATATTCACACTCAAACCTGCAACACAAAACA 662
Db 141 ProGluIleIleThrThrLysAspProIlePheasnThrGlnThrAlaThrGlnThrThr 160
QY 663 GAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 722
Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
QY 723 CCTACTACTCTCTGCTCCAGCTTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT 782
Db 181 ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
QY 783 TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCAATTGTT 842
Db 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
QY 843 GAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 902
Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
QY 903 CTAGTGCTTGCTCTCCTCTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAA 962
Db 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
QY 963 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGATCAGCAGAAAGGAAATGATCGAAACC 1022
Db 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
QY 1023 AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCTAATGAGGAATCAAGAAAACT 1082
Db 281 LysValValLysGluGluLysAlaAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
QY 1083 GATAAAAACCCAGAGTCCAAAGAGTCCAAAGCAAACTACCGTACCGTGGAGAGCT 1142
Db 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
QY 1143 GAAGTT 1148
Db 321 GluVal 322
RESULT 6
AAB87528
ID AAB87528 standard; protein; 322 AA.
XX
AC AAB87528;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human PRO263.
XX
KW Human; PRO protein; mapping.
XX
OS Homo sapiens.
XX
PN WO200116318-A2.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US023328.
XX
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 07-DEC-1999; 99US-0169495P.
PR 09-DEC-1999; 99US-0170262P.
PR 11-JAN-2000; 2000US-0175481P.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 03-MAR-2000; 2000US-0187202P.
PR 21-MAR-2000; 2000US-0191007P.
PR 30-MAR-2000; 2000WO-US008439.
PR 25-APR-2000; 2000US-0199397P.

PR 22-MAY-2000; 2000WO-US014042.
PR 05-JUN-2000; 2000US-0209832P.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2001-183260/18.
DR N-PSDB; AAF92060.
XX
PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT biology, including use as hybridization probes, and in chromosome and
PT gene mapping.
XX
PS Claim 12; Fig 6; 278pp; English.
XX
CC The present sequence is a human PRO polypeptide (secreted and
CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC anti-PRO antibodies are useful for preparation of a medicament useful in
CC the treatment of a condition which is responsive to the PRO protein,
CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC employed as molecular weight markers for protein electrophoresis. The PRO
CC coding sequence has applications in molecular biology, including use as
CC hybridisation probes, and in chromosome and gene mapping
XX
SQ Sequence 322 AA;
Alignment Scores:
Pred. NO.: 3.74e-163 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0
DB: 4 Gaps: 0
US-10-079-111-2 (1-2029) x AAB87528 (1-322)
QY 183 ATGGCCAGGTGCTTCAGCCTGGTGTGTTCTCCTTCCATCTGGACCACGAGGCTCCTG 242
Db 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
QY 243 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGATTATGGGG 302
Db 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
QY 303 ATCACCCCTGTGAGCAAAAAGCGCAACACGACGCTGAATTTACAGAAAGCTAAGAGGCC 362
Db 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
QY 363 TGTAGGCTGTGGGACTAAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 422
Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
QY 423 AGCTTTGAAACTTCAGCTATGGCTGGTGGAGATGGATTCTGGTCACTCTAGGATT 482
Db 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
QY 483 AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTCTGATTTTGGAAGGTTCCAGTG 542
Db 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
QY 543 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACCTTGGACTAATCCTGCATT 602
Db 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
QY 603 CCAGAAATTATCACCAAAAGATCCCATATTCAACTATTCAAACTCAAACACAAACAACA 662
Db 141 ProGluIleIleThrThrLysAspProIlePheasnThrGlnThrAlaThrGlnThrThr 160
QY 663 GAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 722
Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

QY 723 CCTACTACTCCTCCTGCTCCAGCTTCACCTTCTATTCACCGAGAAATAATTGATT 782
Db 181 ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
QY 783 TGTGTACAGAAAGTTTATGGAACTAGCACCATTGTCTACAGAACTGAACCATTTGTT 842
Db 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
QY 843 GAAATAAAGCAGCATTCAAGAATGAAGCTGGCTGGGTTTGGAGGTGTCGCCACGGCTCTG 902
Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
QY 903 CTAGTGCTTGCTCCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGTATGTCAA 962
Db 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
QY 963 AGGTATGTGAAGCCCTTCCCTTTTACAACAAGAATCAGCAGAGGAAGAAATGATCGAAACC 1022
Db 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
QY 1023 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAAACT 1082
Db 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
QY 1083 GATAAAACCAGAAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGGATGCCTGGAAAGCT 1142
Db 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
QY 1143 GAAGTT 1148
Db 321 GluVal 322

RESULT 7
AAB88391
ID AAB88391 standard; protein; 322 AA.
XX
AC AAB88391;
XX
DT 23-MAY-2001 (first entry)
XX
DE Human membrane or secretory protein clone PSEC0135.
XX
KW Human; secretory protein; membrane protein; vaccine; gene therapy;
KW rheumatoid arthritis; diabetes.
XX
OS Homo sapiens.
XX
PN EP1067182-A2.
XX
PD 10-JAN-2001.
XX
PF 07-JUL-2000; 2000EP-00114090.
XX
PR 08-JUL-1999; 99JP-00194179.
PR 11-JAN-2000; 2000JP-00118775.
PR 02-MAY-2000; 2000JP-00183766.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
XX WPI; 2001-093989/11.
DR N-PSDB; AAF93818.
XX
PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT gene therapy or as candidate target molecules in drug development.
XX
PS Claim 1; SEQ ID NO 150; 609pp + Sequence Listing; English.
XX
CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC which encode human secretory or membrane proteins represented by AAB88317
CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and

CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
CC invention. The invention also includes methods for the production of
CC antibodies directed against the proteins, and cDNA sequences, which can
CC be used in vaccines. The polynucleotide sequences can be used in gene
CC therapy. The polynucleotide sequences and the proteins they encode may be
CC used in the prevention, treatment and diagnosis of diseases associated
CC with inappropriate secretory protein/membrane protein expression. The
CC nucleic acids and complementary sequences may also be used as DNA probes
CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
CC and quantitate the presence of similar nucleic acid sequences in samples.
CC They may also be used to study the expression and function of secretory
CC proteins/membrane polypeptides and their role in metabolism. The
CC polypeptides may be used as antigens in the production of antibodies
CC against them and in assays to identify modulators (agonists and
CC antagonists) of expression and activity. The antibodies and antagonists
CC may also be used as therapeutic agents to down regulate expression and
CC activity. The antibodies may also be used as diagnostic agents for
CC detecting the presence of the polypeptides in samples (e.g. by enzyme
CC linked immunosorbant assay (ELISA). Examples of diseases which may be
CC treated include rheumatoid arthritis and diabetes

XX
SQ Sequence 322 AA;

Alignment Scores:
Pred. No.: 3.74e-163 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0
DB: 4 Gaps: 0

US-10-079-111-2 (1-2029) x AAB88391 (1-322)

QY 183 ATGGCCAGGTGCTTCAGCCTGGTGTCTCTCATTCCATCTGGACCAGAGGCTCCTG 242
Db 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 20
QY 243 GTCCAGGCTCTTTGCGTGCAGAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGG 302
Db 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
QY 303 ATCACCTTGTGAGCAAAAGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 362
Db 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
QY 363 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAAACAGCCTTGAAAGCT 422
Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
QY 423 AGCTTTGAAACTTGCAGCTATGCTGGGTTGGAGATGGATTCGTGGTCATCTCTAGGATT 482
Db 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
QY 483 AGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCCTGATTTGGAAGGTTCCAGTG 542
Db 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
QY 543 AGCCGACAGTTTGCAGCCTATGTTTACAACCTCATCTGATCTGACTTAACCTCGTGCATT 602
Db 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
QY 603 CCAGAAATATTATCACCAACAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 662
Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
QY 663 GAATTTATTGTGACGTACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 722
Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
QY 723 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTCTATTCACGGAGAAAAAATTGATT 782
Db 181 ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

QY 783 TGTGTACAGAAAGTTTTATGGAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 842
Db ||||||| CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
QY 843 GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 902
Db ||||||| GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
QY 903 CTAGTGTCTCTCCTCTCTCTTTGGTGCTGCAGCTGGTCTTGATTTTGCTATGTCAA 962
Db ||||||| LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
QY 963 AGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAAATGATCGAAACC 1022
Db ||||||| ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
QY 1023 AAAGTAGTAAAGGAGGAGGAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAACT 1082
Db ||||||| LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
QY 1083 GATAAAACCCAGAAGAGTCCAGAGTCCAAAGCAAACTACCTGCGATGCCCTGGAAGCT 1142
Db ||||||| AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
QY 1143 GAAAGTT 1148
Db ||||||| 321 GluVal 322
RESULT 8
ID ABG95853 standard; protein; 322 AA.
XX
AC ABG95853;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human secreted/transmembrane protein PRO263.
XX
KW Human; secreted protein; transmembrane protein; antirheumatic;
KW antiarthritic; osteopathic; sports-related joint problem;
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN US2002119130-A1.
XX
PD 29-AUG-2002.
XX
PF 06-DEC-2001; 2001US-00006867.
XX
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0064215P.
PR 22-APR-1998; 98US-0082797P.
PR 29-APR-1998; 98US-0083495P.
PR 15-MAY-1998; 98US-0085579P.
PR 02-JUN-1998; 98US-0087759P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 11-JUN-1998; 98US-0088863P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089653P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 24-JUN-1998; 98US-0090444P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090696P.

PR 26-JUN-1998; 98US-0090862P.
PR 02-JUL-1998; 98US-0091628P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097979P.
PR 01-SEP-1998; 98US-0098749P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100930P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101475P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101916P.
PR 30-SEP-1998; 98US-0102570P.
PR 06-OCT-1998; 98US-0103449P.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021194.
PR 22-DEC-1999; 99WO-US030720.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032378.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2002-731348/79.
DR N-PSDB; ABS74380.
XX
PT New isolated secreted and transmembrane PRO polypeptide useful for
PT modulating biological activity of a cell, or for treating sports-related
PT joint problems, osteoarthritis or rheumatoid arthritis.
XX
PS Claim 20; Fig 6; 399pp; English.
XX
CC The invention relates to an isolated secreted and transmembrane PRO
CC polypeptide having 80 % sequence identity to a sequence appearing as
CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
CC extracellular domain of the proteins with their associated signal peptide

CC or lacking its associated signal peptide. Also included are the nucleic
CC acids encoding the proteins, vectors, host cells, fusion proteins and
CC antibodies which specifically bind to the proteins. The proteins are
CC useful for detecting a polypeptide designated as A, B, C or D in a sample
CC suspected of containing an A, B, C or D polypeptide, by contacting the
CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
CC conjugate in the sample, where the formation of the conjugate is
CC indicative of the presence of an A, B, C or D polypeptide in the sample,
CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
CC H or I polypeptide is labeled with a detectable label or is attached to a
CC solid support. The proteins are useful for linking a bioactive molecule
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC or I, or antibodies against them are useful for modulating a biological
CC activity of a cell expressing a polypeptide designated as A, B, C or D or
CC E, F, G, H, or I. The cell is killed. The proteins are useful for
CC identifying agonists or antagonists, for the preparation of a medicament
CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic useful reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence represents a novel secreted or transmembrane protein of the
CC invention

XX
SQ Sequence 322 AA;

Alignment Scores:
Pred. No.: 3.74e-163 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0
DB: 5 Gaps: 0

US-10-079-111-2 (1-2029) x ABG95853 (1-322)

QY	183	ATGCCAGGTGCTTCAGCCTGGTGTGTTGCTCTCACTTCCATCTGGACCACGAGGCTCCTG	242
Db	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu	20
QY	243	GTCCAAGGCTCTTTGCGTGCAGAAAGCTTTCCATCCAGGTGTATGCAGAATTATGGGG	302
Db	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
QY	303	ATCACCCCTTGAGCAAAAAGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAAGGAGCC	362
Db	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
QY	363	TGTAGGCTGCTGGACTAAGTTTGGCCGSCAAGGACCAAGTTGAAACAGCCTGAAAGCT	422
Db	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
QY	423	AGCTTTGAAACTTCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCACTCTAGGATT	482
Db	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
QY	483	AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCCTGATTGTGGAAGTTCCAGTG	542
Db	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120

QY	543	AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCAATT	602
Db	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
QY	603	CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA	662
Db	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
QY	663	GAATTTATTGTTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTACAATACCTGCC	722
Db	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
QY	723	CCTACTACTCTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	782
Db	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
QY	783	TGTGTACAGAAAGTTTTTATGGAACTAGCACCATGTCTACAGAACTGAACCATTTGTT	842
Db	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal	220
QY	843	GAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG	902
Db	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
QY	903	CTAGTGTGCTCTCTCTTCTTTTGGTGTGTCAGCTGGTCTTGGATTGCTATGTCAAA	962
Db	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
QY	963	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAATGATCGAAACC	1022
Db	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
QY	1023	AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCTAATGAGGAATCAAGAAACT	1082
Db	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
QY	1083	GATAAAACCCAGAGAGTCCAAGAGTCCAAGCTCAAGCAAACTACCGTGCATCGCTGGAAGCT	1142
Db	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
QY	1143	GAAGTT 1148	
Db	321	GluVal 322	
RESULT 9			
ABB84832			
ID	ABB84832	standard; protein; 322 AA.	
XX	AC	ABB84832;	
XX	DT	16-MAY-2002 (first entry)	
XX	DE	Human PRO263 protein sequence SEQ ID NO:32.	
XX	KW	Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;	
KW	KW	vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;	
KW	KW	gene therapy; cardiovascular disorder; endothelial disorder; cancer;	
KW	KW	angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;	
KW	KW	age-related macular degeneration; arterial restenosis; angina;	
KW	KW	rheumatoid arthritis; myocardial infarction; thrombophlebitis;	
KW	XX	lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;	
OS	XX	wound healing; chromosome mapping; gene mapping.	
XX	PN	Homo sapiens.	
XX	XX	WO200200690-A2.	
PD	XX	03-JAN-2002.	
XX	PF	20-JUN-2001; 2001WO-US019692.	
XX	PR	23-JUN-2000; 2000US-0213637P.	

PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
XX WPI; 2002-090516/12.
DR N-PSDB; ABL88087.
DR
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 11; Fig 32; 565pp; English.
XX
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiac, cytostatic,
CC antiangiogenic, hypotensive, vulnery and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The PRO polynucleotides have applications in molecular biology,
CC including use as hybridisation probes, and in chromosome and gene
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC exemplification of the present invention
XX
SQ Sequence 322 AA;

Alignment Scores:
Pred. No.: 3.74e-163 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0

DB: 5 Gaps: 0
US-10-079-111-2 (1-2029) x ABB84832 (1-322)
QY 183 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 242
|||||
Db 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
243 GTCCAAGGCTCTTTCGCTGCAGAAAGAGCTTTCATCCAGGTGTCATGCAGAATTATGGGG 302
|||||
Db 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
303 ATCACCCCTTGTGAGCAAAAAGCGGAACCCAGCAGCTGAATTTACAGAAGCTAAGAGGCC 362
|||||
Db 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
363 TGTAGGCTGTGGGACTAAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGACT 422
|||||
Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
423 AGCTTTGAAACTTGCAGCTATGGCTGGTGGTGGAGATGGATTGCTGGTCATCTCTAGGATT 482
|||||
Db 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
483 AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTGATTGGGAAGGTTCCAGTG 542
|||||
Db 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
543 AGCCGACAGTTTGACGCTATTGTTACAACCTCATCTGATACTTGGACTAATCGTGCATT 602
|||||
Db 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
603 CCAGAAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 662
|||||
Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
663 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGATCCCTTACTCTACAATACCTGCC 722
|||||
Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
723 CCTACTACTCCTCCTGCTCCAGCTTCCACCTTCTATTCCACGGAGAAAAAATTGATT 782
|||||
Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
783 TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 842
|||||
Db 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
843 GAAAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGAGGTGTCCCCACGGCTCTG 902
|||||
Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
903 CTAGTGCTTGCTCCTCCTTCTTTTGGTGTGCAGCTGGTCTTTGGATTTTGTATGTCAAA 962
Db 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
963 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAAATGATCGAAACC 1022
Db 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
1023 AAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAAC 1082
Db 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
1083 GATAAAACCCAGAAAGAGTCCAAGAGTCCAAGCAAAACTACCGTCGATGCTGGAGGCT 1142
Db 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
1143 GAAGTT 1148
Db 321 GluVal 322
RESULT 10

ABB95438
ID ABB95438 standard; protein; 322 AA.
XX
AC ABB95438;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related protein PRO263 SEQ ID NO: 32.
XX
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
KW antiarteriosclerotic.
XX
OS Homo sapiens.
XX
PN WO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US021735.
XX
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
XX
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.

PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-171999/22.
DR N-PSDB; ABL95576.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 11; Fig 32; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including a
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention
XX
SQ Sequence 322 AA;

Alignment Scores:
Pred. No.: 3.74e-163 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0
DB: 5 Gaps: 0

US-10-079-111-2 (1-2029) x ABB95438 (1-322)

QY 183 ATGGCCAGGTGCTTCAGCCTGGTGTCTCTCATTCCATCTGGACCAGGCTCCTG 242
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||
1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 20

QY 243 GTCCAGGCTCTTTGCGTGCAGAAAGGCAACAGCTTTCCATCCAGGTGTCAGAAATTATGGGG 302
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||
21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

QY 303 ATCACCTTGTGAGCAAAAAGGCAACAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 362
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||
41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60

QY 363 TGTAGGCTGCTGGACTAAGTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 422
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||
61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

QY 423 AGCTTTGAAACTTGACGCTATGGCTGGGTTGGAGATGGATTCTGTGCTCATCTTAGGATT 482
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||
81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

QY 483 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTTGGGTGCTCTGATTGGAGGTTCCAGTG 542
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||
101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

QY 543 AGCCGACAGTTTGCAGCCTATTGTTACAACATCATCTGATACTTGGACTAAGTTCGTGCATT 602
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||
121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

QY 603 CCAGAAATTATCACCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 662
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||
141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

QY 663 GAATTATTGTGTCAGTGACGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 722
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||
161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

QY 723 CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 782

Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
QY 783 TGTGTCACAGAAAGTTTATGGAAGCTAGCACCATGTCTACAGAAACTGAACATTTGTT 842
Db 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
QY 843 GAAATAAAGCAGCAATCAAGAATGAAGCTGCTGGGTTTGAGGTGTCCTCCACGGCTCTG 902
Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
QY 903 CTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAA 962
Db 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
QY 963 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGATCAGCAGAGGAATGATCGAAACC 1022
Db 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
QY 1023 AAAGTAGTAAAGGAGAGAGGCCAATGATAGCAACCTAATGAGGAATCAAGAAAAC 1082
Db 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
QY 1083 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTCCGATCGCTGGAAGCT 1142
Db 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
QY 1143 GAAGTT 1148
Db 321 GluVal 322
RESULT 11
ABU71625
ID ABU71625 standard; protein; 322 AA.
XX
AC ABU71625;
XX
DT 16-JUN-2003 (first entry)
XX
DE Human PRO polypeptide #36.
XX
KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
KW pathological disorder; cardiac insufficiency disorder; protein secretion;
KW pancreas; diabetes; gastrointestinal mucosa; mucosal lesion; psoriasis;
KW skin disease; keratinocyte differentiation; epithelial cancer; tumour;
KW lung squamous cell carcinoma; epidermoid carcinoma; vulva; glioma;
KW cytostatic; cardiant; endocrine; antidiabetic; gastrointestinal;
KW antiulcer; dermatological; vulnerary.
XX
OS Homo sapiens.
XX
PN US2002146709-A1.
XX
PD 10-OCT-2002.
XX
PF 18-JUL-2001; 2001US-00909088.
XX
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.

PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
PR WPI; 2003-328338/31.

DR N-PSDB; ACA59060.
XX
PT Isolated nucleic acid useful for e.g., treating pathological disorders
PT encodes a secreted or transmembrane protein.
XX
PS Claim 12; Fig 74; 473pp; English.
XX
CC The invention relates to human PRO polypeptides (secreted or
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC PRO polypeptides and polynucleotides can be used in treating pathological
CC disorders and tumours, in therapeutic treatment of cardiac insufficiency
CC disorders and in therapeutic treatment of disorders involving protein
CC secretion by the pancreas, including diabetes. They can also be used in
CC treating disorders associated with the preservation and maintenance of
CC gastrointestinal mucosa and the repair of acute and chronic mucosal
CC lesions, and skin diseases associated with abnormal keratinocyte
CC differentiation (e.g., psoriasis, epithelial cancers such as lung
CC squamous cell carcinoma, epidermoid carcinoma of the vulva and gliomas).
CC The sequences can be used as molecular markers for protein
CC electrophoresis purposes and can be utilised in protein-protein binding
CC assays, biochemical screening assays, immunoassays and cell-based assays.
CC This sequence represents a human PRO polypeptide of the invention
XX
SQ Sequence 322 AA;

Alignment Scores:
Pred. No.: 3.74e-163 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0
DB: 6 Gaps: 0

US-10-079-111-2 (1-2029) x ABU71625 (1-322)

QY 183 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 242
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 20

QY 243 GTCCAAGGCTCTTTGGTGCAGAGAGCTTCCATCCAGTGTCAATGAGGCTTAAGGGG 302
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

QY 303 ATCACCCTGTGAGCAAAAAGGCGAACAGCAGCTGAATTCACAGAAGCTAAGGAGGCC 362
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60

QY 363 TGTAGGCTGCTGGGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 422
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

QY 423 AGCTTTGAAACTTGCAGCTATGGCTGGTGGTGGAGATGGATTGGTGCATCTCTAGGATT 482
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgile 100

QY 483 AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCCTGATTTGGAAGGTTCCAGTG 542
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

QY 543 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTGGACTAATCGTGCAATT 602
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysile 140

QY 603 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 662
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

QY 663 GAATTTATTGTCAAGTACACTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 722
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

QY 723 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 782
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
QY 783 TGTGTCACAGAAAGTTTTTATGGAACTAGCACCATTGTCTACAGAAACTGAACCATTTGTT 842
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

QY 843 GAAATATAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 902
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240

QY 903 CTAGTGTCTGCTCTCCTCTTTTGGTGTCTGCAGCTGGTCTTGGATTTTGTATGTCAA 962
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260

QY 963 AGGTATGTGAAGGCCTTCCCTTTTACAAAACAAGATCAGCAGAGGAAATGATCGAAACC 1022
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280

QY 1023 AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCCTAATGAGGAATCAAAGAAACT 1082
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300

QY 1083 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGCATGCCTGGAAGCT 1142
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320

QY 1143 GAAGTT 1148
Db |||||||
321 GluVal 322

RESULT 12
ABU71480
ID ABU71480 standard; protein; 322 AA.
XX
AC ABU71480;
XX 10-JUN-2003 (first entry)
XX Human PRO polypeptide #36.
DE
XX
KW Human; secreted and transmembrane protein; PRO polypeptide; cancer;
KW Alzheimer's disease; ischaemia; cytostatic; nootropic; vasotropic;
KW neuroprotective.
XX Homo sapiens.
OS
XX US2002192659-A1.
FN
XX
PD 19-DEC-2002.
XX
PF 10-JUL-2001; 2001US-00902853.
XX
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.

PR 27-OCT-1997; 97US-00633329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-361832/34.
DR N-PSDB; ACA58457.
XX
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or
PT PRO1868, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.

XX
PS Claim 12; Fig 74; 474pp; English.
XX
CC The present invention relates to the isolation of novel human secreted
CC and transmembrane proteins (PRO polypeptides), and the polynucleotide
CC sequences encoding them. The polynucleotide sequences are useful in
CC molecular biology, as hybridisation probes, in chromosome and gene
CC mapping, in generating antisense RNA and DNA, and in gene therapy. The
CC polynucleotide sequences may also be used in preparing PRO polypeptides
CC by recombinant techniques, and in generating either transgenic animals or
CC knock-out animals which, in turn, are useful in the development and
CC screening of therapeutically useful reagents. The PRO polypeptides or
CC their antibodies are useful in preparing a medicament for treating a
CC condition responsive to the polypeptide or antibody, such as cancer,
CC Alzheimer's disease or ischaemia, and in various diagnostic assays.
CC ABU71445-ABU71505 represent human PRO polypeptides of the invention
XX
SQ Sequence 322 AA;

Alignment Scores:
Pred. No.: 3.74e-163 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0
DB: 6 Gaps: 0

US-10-079-111-2 (1-2029) x ABU71480 (1-322)

QY 183 ATGGCCAGGTCTTCAGCCTGGTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCTGTG 242
Db 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20

QY 243 GTCCAAGGCTCTTTGGTCGAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG 302
Db 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

QY 303 ATCACCCCTTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTACAGAAGCTAAGGAGGCC 362
Db 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60

QY 363 TGTAGGCTGTGGGACTAAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGACT 422
Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

QY 423 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCTGTCATCTCTAGGATT 482
Db 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

QY 483 AGCCCAAACCCCAAGTGTGGGAAAAAATGGGGTGGTGTCTCTGATTTTGGAAGGTTCCAGTG 542
Db 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

QY 543 AGCCGACAGTTTGACGCCTATTGTTACAACCTCATCTGATACCTTGGACTAATCGTGCAATT 602
Db 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

QY 603 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACCTGCACACAAACAACA 662
Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

QY 663 GAATTTATTGTCAGTACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 722
Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

QY 723 CCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 782
Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

QY 783 TGTGTCACAGAAGTTTTATGGAAACTAGACCATGTCTACAGAAACTGAACCATTTGTT 842
Db 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

CC the PRO nucleic acid, a host cell comprising the vector, producing a PRO
CC polypeptide (by culturing the host cell for the expression of the PRO
CC polypeptide, and recovering the PRO polypeptide from the cell culture),
CC an isolated PRO polypeptide (having at least 80% sequence identity to: (a)
CC a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino
CC acid sequence encoded by a nucleic acid molecule deposited with an ATCC
CC number (detailed in the specification); or (c) an extracellular domain of
CC a PRO polypeptide or to a PRO polypeptide lacking its associated signal
CC peptide), a chimaeric molecule comprising a PRO polypeptide of fused to a
CC heterologous amino acid sequence, an anti-PRO antibody, detecting a
CC linking a bioactive molecule to a sample suspected of containing the polypeptide,
CC modulating at least one biological activity of a cell expressing a PRO1868 and
CC or PRO1868. Nucleic acids which encode PRO can be used to generate either
CC transgenic animals or knock-out animals which may be used in the
CC development and screening of therapeutically useful reagents. The nucleic
CC acids may also be used in gene therapy, in chromosome identification, as
CC chromosome markers, or in generating probes. The PRO polypeptides are
CC useful as molecular markers for protein electrophoresis, and the isolated
CC nucleic acids may be used for recombinantly expressing those markers. The
CC PRO polypeptides and nucleic acids may also be used in tissue typing.
CC Anti-PRO antibodies are useful in diagnostic assays for PRO, and in
CC affinity purification of PRO from recombinant cell culture or natural
CC sources. The present sequence represents a PRO protein
XX
SQ Sequence 322 AA;

Alignment Scores:
Pred. No.: 3.74e-163 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0
DB: 6 Gaps: 0

US-10-079-111-2 (1-2029) x ABU71926 (1-322)

QY	183	ATGCCAGGTGCTTCAGCCCTGGTGTCTCTCATTCCATCTGGACCACGAGGCTCCTG	242
Db	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu	20
QY	243	GTCCAAGGCTCTTTGGCGTGCAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGG	302
Db	21	ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly	40
QY	303	ATCACCTTGTGAGCAAAAAGCGAACCAACGACGCTGAATTCACAGAAGCTAAGGAGCC	362
Db	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
QY	363	TGTAGGCTGTGGGACTAAGTTTGGCCGGCAAGGACCAAGTGAACAGCCTTGAAGCT	422
Db	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
QY	423	AGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGGATTGGTGCATCTCTAGGATT	482
Db	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
QY	483	AGCCCAACCCCAAGTGTGGGAAAAATGGGTGGTGCCTGATTGTGAAGGTTCCAGTG	542
Db	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
QY	543	AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATT	602
Db	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
QY	603	CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA	662
Db	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
QY	663	GAATTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	722
Db	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180

QY	723	CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	782
Db	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgLysLysLeuIle	200
QY	783	TGTGTACAGAAAGTTTTTATGGAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	842
Db	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
QY	843	GAATAATAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG	902
Db	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
QY	903	CTAGTGCTTGCTCTCTCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAA	962
Db	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
QY	963	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAAATGATCGAAACC	1022
Db	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
QY	1023	AAAGTAGTAAAGGAGGAGGAGCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACT	1082
Db	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
QY	1083	GATAAAACCCAGAGAGTGCCAGAGTCCAAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAAGCT	1142
Db	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
QY	1143	GAAAGTT 1148	
Db	321	GluVal 322	
RESULT 14			
ABO01809			
ID	ABO01809 standard; protein; 322 AA.		
XX			
AC	ABO01809;		
XX			
DT	07-AUG-2003 (first entry)		
XX			
DE	Novel human secreted and transmembrane protein PRO263.		
XX			
KW	Human; secreted and transmembrane protein; PRO; pharmaceutical;		
KW	diagnostic; biosensor; bioreactor; Parkinson's disease;		
KW	Alzheimer's disease; inflammation; nephritis; wound healing;		
KW	nerve repair; collateral blood vessel formation; cancer;		
KW	colorectal cancer; haemorrhage; rheumatoid arthritis; diabetes;		
KW	cirrhosis; fibrosis; restenosis; dermal fibrotic condition; keloid;		
KW	scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis;		
XX	infertility; gene therapy.		
OS	Homo sapiens.		
XX			
PN	US2002197671-A1.		
XX			
PD	26-DEC-2002.		
XX			
PF	17-JUL-2001; 2001US-00907824.		
XX			
PR	17-SEP-1997; 97US-0059113P.		
PR	17-SEP-1997; 97US-0059115P.		
PR	17-SEP-1997; 97US-0059117P.		
PR	17-SEP-1997; 97US-0059119P.		
PR	17-SEP-1997; 97US-0059121P.		
PR	17-SEP-1997; 97US-0059122P.		
PR	17-SEP-1997; 97US-0059184P.		
PR	18-SEP-1997; 97US-0059263P.		
PR	18-SEP-1997; 97US-0059266P.		
PR	15-OCT-1997; 97US-0062125P.		
PR	17-OCT-1997; 97US-0062285P.		
PR	17-OCT-1997; 97US-0062287P.		
PR	21-OCT-1997; 97US-0063486P.		
PR	24-OCT-1997; 97US-0062814P.		

PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 02-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
FA (GETH) GENENTECH INC.

XX
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;

XX WPI; 2003-370793/35.
DR N-PSDB; ACD07564.
XX
PT New genes and secreted and transmembrane polypeptides (e.g. PRO245 or PRO335), useful for treating or diagnosing e.g. Alzheimer's disease, cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia or strokes.
XX
PS Claim 12; Fig 74; 482pp; English.
XX
CC The invention describes a new isolated nucleic acid molecule comprising the full length coding sequence of the DNA deposited with the American Type Culture Collection (e.g. ATCC Deposit No. 209258), or a sequence with at least 80% identity to a DNA encoding a PRO polypeptide comprising any of 61 sequences having 164-1119 amino acids fully defined in the specification. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating e.g. Parkinson's disease, Alzheimer's disease, inflammations, nephritis, wound healing, nerve repair, collateral blood vessel formation, cancers (e.g. colorectal cancer), haemorrhage (or reduce risk for haemorrhage), rheumatoid arthritis, diabetes, cirrhosis of the liver, fibrosis of the lungs, restenosis, dermal fibrotic conditions (e.g. keloids or scarring), ischaemia, strokes, hypertension, heart attacks, atherosclerosis, or infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats, or rabbits) The PRO polypeptides are useful as targets for therapeutic intervention in these diseases, and diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
XX
SQ Sequence 322 AA;

Alignment Scores:

Pred. No.: 3.74e-163 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0
DB: 6 Gaps: 0

US-10-079-111-2 (1-2029) x ABO01809 (1-322)

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Db 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 20
QY 243 GTCCAAGGCTCTTTCGGTGCAGAAAGCGAACCCAGCAGCTGAATTCACAGAAGCTAAGGAGGCC 302
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|||
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QY 483 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTCTGATTGGAGGTTCCAGTG 542
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Db	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
QY	843	GAAAAATAAGCAGCATTTCAAGAATGAAGCTGCTGGTTTGGAGGTGTCCCCACGGCTCTG	902
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QY	963	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAGAAGGAAATGATCGAAACC	1022
Db	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
QY	1023	AAAGTAGTAAAGGAGGAGAAGCCCAATGATAGCAACCCTAATGAGGAATCAAGAAAAACT	1082
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QY	1083	GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTCGGATGCCTCGAAGCT	1142
Db	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
QY	1143	GAAATT	1148
Db	321	GluVal	322

Search completed: September 13, 2004, 10:13:22
Job time : 231 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: September 13, 2004, 10:06:01 ; Search time 201.5 Seconds
(without alignments)
6458.355 Million cell updates/sec

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Perfect score: 3604
Sequence: 1 ccttgacaagtccagaagctt.....aacatttaaaaaaaaaa 2029

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 2670352

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published Applications AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10079111@cgn_1_1_342@runat_13092004_102128_1879
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description

1	1772	49.2	344	12	US-10-276-774-2349	Sequence 2349, Ap
2	1657	46.0	322	9	US-09-909-320-201	Sequence 201, App
3	1657	46.0	322	9	US-09-909-088B-201	Sequence 201, App
4	1657	46.0	322	9	US-09-905-291A-201	Sequence 201, App
5	1657	46.0	322	9	US-09-902-853-201	Sequence 201, App
6	1657	46.0	322	9	US-09-907-824-201	Sequence 201, App
7	1657	46.0	322	9	US-09-907-841-201	Sequence 201, App
8	1657	46.0	322	10	US-09-904-011-201	Sequence 201, App
9	1657	46.0	322	10	US-09-906-742-201	Sequence 201, App
10	1657	46.0	322	10	US-09-906-838-201	Sequence 201, App
11	1657	46.0	322	10	US-09-907-613-201	Sequence 201, App
12	1657	46.0	322	10	US-09-907-942-201	Sequence 201, App
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15	1657	46.0	322	10	US-09-904-820-201	Sequence 201, App
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35	1657	46.0	322	10	US-09-905-088-201	Sequence 201, App
36	1657	46.0	322	10	US-09-907-575-201	Sequence 201, App
37	1657	46.0	322	10	US-09-905-075-201	Sequence 201, App
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39	1657	46.0	322	10	US-09-902-634-201	Sequence 201, App
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41	1657	46.0	322	10	US-09-907-979-201	Sequence 201, App
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45	1657	46.0	322	10	US-09-903-823-201	Sequence 201, App

ALIGNMENTS

RESULT 1
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; Sequence 2349, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2349
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2349
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US-10-079-111-2 (1-2029) x US-10-276-774-2349 (1-344)			
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Db	1	AlaSerAlaSerHisIleThrSerGlyHisLeuArgCysPheProGlySerGluGlyVal	20
QY	177	GGCAGATGGCCAGGTGCTTCAGCCTGGTGTGTTGCTTCTCACTTCCATCTGGACCACGAGG	236
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; Sequence 201, Application US/09909320			
; Patent No. US20020132240A1			
; GENERAL INFORMATION:			
; APPLICANT: Genentech, Inc.			
; APPLICANT: Ashkenazi, Avi			
; APPLICANT: Botstein, David			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Eaton, Dan L.			
; APPLICANT: Ferrara, Napoleone			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Fong, Sherman			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Gerber, Hanspeter			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, A.			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, Christopher J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Hillan, Kenneth, J.			
; APPLICANT: Kljavin, Ivar J.			
; APPLICANT: Mather, Jennie P.			
; APPLICANT: Pan, James			
; APPLICANT: Paoni, Nicholas F.			
; APPLICANT: Roy, Margaret Ann			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Williams, P. Mickey			
; APPLICANT: Wood, William, I.			
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
; TITLE OF INVENTION: Acids Encoding the Same			
; FILE REFERENCE: 10466-14			
; CURRENT APPLICATION NUMBER: US/09/909,320			
; CURRENT FILING DATE: 2002-01-04			
; PRIOR APPLICATION NUMBER: PCT/US00/04414			
; PRIOR FILING DATE: 2000-02-22			
; PRIOR APPLICATION NUMBER: US 60/143,048			
; PRIOR FILING DATE: 1999-07-07			
; PRIOR APPLICATION NUMBER: US 60/145,698			
; PRIOR FILING DATE: 1999-07-26			
; PRIOR APPLICATION NUMBER: US 60/146,222			
; PRIOR FILING DATE: 1999-07-28			
; PRIOR APPLICATION NUMBER: PCT/US99/20594			
; PRIOR FILING DATE: 1999-09-08			
; PRIOR APPLICATION NUMBER: PCT/US99/20944			
; PRIOR FILING DATE: 1999-09-13			
; PRIOR APPLICATION NUMBER: PCT/US99/21090			
; PRIOR FILING DATE: 1999-09-15			
; PRIOR APPLICATION NUMBER: PCT/US99/21547			
; PRIOR FILING DATE: 1999-09-15			
; PRIOR APPLICATION NUMBER: PCT/US99/23089			
; PRIOR FILING DATE: 1999-10-05			
; PRIOR APPLICATION NUMBER: PCT/US99/28214			
; PRIOR FILING DATE: 1999-11-29			
; PRIOR APPLICATION NUMBER: PCT/US99/28313			
; PRIOR FILING DATE: 1999-11-30			
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; PRIOR FILING DATE: 1999-12-02			
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; PRIOR FILING DATE: 1999-12-02			
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; PRIOR FILING DATE: 1999-12-20
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; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
US-09-909-320-201

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US-10-079-111-2 (1-2029) x US-09-909-320-201 (1-322)

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QY 423 AGCTTTGAAACTTGACGCTATGGCTGGTTGGATGGATTCGTGGTCATCTCAGGATT 482
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QY 543 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATT 602
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QY 663 GAATTTATTGTCAGTGACGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 722
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QY 723 CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATGATT 782
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US-09-909-088B-201
; Sequence 201, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,088B
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
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; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201

; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:

; OTHER INFORMATION: Synthetic protein
US-09-909-088B-201

Alignment Scores:

Pred. No.:	4,44e-148	Length:	322
Score:	1657.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	45.98%	Indels:	0
DB:	9	Gaps:	0

US-10-079-111-2 (1-2029) x US-09-909-088B-201 (1-322)

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Db	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu	20
QY	243	GTCCAAGCTCTTTGCGTGCAGAGAGCTTTCATCCAGGTGTCATGCAGAATTATGGGG	302
Db	21	ValGlnGlySerLeuArgAlaGluGluSerIleGlnValSerCysArgIleMetGly	40
QY	303	ATCACCTTGTGAGCAAAAAGCGAACAGCAGCTGAATTCACAGAAGCTAAGGAGGCC	362
Db	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
QY	363	TGTAGGCTGTGGGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT	422
Db	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
QY	423	AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGGTCATCTCTAGGATT	482
Db	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle	100
QY	483	AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCTCGATTGGAAGGTTCCAGTG	542
Db	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
QY	543	AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTTAACCTCGTGCA	602
Db	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
QY	603	CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA	662
Db	141	ProGluIleIleThrThrLysAspProllePheAsnThrGlnThrAlaThrGlnThrThr	160
QY	663	GAATTTATGTGACGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	722
Db	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
QY	723	CCTACTACTCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	782
Db	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200

QY	783	TGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	842
Db	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
QY	843	GAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCACGGCTCTG	902
Db	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
QY	903	CTAGTGTCTCTCTCTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGTCTATGTCAAA	962
Db	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
QY	963	AGGTATGTGAAGGCCTTCCCTTTTACAAAACAAGAAATCAGCAGAAAGAAATGATCGAAAC	1022
Db	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
QY	1023	AAAGTAGTAAAGGAGGAGGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT	1082
Db	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
QY	1083	GATAAAACCCAGAGAGTCCCAAGACTCCAAGCAAAACTACCGTCGATGCCTGGAAGCT	1142
Db	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
QY	1143	GAAGTT 1148	
Db	321	GluVal 322	

RESULT 4
US-09-905-291A-201
; Sequence 201, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
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; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
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; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
US-09-905-291A-201

Alignment Scores:
Pred. No.: 4.44e-148 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0
DB: 9 Gaps: 0

US-10-079-111-2 (1-2029) x US-09-905-291A-201 (1-322)

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QY 243 GTCCAAGGCTCTTTGCGTGCGACAAGAGCTTTCCATCCAGGTGTATGCAGAAATTATGGG 302
Db 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
QY 303 ATCACCTTGTGAGCAAAAAGGCGAACCAAGAGCTGAATTCACAGAAGCTAAGAGGCC 362
Db 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
QY 363 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 422
Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
QY 423 AGCTTTGAAACTTGACGCTATGGCTGGTGGTGGAGATGGATTCGTGGTCACTCTCAGGATT 482
Db 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
QY 483 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGCTGCTGATTTTGGAAAGTTCCAGTG 542
Db 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
QY 543 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAAGTTCGTGCATT 602
Db 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
QY 603 CCAGAAATTATCACCCACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACA 662

Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
QY 663 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACTGCC 722
Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
QY 723 CCTACTACTCTCTCTGCTCCAGCTTCCACCTTCTATTCACGGAGAAAAATTGATT 782
Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
QY 783 TGTGTCACAGAAGTTTTTATGGAAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 842
Db 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
QY 843 GAAAAATAAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 902
Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
QY 903 CTAGTGCTTGCTCTCTCTCTTCTTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAA 962
Db 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
QY 963 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGATCAGCAGAAGGAATGATCGAAACC 1022
Db 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
QY 1023 AAAGTAGTAAAGGAGGAGGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT 1082
Db 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluSerLysLysThr 300
QY 1143 GAAGTT 1148
Db 321 GluVal 322

RESULT 5

US-09-902-853-201
; Sequence 201, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10

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; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-902-853-201

Alignment Scores:
Pred. No.:          4,44e-148      Length:          322
Score:              1657.00        Matches:         322
Percent Similarity: 100.00%        Conservative:    0
Best Local Similarity: 100.00%      Mismatches:     0
Query Match:        45.98%         Indels:          0
DB:                 9              Gaps:           0

US-10-079-111-2 (1-2029) x US-09-902-853-201 (1-322)

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Db 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 20

QY 243 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 302
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Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

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Db 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

QY 483 AGCCCCAAACCCCAAGTGTGGGAAAAAATGGGGTGGGTGTCTCGATTGTGGAGGTTCCAGTG 542
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Db 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
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Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
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Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
QY 723 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 782
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Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
QY 783 TGTGTCACAGAAAGTTTATTGAAACTAGCACCACCATGTCTACAGAAACTGAACCATTTGTT 842
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Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
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Db 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
QY 1083 GATAAAACCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTCGATGCCGTGAAGCT 1142
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Db 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
QY 1143 GAAGTT 1148
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Db 321 GluVal 322

RESULT 6
US-09-907-824-201
; Sequence 201, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
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; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
```

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; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-907-824-201

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Alignment Scores:	
Pred. No.:	4.44e-148
Score:	1657.00
Length:	322
Percent Similarity:	100.00%
Matches:	322
Best Local Similarity:	100.00%
Conservative:	0
Mismatches:	0
Query Match:	45.98%
Indels:	0
DB:	9
Gaps:	0

US-10-079-111-2 (1-2029) x US-09-907-824-201 (1-322)

[illegible]

QY	363	TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCT	422
Db	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
QY	423	AGCTTTGAAACTTGCAGCTATGGCTGGSTTGGAGATGGATTTCGTGGTCATCTCTAGGATT	482
Db	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
QY	483	AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTTGGAAGGTTCCAGTG	542
Db	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
QY	543	AGCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACCTTGGACTAATCTCGTCGATT	602
Db	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
QY	603	CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAACAACA	662
Db	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
QY	663	GAATTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	722
Db	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
QY	723	CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	782
Db	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
QY	783	TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	842
Db	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
QY	843	GAAATAAAGCAGCATTTCAAGAATGAAGTCTGGGTGGAGGTGTCCCCACGGCTCTG	902
Db	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
QY	903	CTAGTGCTTGTCTCTCTCTTTTGGTGTGCTGAGCTGGTCTTGGATTTTGTATGTCAA	962
Db	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
QY	963	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAATGATCGAAACC	1022
Db	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr	280
QY	1023	AAAGTAGTAAAGGAGGAGGAGGCCCATGATAGCAACCTTAATGAGGAATCAAAGAAACT	1082
Db	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
QY	1083	GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCTGTGGAAGCT	1142
Db	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
QY	1143	GAAGTT 1148	
Db	321	GluVal 322	

RESULT 7

US-09-907-841-201

; Sequence 201, Application US/09907841

; Publication No. US20020198366A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
US-09-907-841-201

Alignment Scores:
Pred. No.: 4.44e-148 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0
DB: 9 Gaps: 0

US-10-079-111-2 (1-2029) x US-09-907-841-201 (1-322)

QY 183 ATGCCAGGTGCTTCAGCCGTGGTGTGCTTCTCACTTCCATCTGCACACGAGGCTCCTG 242
Db 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 20

QY 243 GTCCAAGGCTCTTTGCGTGCAGAGAGCTTCCATCCAGGTGTCATGCAGAATTATGGGG 302
Db 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

QY 303 ATCACCTTGTGAGCAAAAGCGGACGAGCTGAATTTCCAGAGCTAAGGAGGCC 362
Db 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60

QY 363 TGTAGGCTGTGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 422
Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

QY 423 AGCTTTGAAACTTGCAGCTAAGGCTGGTGGAGATGGATTTCGTGTCATCTCTAGGATT 482
Db 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

QY 483 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTCGAAGGTTCCAGTG 542
Db 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

QY 543 AGCCGACAGTTTGCAGCCCTATTGTTACAACTCATCTGATACCTTGGACTAACTCGTGCAATT 602
Db 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

QY 603 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACACTGCAACACAAACAACA 662
Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

QY 663 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 722
Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

QY 723 CCTACTACTCTCTCTGCTCCAGTTCACGTTCCACTTCTATTCCACGAGAAAAAATTGATT 782
Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

QY 783 TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 842
Db 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

QY 843 GAAATAAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 902
Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240

QY 903 CTAGTGCTTGCTCTCTCTCTCTTTGGTGTGCTGCAGCTGGTCTTGGATTTTGTATGTCAA 962
Db 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260

QY 963 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAAATGATCGAAACC 1022
Db 261 ArgIyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280

QY 1023 AAAGTAGTAAGGAGGAGAGGCAATGATAGCAACCCCTAATCAGGAATCAAAGAAACT 1082
Db 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300

QY 1083 GATAAAAACCCAGAGAGTCCAGAGTCCAAGCAAACTACCGTCGATGCCTGGAAGCT 1142
Db 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320

QY 1143 GAAGTT 1148
Db 321 GluVal 322

RESULT 8
US-09-904-011-201
; Sequence 201, Application US/09904011
; Publication No. US20030003530A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.


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; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-742-201

Alignment Scores:
Pred. No.: 4,44e-148 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Query Match: 45.98% Indels: 0
DB: 10 Gaps: 0
US-10-079-111-2 (1-2029) x US-09-906-742-201 (1-322)
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Db 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu 20
QY 243 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 302
Db 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
QY 303 ATCACCCCTTGTGAGCAAAAAGGCGAACCAAGCAGCTGAATTTTCAGAAAGCTAAGGAGGCC 362
Db 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
QY 363 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCT 422
Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
QY 423 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGGTGCATCTCTAGGATT 482
Db 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
QY 483 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTGGAAGGTTCCAGTG 542
Db 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
QY 543 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGGACTAACTCGTGCATT 602
Db 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
QY 603 CCAGAAATATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACACAACA 662
Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
QY 663 GAATTTATGTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 722
Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
QY 723 CCTACTACTCTCTCTCTCCAGTCCAGTTCCTCTCTATTCACGGAGAAAAAATTGATT 782
Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
QY 783 TGTGTCACAGAAAGTTTTATGAAACTAGCACCACCATGTCTACAGAAACTGAACCATTTGTT 842
Db 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
QY 843 GAAATATAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 902
Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
QY 903 CTAGTGTCTCTCTCTCTCTCTTTTGGTGTCTGCAGCTGGTCTTGGATTGCTATGTCAA 962
Db 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
QY 963 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAAATGATCGAAACC 1022
Db 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
QY 1023 AAAGTAGTAAAGGAGGAGGAGGCCAATGATAGCAACCCCTAATAGGAATCAAAGAAACT 1082
Db 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
QY 1083 GATAAAACCCAGAAAGAGTCCAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCTGGAAGCT 1142
Db 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
QY 1143 GAAGTT 1148
Db 321 GluVal 322
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RESULT 10
US-09-906-838-201
; Sequence 201, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,838
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
```

```
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-838-201

Alignment Scores:
Pred. No.:      4.44e-148      Length:      322
Score:          1657.00      Matches:     322
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      45.98%      Indels:      0
DB:               10      Gaps:      0

US-10-079-111-2 (1-2029) x US-09-906-838-201 (1-322)

QY      183  ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCAGTCTCCATCTGGACCACGAGGCTCCTG 242
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Db      1  MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20

QY      243  GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCAATGCAGAAATATGGGG 302
      |||
Db      21  ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

QY      303  ATCACCCCTTGTAGCAAAAAAGCGCAACAGCAGCTGAATTTTCACAGAAGCTAAGGAGGCC 362
      |||
Db      41  IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60

QY      363  TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 422
      |||
Db      61  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

QY      423  AGCTTTGAAACTTGACAGCTATGGCTGGCTGGTTGGAGATGGATTTCGTGGTCATCTTAGGATT 482
      |||
Db      81  SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

QY      483  AGCCCAAACCCCAAGTGTGGGAAAAAATGGGTGGGTGTCCTGATTGGAAGGTTCCAGTG 542
      |||
Db      101  SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

QY      543  AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATGACTATTGGACTAACTCGTCATT 602
      |||
Db      121  SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

QY      603  CCAGAAATTATCACCAACCAAGATCCCATATTTCAACACTCAAACCTCAAACACACAACAACA 662
      |||
Db      141  ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

QY      653  GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 722
      |||
Db      161  GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

QY      723  CCTACTACTACTCCTCTGCTCCAGCTTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 782
      |||
Db      181  ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

QY      783  TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 842
      |||
Db      201  CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

QY      843  GAAAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 902
      |||
Db      221  GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240

QY      903  CTAGTGTCTTCTCTCTCTTCTTTTGGTGTCTGAGCTGGTCTTTGGATTTTGTATGTCAA 962
      |||
Db      241  LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260

QY      963  AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAATGATCGAAACC 1022
      |||
Db      261  ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280

QY      1023  AAAGTAGTAAAGGAGAGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAAACT 1082
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Db 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
QY 1083 GATAAAACCCAGAGTCCAAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCT 1142
Db 301 AspLysAsnProGluGluSerLysSerProSerLysThrValArgCysLeuGluAla 320
QY 1143 GAAGTT 1148
Db 321 GluVal 322

RESULT 11
US-09-907-613-201
; Sequence 201, Application US/09907613
; Publication No. US20030027145A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,613
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
US-09-907-613-201
Alignment Scores:
Pred. No.: 4.44e-148 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0
DB: 10 Gaps: 0
US-10-079-111-2 (1-2029) x US-09-907-613-201 (1-322)
QY 183 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCATTCCATCTGCACCACGAGGCTCCTG 242
Db 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
QY 243 GTCCAAAGGCTCTTTGCGTGCAGAAAGCGAACCCAGCAGCTGAATTTTCAGAAAGCTAAGGAGGCC 302
Db 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
QY 303 ATCACCCCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTTCAGAAAGCTAAGGAGGCC 362
Db 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
QY 363 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTGAACAGCCCTTGAAAGCT 422
Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
QY 423 AGCTTTGAAACTTGACGCTATGGCTGGGTTGGAGATGGATTCCGGTCACTCTAGGATT 482
Db 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
QY 483 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTTGGGTGCTCCTGATTTGGAAGGTTCCAGTG 542
Db 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
QY 543 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGACTTAACCTCGTGCAATT 602
Db 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
QY 603 CCAGAAATTATCACCACCAAGATCCCATATTTCACACTCAAACTGCAACACAAACAACA 662
Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
QY 663 GAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 722
Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
QY 723 CCTACTACTCTCCTCCTGCTCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 782
Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
QY 783 TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAAACTGAACCATTTGTT 842
Db 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
QY 843 GAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 902
Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240

QY 903 CTAGTGTGCTCTCCTCTCTTTGGTGTGCAGCTGGTCTTGATTTTGATGTCAA 962
Db |||||||
241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
QY 963 AGGTATGTAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAATGATCGAAACC 1022
Db |||||||
261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
QY 1023 AAAGTAGTAAAGGAGGAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAACT 1082
Db |||||||
281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
QY 1083 GATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGGATGCCTGGAAGCT 1142
Db |||||||
301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
QY 1143 GAAGTT 1148
Db |||||||
321 GluVal 322

RESULT 12

US-09-907-942-201
; Sequence 201, Application US/09907942
; Publication No. US20030027146A1

GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US/09/907,942
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
US-09-907-942-201

Alignment Scores:

Pred. No.: 4.44e-148 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-2 (1-2029) x US-09-907-942-201 (1-322)

QY 183 ATGGCCAGGTGCTTCAGCTGGTGTGTTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 242
Db |||||||
1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
QY 243 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATATGGGG 302
Db |||||||
21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
QY 303 ATCACCCCTTGTGAGCAAAAAGCGGAACCCAGCAGCTGAATTTACAGAAGCTAAGAGGCC 362
Db |||||||
41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
QY 363 TGTAGGCTGTGGACTAAGTTTGGCCGGCAAGACCAAGTTGAAACAGCCTTGAAAGCT 422
Db |||||||
61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
QY 423 AGCTTTGAAACTTGACAGCTATGGCTGGTGGGTTGGAGATGGATTTCGTGGTCATCTCTAGGATT 482
Db |||||||
81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
QY 483 AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCTCTGATTTTGGAGGTTCCAGTG 542
Db |||||||
101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
QY 543 AGCCGACAGTTTGCAGCCCTATTGTTACAACATCATCTGATACCTTGGACTAAGTTCGTGCATT 602
Db |||||||
121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
QY 603 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACAACA 662
Db |||||||
141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
QY 663 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCC 722
Db |||||||
161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
QY 723 CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 782
Db |||||||

Db	181	ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
QY	783	TGTGTACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	842
Db	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
QY	843	GAAAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG	902
Db	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
QY	903	CTAGTGTCTGCTCTCTCTCTCTTTGGTGTCTGCAGCTGGTCTTTGGATTTTGTCTATGTCAAA	962
Db	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
QY	963	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAAGGAATGATCGAAACC	1022
Db	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
QY	1023	AAAGTAGTAAAGGAGGAGGCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACT	1082
Db	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
QY	1083	GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAACTACCGTGGATGCCTGGAAGCT	1142
Db	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
QY	1143	GAAGTT	1148
Db	321	GluVal	322

RESULT 13

US-09-904-859-201
; Sequence 201, Application US/09904859
; Publication No. US20030036060A1

: GENERAL INFORMATION:

APPLICANT:	Genentech, Inc.	
APPLICANT:	Ashkenazi, Avi	
APPLICANT:	Botstein, David	
APPLICANT:	Desnovers, Luc	
APPLICANT:	Eaton, Dan L.	
APPLICANT:	Ferrara, Napoleone	
APPLICANT:	Filvaroff, Ellen	
APPLICANT:	Fong, Sherman	
APPLICANT:	Gao, Wei-Qiang	
APPLICANT:	Gerber, Hanspeter	
APPLICANT:	Gerritsen, Mary E.	
APPLICANT:	Goddard, A.	
APPLICANT:	Godowski, Paul J.	
APPLICANT:	Grimaldi, Christopher J.	
APPLICANT:	Gurney, Austin L.	
APPLICANT:	Hillan, Kenneth, J.	
APPLICANT:	Kljavin, Ivar J.	
APPLICANT:	Mather, Jennie P.	
APPLICANT:	Pan, James	
APPLICANT:	Paoni, Nicholas F.	
APPLICANT:	Roy, Margaret Ann	
APPLICANT:	Stewart, Timothy A.	
APPLICANT:	Tumas, Daniel	
APPLICANT:	Williams, P. Mickey	
APPLICANT:	Wood, William, I.	
TITLE OF INVENTION:	Secreted and Tra	
TITLE OF INVENTION:	Acids Encoding	
FILE REFERENCE:	10466-14	
CURRENT APPLICATION NUMBER:	US/09/90	
CURRENT FILING DATE:	2001-07-12	
PRIOR APPLICATION NUMBER:	09/665,350	
PRIOR FILING DATE:	2000-09-18	
PRIOR APPLICATION NUMBER:	PCT/US00/0	
PRIOR FILING DATE:	2000-02-22	
PRIOR APPLICATION NUMBER:	US 60/143,	
PRIOR FILING DATE:	1999-07-07	
PRIOR APPLICATION NUMBER:	US 60/145,	
PRIOR FILING DATE:	1999-07-26	

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; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PR1
; ORGANISM: Homo Sapien
;

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QY 603 CCAGAAATTATCACCAAAAGATCCCATATTCAACACTCAAACCTGCAACACAAACAACA 662
Db 141 ProGluIleIleThrThrLysAspProIlePheasnThrGlnThrAlaThrGlnThrThr 160
QY 663 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 722
Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
QY 723 CCTACTACTCTCCTCTCCAGCTTCCACTTCTATCCACGGAGAAAAAATTTGATT 782
Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
QY 783 TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCAATGCTCTACAGAAACTGAACCAATTTGTT 842
Db 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
QY 843 GAAAAATAAGCAGCATTCAAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 902
Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
QY 903 CTAGTGCTTGCTCTCCTCTCTTTTGGTGCTGCAGCTGGTCTTGGATTTTGGCTATGTCAA 962
Db 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
QY 963 AGGTATGTGAAGGCCCTCCCTTTTACAAAACAAGATCAGCAGAAAGGAATGATCGAAACC 1022
Db 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
QY 1023 AAAGTAGTAAAGGAGGAGCAAGGCCAATGATAGCAACCTAATGAGGAATCAAAGAAACT 1082
Db 281 LysValValLysGluGluLysAlaAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
QY 1083 GATAAAAACCCAGAGAGTCCAAAGAGTCCAAAGCAAAACTACCGTGCAGTCCCTGGAAAGCT 1142
Db 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
QY 1143 GAAGTT 1148
Db 321 GluVal 322

RESULT 14
US-09-909-204-201
; Sequence 201, Application US/09909204
; Publication No. US20030036061A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/909,204
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
US-09-909-204-201

Alignment Scores:
Pred. No.: 4.44e-148 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-2 (1-2029) x US-09-909-204-201 (1-322)

QY 183 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 242
Db 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20

QY 243 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTTCATGCAGATTATGGGG 302
Db 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

QY 303 ATCACCCCTTGTGAGCAAAAAGCGCAACCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 362
Db 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60

QY 363 TGTAGGCTGCTGGACTAAGTTTGGCCGGCAGCACCAGTGAACAGCCTTGAAAGCT 422
Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

QY 423 AGCTTTGAAACTTGACGCTATGGCTGGTGGGATGGATTCGTGGTTCATCTCTAGGATT 482

Db 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
QY 483 AGCCCAAAACCCAAAGTGTGGGAAAAATGGGGTGGGTGCTCCTGATTTGGAAGGTTCCAGTG 542
Db 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValIleTrpLysValProVal 120
QY 543 AGCCGACAGTTTGCAGCCTATTGTTACAACACTCATCTGATACTTGGACTAACTCGTGCATT 602
Db 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
QY 603 CCAGAAATTATCACCAACCAAGATCCCAATATTCAAACACTCAAACCTGCAACACAAACA 662
Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
QY 663 GAATTTATGTTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTTACAAATACCTGCC 722
Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
QY 723 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCACAGAACTGAACCAATTTGATT 782
Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgLysLysLeuIle 200
QY 783 TGTGTACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAACTGAACCAATTTGTT 842
Db 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
QY 843 GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 902
Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
QY 903 CTAGTGCTTGCTCTCCTCTCTTCTTTGGTGCTGCAGCTGGTCTTGAAATTTTGCTATGCAAA 962
Db 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
QY 963 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAAGAAATGATCGAAACC 1022
Db 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
QY 1023 AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT 1082
Db 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
QY 1083 GATAAAACCCAGAGAGTCCAGAGTCCAAGACTCCAAGCAAAACTACCGTCGATGCCTGGAAGCT 1142
Db 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
QY 1143 GAAGTT 1148
Db 321 GluVal 322

RESULT 15

US-09-904-820-201
; Sequence 201, Application US/09904820
; Publication No. US20030036094A1
; GENERAL INFORMATION:

- ; APPLICANT: Genentech, Inc.
- ; APPLICANT: Ashkenazi, Avi
- ; APPLICANT: Botstein, David
- ; APPLICANT: Desnoyers, Luc
- ; APPLICANT: Eaton, Dan L.
- ; APPLICANT: Ferrara, Napoleone
- ; APPLICANT: Filvaroff, Ellen
- ; APPLICANT: Fong, Sherman
- ; APPLICANT: Gao, Wei-Qiang
- ; APPLICANT: Gerber, Hanspeter
- ; APPLICANT: Gerritsen, Mary E.
- ; APPLICANT: Goddard, A.
- ; APPLICANT: Godowski, Paul J.
- ; APPLICANT: Grimaldi, Christopher J.
- ; APPLICANT: Gurney, Austin L.
- ; APPLICANT: Hillan, Kenneth, J.
- ; APPLICANT: Kljavin, Ivar J.
- ; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,820
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT

; ORGANISM: Homo Sapien

US-09-904-820-201

Alignment Scores:

Pred. No.: 4,44e-148 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-2 (1-2029) x US-09-904-820-201 (1-322)

QY 183 ATGCCAGGTGCTTCAGCCTGGTGTCTCAGCTTCCATCTCTCAGCTTCCATCTGGACCACGAGGCTCCTG 242
Db 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
QY 243 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 302
Db 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40

QY	303	ATCACCCCTTGTGACGACAAAAAGCGCAACCCAGCAGCTGAATTTTCACAGAAGCTCAAGGAGGCC	362
DB	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
QY	363	TGTAGGCTGCTGGGACTAAGTTTGGCCGCGCAAGGACCAAGTTTGAACAGCCTTGAAGCT	422
DB	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
QY	423	AGCTTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCTGTGTCATCTCTAGGATT	482
DB	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
QY	483	AGCCCAACCCCAAGTGTGGGAAAAAATGGGGTGGTGTCTGATTTTGGAGGTTCCAGTG	542
DB	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
QY	543	AGCCGACAGTTTGAGCCTATTGTTTCAACTCATCTGATACCTTGGACTAACTCGTGCATT	602
DB	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
QY	603	CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACAACA	662
DB	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
QY	663	GAATTTATTGTGACGTACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	722
DB	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
QY	723	CCTACTACTACTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	782
DB	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
QY	783	TGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	842
DB	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
QY	843	GAAAATAAGCAGCATTCAGAATGAAGCTGTCTGGTTTGGAGGTGTCCCCACGGCTCTG	902
DB	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
QY	903	CTAGTGTCTGCTCTCTCTCTTTTGGTGTGCTGAGCTGTCTTGGATTGTGCTATGTCAAA	962
DB	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
QY	963	AGGTATGTGAAGCCTTCCCTTTTACAAACAAGATCAGCAGAAGGAAATGATCGAAACC	1022
DB	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
QY	1023	AAAGTAGTAAAGGAGGAGGCGCCCAATGATAGCAACCTTAATGAGGAATCAAGAAAACT	1082
DB	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
QY	1083	GATAAAAAACCCAGAGTCCAAGAGTCCAAGCAAAAACTACCGTGCATGCCTTGAAGCT	1142
DB	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
QY	1143	GAAGTT	1148
DB	321	GluVal	322

Blank

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 13, 2004, 10:05:16 ; Search time 74.5 Seconds
(without alignments)
5239.533 Million cell updates/sec

Title: US-10-079-111-2
Perfect score: 3604
Sequence: 1 ccttgacaagtcagaagctt.....aaacatttaaaaaaaaaa 2029

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 566732

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10079111/runat_13092004_102127_1835/app_query.fasta_1.2183
-DB=PIR_78 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosu62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10079111@cgn_1_1_104 @runat_13092004_102127_1835 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length	ID	Description

1	229.5	6.4	363	2 A37009	CD44 homolog membr
2	228.5	6.3	503	2 B38745	cell adhesion mole
3	222.5	6.2	362	2 A30901	lymphocyte adhesio
4	222.5	6.2	365	2 A34424	CD44 membrane gly
5	217.5	6.0	362	2 A35616	T-cell surface gly
6	215.5	6.0	742	2 A47195	lymphocyte homing
7	208.5	5.8	366	2 A53286	cell-surface glyco
8	208	5.8	699	2 I37369	epican - human
9	205	5.7	361	2 JH0417	cell adhesion mole
10	204	5.7	493	2 S13530	CD44E protein, epi
11	202.5	5.6	351	2 S45305	CD44 antigen precu
12	202.5	5.6	426	2 JH0518	lymphocyte homing
13	198	5.5	395	2 I77371	CD44R5 - human
14	186	5.2	359	2 S24240	lymphocyte surface

15	152.5	4.2	3562	2 A47171	chondroitin sulfat
16	148.5	4.1	2109	1 I50421	aggrecan precursor
17	145	4.0	277	2 A41735	hyaluronate-bindin
18	145	4.0	1069	2 T42681	hypothetical prote
19	144	4.0	275	2 JC6506	tumor necrosis fac
20	143.5	4.0	1340	2 A39808	proteoglycan core
21	143	4.0	2327	2 T42630	aggrecan - bovine
22	138.5	3.8	2415	1 A39086	aggrecan precursor
23	137	3.8	276	2 A47290	TSG-6 homolog PS4
24	136.5	3.8	2124	2 A28452	proteoglycan core
25	132.5	3.7	2132	1 A55182	aggrecan precursor
26	131.5	3.6	912	2 A54423	brevican precursor
27	130.5	3.6	883	2 S49126	brevican precursor
28	130.5	3.6	883	2 S57653	brevican precursor
29	126	3.5	1257	2 S28764	neurocan precursor
30	122	3.4	2397	1 A55535	versican precursor
31	117	3.2	340	2 JC7505	brain link protein
32	116	3.2	846	2 T21700	hypothetical prote
33	115	3.2	370	2 S29139	aggrecan - pig (fr
34	115	3.2	1360	2 T33922	hypothetical prote
35	115	3.2	1643	2 T14274	versican precursor
36	115	3.2	3381	2 T42389	versican precursor
37	114.5	3.2	660	2 JW0067	chitinase [EC 3.2.
38	113	3.1	645	2 T29818	hypothetical prote
39	112	3.1	390	1 QQBE77	glycoprotein I pre
40	112	3.1	1268	2 S52781	neurocan - mouse
41	111.5	3.1	402	2 S73773	dihydrolipoamide a
42	111.5	3.1	909	1 QRXL12	LDL receptor 2 pre
43	111	3.1	2409	1 A60979	versican precursor
44	110	3.1	354	1 LKHU	proteoglycan link
45	109.5	3.0	355	1 LKCH	proteoglycan link

ALIGNMENTS

RESULT 1

A37009
CD44 homolog membrane glycoprotein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 21-Jul-2000
C;Accession: A37009
R;Zhou, D.F.H.; Ding, J.F.; Picker, L.J.; Bargatzke, R.F.; Butcher, E.C.; Goeddel, D.V.
J. Immunol. 143, 3390-3395, 1989
A;Title: Molecular cloning and expression of Pgp-1. The mouse homolog of the human H-CAM
A;Reference number: A37009; MUID:90038499; PMID:2681416
A;Accession: A37009
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-363 <ZHO>
A;Cross-references: GB:M30655; NID:g200332; PIDN:AAA39922.1; PID:g200333
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cell adhesion; glycoprotein; membrane protein

Alignment Scores:			
Pred. No.:	6.93e-12	Length:	363
Score:	229.50	Matches:	89
Percent Similarity:	40.90%	Conservative:	57
Best Local Similarity:	24.93%	Mismatches:	148
Query Match:	6.37%	Indels:	63
DB:	2	Gaps:	14

US-10-079-111-2 (1-2029) x A37009 (1-363)

QY	225	TGGACCA	CGAGG	-----CTCCTGGTCCAGGCTCTTTGGTGCAGAGAGCTTTCC	275
				:::	:::
Db	6	TrpHisThrAlaTrpGlyLeuCysLeuLeuGlnLeuSerLeuAlaHisGlnGlnIleAsp			25
				:::	:::
QY	276	ATCCAGGTGTCAGAGAATTATGGGGATCACCCCTTGTGAGCAAAAAGCGCAACACGACAG			335
		:::	:::	:::	
Db	26	LeuAsnValThrCysArgTyrAlaGlyValPheHisValGluLysAsnGlyArgTyrSer			45
				:::	
QY	336	CTGAATTTCACAGACGCTAAGGAGGCCTGTAGCTGCTGGACTAAGTTTGGCGGCAAG			395
		:::		:::	:::

Db 46 IleSerArgThrGluAlaAlaAspLeuCysGlnAlaPheAsnSerThrLeuProThrMet 65
QY 396 GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGTTGGA 455
Db 66 AspGlnMetLysLeuAlaLeuSerLysGlyPheGluThrCysArgTyrGlyPheIle--- 84
QY 456 GATGGATTCTGGTTCATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGGAAAAAATGGGGTG 515
Db 85 GluGlyAsnValValIleProArgIleHisProAsnAlaIleCysAlaAlaAsnHisThr 104
QY 516 GGTGTCCTGAFTTGGAAAGGTTCCAGTGAGCGGACAGATTTGCAGCCCTATTGTTACAACCTCA 575
Db 105 GlyValTyrIleLeuValThrSerAsnThrSerHisTyrAspThrTyrCysPheAsnAla 124
QY 576 TCTGATACTTGGACTAACTCGTGCATTCAGAGAAATATCACCAACCAAGATCCCATATTC 635
Db 125 SerAlaProProGluGluAspCys-----ThrSerValThrAspLeuPro 139
QY 636 AACACTCAAACTGCAACACAAACAACAGAAATTATTGTGAGTGACAGTACC---TACTCG 692
Db 140 AsnSerPheAspGlyProValThrIleThrIleValAsnArgAspGlyThrArgTyrSer 159
QY 693 GTGGCATCCCTTACTCTACA-----ATACCTGCCCTTACT----- 728
Db 160 LysLysGlyGluTyrArgThrHisGlnGluAspIleAspAlaSerAsnIleIleAspAsp 179
QY 729 -----ACTACTCCTCCTGCT---ACTACTCCTCCTGCT---CCAGCTTCCACT 755
Db 180 AspValSerSerGlySerThrIleGluLysSerThrProGluGlyTyrIleLeuHisThr 199
QY 756 TCTATTCCACGGAGAAAAAATTGATTGTGTGCACAGAAGTTTTTATGGAAACTAGCACCC 815
Db 200 TyrLeuProThrGluGlnProThrGlyAspGlnAspAspSerPhePheIleArgSerThr 219
QY 816 ATGTCTACA---GAAACTGAACCATTTGTTGAAAAATAAAGCAGCATTTCAAG----- 863
Db 220 LeuAlaThrArgAspArgAspSerSerLysAspSerArgGlySerSerArgThrValThr 239
QY 864 -----AATGAAGCTGCTGGGTTTGGAGT----- 887
Db 240 HisGlySerGluLeuAlaGlyHisSerSerAlaAsnGlnAspSerGlyValThrThrThr 259
QY 888 -----GTCCCCACGGCTCTGCTAGTGTGCTAGTGTGCTCTCCTCTTC 923
Db 260 SerGlyProMetArgArgProGlnIleProGluTrpLeuIleIleLeuAlaSerLeu--- 278
QY 924 TTTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAAAGGTATGTGAAGGCCTTCCCT 983
Db 279 LeuAlaLeuAlaLeuIleLeuAlaValCys-----IleAlaValAsnSer 293
QY 984 TTTACAAACAAGAATCAGCAGAGAAGGAATGATC-----GAAACCAAGTAGTAAAG 1034
Db 294 ArgArgCysGlyGlnLysLysLysLeuValIleAsnGlyGlyAsnGlyThrValGlu 313
QY 1035 GAGGAGAAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACTGATAAAACCCA 1094
Db 314 AspArgLysProSerGluLeuAsn---GlyGluAlaSerLysSerGlnGluMetValHis 332
QY 1095 GAAGAGTCCAAAGAGTCCAAAGCAAAACTACCGTGCGATGCCTGGAAGCTGAA 1145
Db 333 LeuValAsnLysGluProSerGluThrProAspGlnCysMetThrAlaAsp 349
RESULT 2
B38745
cell adhesion molecule CD44 precursor, long form (meta-1) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 05-Nov-1999
C;Accession: B38745; A38745
R;Guenther, U.; Hofmann, M.; Rudy, W.; Reber, S.; Zoeller, M.; HauBmann, I.; Matzku, S.
Cell 65, 13-24, 1991
A;Title: A new variant of glycoprotein CD44 confers metastatic potential to rat carcinom
A;Reference number: A38745; MUID:91191552; PMID:1707342
A;Accession: B38745

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-503 <GUE>
A;Cross-references: GB:M61874; NID:g576534; PIDN:AAA53534.1; PID:g576535
A;Accession: A38745
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-223,386-503 <GU2>
A;Cross-references: GB:M61875
C;Keywords: cell adhesion
Alignment Scores:
Pred. No.: 8.92e-12 Length: 503
Score: 228.50 Matches: 126
Percent Similarity: 36.19% Conservative: 60
Best Local Similarity: 24.51% Mismatches: 242
Query Match: 6.34% Indels: 86
DB: 2 Gaps: 21
US-10-079-111-2 (1-2029) x B38745 (1-503)
QY 225 TGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCATCCAGGTG 284
Db 10 TrpGlyLeuLeuCysLeuLeuGlnLeuSerLeuAlaGlnGlnIleAspLeuAsnIle 29
QY 285 TCATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAGCGCAACCCAGCAGCTGAATTC 344
Db 30 ThrCysArgTyrAlaGlyValPheHisValGluLysAsnGlyArgTyrSerIleSerArg 49
QY 345 ACAGAAGCTAAGGAGGCCCTGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTT 404
Db 50 ThrGluAlaAlaAspLeuCysGluAlaPheAsnThrThrLeuProThrMetAlaGlnMet 69
QY 405 GAAACAGCCTTGAAAGCTAGCTTTGAAAACCTTGCAGCTATGGCTGGGTGGAGATGGATTC 464
Db 70 GluLeuAlaLeuArgLysGlyPheGluThrCysArgTyrGlyPheIle---GluGlyHis 88
QY 465 GTGGTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTG 524
Db 89 ValValIleProArgIleHisProAsnAlaIleCysAlaAlaAsnAsnThrGlyValTyr 108
QY 525 ATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACT 584
Db 109 IleLeuLeuAlaSerAsnThrSerHisTyrAspThrTyrCysPheAsnAlaSerAlaPro 128
QY 585 TGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAA 644
Db 129 LeuGluGluAspCys-----ThrSerValThrAspLeuProAsnSerPhe 143
QY 645 ACTGCAACACAACAACAGAATTTATTGTCAGTGACAGTACC---TACTCGGTGGCATCC 701
Db 144 AspGlyProValThrIleThrIleValAsnArgAspGlyThrArgTyrSerLysLysGly 163
QY 702 CCTTACTCTACA-----ATACCTGCCCTTACT----- 728
Db 164 GluTyrArgThrHisGlnGluAspIleAspAlaSerAsnIleIleAspGluAspValSer 183
QY 729 -----ACTACTCCTCCTGCT---CCAGCTTCCACTTCTATTCCA 764
Db 184 SerGlySerThrIleGluLysSerThrProGluGlyTyrIleLeuHisThrAspLeuPro 203
QY 765 CGGAGAAAAAAATTTGTTGTGCACAGAAGTTTTTATGGAAAACTAGCACCATGTCTACA 824
Db 204 ThrSerGlnProThrGlyAspArgAspAspAlaPhePheIleGlySerThrLeuAlaThr 223
QY 825 ---GAAACTGAACCATTTGTTGAAAAATAAAGCAGCATTCACAGAATGAAGCTGCTGGGTTT 881
Db 224 IleAlaThrThrProTrpValSerAlaHisThrLysGlnAsnGlnGluArgThrGlnTrp 243
QY 882 GGAGGTGTC-----CCCACGGCTCTGCTAGTGTGCTTCTCTCTCTCTCTTTGGTGCT 932
Db 244 AsnProIleHisSerAsnProGluValLeuLeuGlnThrThrThrArgMetThrAspIle 263

QY 933 GCAGCTGGTCTTGGATTTCGTATGTCAAAAGGTATGTGAAG-----GCCTTCCCTTTT 986
Db 264 AspArgAsnSerThrSerAlaHisGlyGluAsnTrpThrGlnGluProGlnProPhe 283
QY 987 ACAAACAAGAAATCAGCAGAGGAA-----ATGATC 1016
Db 284 AsnAsnHisGluTyrGlnAspGluGluThrProHisAlaThrSerThrTrpAla 303
QY 1017 GAAACCAAGTAGTAAAGGAGAGAGGCCAATGATAGCAACCCTAATGAGGAATCAAAG 1076
Db 304 AspProAsnSerThrThrGluAlaAlaThrGlnLysGluLysTrpPheGluAsnGlu 323
QY 1077 AAAACTGATAAAAACCCA-----GAAGAGTCCAAGAGTCCAAGCAAAACTACC 1124
Db 324 TrpGlnGlyLysAsnProProThrProSerGluAspSerHisValThrGluGlyThrThr 343
QY 1125 GTGCGATGCTGGAAGCTGAAGTTTAGATGAGA-----CAGAAATGAGGAGACACA 1175
Db 344 AlaSerAlaHisAsnAsnHisProSerGlnArgMetThrThrGlnSerGlnGluAspVal 363
QY 1176 CCTGAGGCTGGTTTCTTTCATGCTCCTTACCCTGCCCCAGCTGGGAAATCAAAAGGCC 1235
Db 364 SerTrpThrAspPheAsp---ProIleSerHisProMetGlyGln-----Gly 379
QY 1236 AAAGAACCAAGAAGAAAGTCCACCCTTGTTCTCTAACTGGAATCAGCTCAGGACTGCCA 1295
Db 380 HisGlnThrGluSerLysGlyHis-----SerSerGly---Asn 391
QY 1296 TTGACTATGGAGTGCACCAAGAGAAATGCCCTTCT-----CCTTATTGTAACCCGTGC 1349
Db 392 GlnAspSerGlyValThrThrThrSerGlyProAlaArgArgProGlnIle---ProGlu 410
QY 1350 TGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCTTTCTAGCCTGGCTATGTCCTA 1409
Db 411 TrpLeu--IleIleLeuAlaSerLeuLeuAlaLeuAlaLeuIleLeuAlaValCys--- 428
QY 1410 ATAATATCCACTGGGAGAAAGGAGTTTTGCAAGTGCAGGACCTAAACATCTCATCA 1469
Db 429 -----IleAlaValAsnSerArgArgCysGlyGlnLysLysLeuVal- 444
QY 1470 GTATCCAGTGGTAA-----AAGGCC 1490
Db 445 IleAsnSerGlyAsnGlyThrValGluAspArgLysProSerGluLeuAsnGlyGluAla 464
QY 1491 TCCTGGCTGTCTGAGGCTAGTGGGTTGAAAGCCAGGAGTCACTGAGACC---AAGGCT 1547
Db 465 SerLysSerGlnGluMetValHisLeuValAsnLysGluProThrGluThrProAspGln 484
QY 1548 TTCTCTACTGATTCGCGAGCTCAGACCCTTTCTTCA 1583
Db 485 PheMetThrAlaAspGluThrArgAsnLeuGlnSer 496
RESULT 3
A30901
lymphocyte adhesion receptor precursor - baboon
C;Species: Papio sp. (baboon)
C;Date: 18-Apr-1989 #sequence_revision 18-Apr-1989 #text_change 21-Jul-2000
C;Accession: A33935; A30901
R;Idzerda, R.L.; Carter, W.G.; Nottenburg, C.; Wayne, E.A.; Gallatin, W.M.; St. John, T
Proc. Natl. Acad. Sci. U.S.A. 86, 4659-4663, 1989
A;Title: Isolation and DNA sequence of a cDNA clone encoding a lymphocyte adhesion recep
A;Reference number: A33935; MUID:89282830; PMID:2471974
A;Accession: A33935
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-362 <IDZ>
A;Cross-references: GB:M22452; NID:gl76576; PID:gl76577
C;Comment: This protein was isolated from the herpes papio induced B cell lymphoma.
C;Genetics:
A;Gene: CD44; ECMRIII; Hermes-1 antigen
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cytoskeleton; extracellular matrix; glycoprotein; lipoprotein; surface antig
F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-362/Product: lymphocyte adhesion receptor #status predicted <MAT>
F;21-270/Domain: extracellular #status predicted <EXT>
F;271-290/Domain: transmembrane #status predicted <TMM>
F;291-362/Domain: intracellular #status predicted <CVT>
F;25,57,100,110,120,256/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;296/Binding site: palmitate (Cys) (covalent) #status predicted

Alignment Scores:
Pred. No.: 2.89e-11 Length: 362
Score: 222.50 Matches: 92
Percent Similarity: 37.40% Conservative: 43
Best Local Similarity: 25.48% Mismatches: 127
Query Match: 6.17% Indels: 99
DB: 2 Gaps: 16

US-10-079-111-2 (1-2029) x A30901 (1-362)

QY 240 CTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATG 299
Db 14 LeuValGlnLeuSerLeu-----AlaGlnIleAspLeuAsnIleThrCysArgPheGlu 31
QY 300 GGGATCACCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAGAAGCTAAGGAG 359
Db 32 GlyIleTyrHisValGluLysAsnGlyArgTyrSerIleSerArgThrGluAlaAlaAsp 51
QY 360 GCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAA 419
Db 52 LeuCysLysAlaPheAsnSerThrLeuProThrMetAlaGlnMetGluLysAlaLeuSer 71
QY 420 GCTAGCTTTGAAACCTTGCACTATGGCTGGTGGAGATGGATTCGTGGTCATCTCTAGG 479
Db 72 IleGlyPheGluThrCysArgTyrGlyPheIle---GluGlyHisValIleProArg 90
QY 480 ATTAGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTCTGATTGGAAAGTTCCA 539
Db 91 IleHisProAsnSerIleCysAlaAlaAsnAsnThrGlyValTyrIleLeuThrSerAsn 110
QY 540 GTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGC 599
Db 111 ThrSer---GlnTyrAspThrTyrCysPheAsnAlaSerAlaProProGlyGluAspCys 129
QY 600 ATTCCAGAAATTATCACCAACAAAGATCCCATATTTCAACACTCAAACCTGCAACACAAACA 659
Db 130 -----ThrSerValThrAspLeuProAsnAlaPheAspGlyProIleThr 144
QY 660 ACAGAATTTATTGTCTAGTGACAGTACC---TACTCGGTGGCATCCCCCTTACTCTACAATA 716
Db 145 IleThrIleValAsnArgAspGlyThrArgTyrValLysLysGlyGluTyrArgThrAsn 164
QY 717 CCT-----GCCCTACT----- 728
Db 165 ProGluAspIleAsnProSerSerProThrAspAspValSerSerGlySerSerSer 184
QY 729 -----ACTACTCTCCT 740
Db 185 GluArgSerSerThrLeuGlyGlyTyrIlePheTyrAsnHisPheSerThrSerProPro 204
QY 741 GCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATGATTTGTGTCAACAGAGTTT 800
Db 205 IleProAspGluAspGly----- 210
QY 801 ATGGAAGCTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAGCAGCATTC 860
Db 211 ---ProTrpIleThrAspSerThrAspArgThrProAlaThrArgAspGlnGlyAlaPhe 229
QY 861 AAG-----AATGAAGCTGCTGGGTT----- 881
Db 230 AspProSerGlyGlySerHisThrThrHisGlySerGluSerAlaGlyHisSerHisGly 249
QY 882 -----GGAGGT-----GTCCCCACG 896
Db 250 SerArgGluGlyGlyAlaAsnThrThrSerGlyProLeuArgThrProGlnIleProGlu 269

Alignment Scores:

Pred. No.: 8.01e-11 Length: 362
Score: 217.50 Matches: 88
Percent Similarity: 38.73% Conservative: 46
Best Local Similarity: 25.43% Mismatches: 149
Query Match: 6.03% Indels: 63
DB: 2 Gaps: 12

US-10-079-111-2 (1-2029) x A35616 (1-362)

QY	252	TC	TTGCGTGCAGAA	GAGCTT	CCATCC	AGGTG	TCATG	CAGA	AATTAT	GGGAT	CAC	CCCT	311
Db	18	Ser	Leu	Ala	His	Glu	Gln	Ile	Asp	Leu	Asn	Ile	Thr
QY	312	GT	GAGCA	AAAGG	CGAAC	CAGC	AGTGA	ATTTC	CAGA	AGCTA	AGGAG	GCCTG	371
Db	38	Val	Glu	Lys	Asn	Gly	Arg	Tyr	Ser	Ile	Ser	Arg	Thr
QY	372	CT	GGGACTA	AGTTT	GGCCG	CAAGG	ACCA	AGTTG	AAAC	ACGCTT	GAAAG	CTAGC	431
Db	58	Phe	Asn	Ser	Thr	Leu	Pro	Thr	Met	Asp	Gln	Met	Val
QY	432	AC	TG	CAGCTA	TGGCT	GGTGG	AGATG	GA	TTTC	GTG	TCTCT	CTAGG	491
Db	78	Thr	Cys	Arg	Tyr	Gly	Phe	Ile	---	Glu	Gly	His	Val
QY	492	CC	CAAGT	GTGGG	AAAA	TGGG	TGGT	GTCT	CTG	ATTG	GGA	AGGTT	551
Db	97	Ala	Ile	Cys	Ala	Ala	Asn	His	Thr	Gly	Val	Tyr	Ile
QY	552	TT	TG	CAGC	CTATT	GT	TAC	AACT	CATCT	GATAC	TCTG	TGCTA	611
Db	116	Tyr	Asp	Thr	Tyr	Cys	Phe	Asn	Ala	Ser	Ala	Pro	Leu
QY	612	AT	CACC	ACCA	AGAT	CCCAT	ATTTC	AACT	CAAA	CTCA	AAAC	ACAC	671
Db	132	---	Thr	Ser	Val	Thr	Asp	Leu	Pro	Asn	Ser	Phe	Glu
QY	672	GT	CAGT	GAC	AGT	ACC---	TAC	T	CGT	GCG	ATC	CCCTT	716
Db	151	Asn	Arg	Asp	Gly	Thr	Arg	Tyr	Ser	Lys	Gly	Glu	Tyr
QY	717	CT	G	CCCC	CTACT	ACTCT	CTCT	CTG	CTC	AGCT	TTCC-----	-----	752
Db	171	Asp	Ala	Ser	Asn	Thr	Thr	Asp	Asp	Val	Ser	Ser	Ser
QY	753	---	-----	-----	ACTT	CTAT	TTCC	ACG	GAAAA	AAAA	ATTG	ATTG	791
Db	191	Ser	Gly	Gly	Tyr	Val	Phe	His	Thr	Tyr	Leu	Pro	Thr
QY	792	GA	AGT	TTTT	TAT	GGAA	CTAG	CAC	CATG	TCTAC	AGAA-----	-----	827
Db	211	Asp	Pro	Tyr	Phe	Ile	Gly	Ser	Thr	Met	Ala	Thr	Arg
QY	828	---	-----	-----	---	ACT	GA	ACC	ATT	TTG	TG	AAAA	848
Db	231	Arg	Gly	Asn	Ser	Leu	Thr	Val	Thr	Asp	Gly	Ser	Lys
QY	849	AA	AGC	AGCAT	TTCA	AGA	ATGA	AGT	CGT	GGT	TTT	TGGA-----	899
Db	251	Gln	Asp	Ser	Gly	Ala	Asn	Thr	Thr	Ser	Arg	Pro	Gly
QY	900	CT	G	TAGT	GCTT	GCTCT	CTCT	CTT	TTT	GGT	GCTG	CGCTT	959
Db	271	Leu	Ile	Val	Leu	Ala	Ser	Leu---	Leu	Ala	Leu	Ala	Val
QY	960	AAA	AGT	ATG	TGA	AGG	CCCTT	CCCTTT	TAC	AAAC	AA	GAAT	1019
Db	288	-----	---	Ile	Ala	Val	Asn	Ser	Arg	Arg	Cys	Gly	Gln
QY	1020	ACC	AAAG	TAGT	AAAG	GAG	GAGG	CCCA	ATG	ATAG	CAAC	CCCTA	1079
Db	305	Asn	Ser	-----	Gly	Asn	Gly	Lys	Val	Glu	Asp	Arg	Lys

QY	1080	ACT	GATA	AAAA	ACCC	CAGAA-----	-----	GAGT	CCA	AGAGT	CCA	AGAAA	ACT
Db	323	Ala	Ser	Lys	Ser	Gln	Glu	Met	Val	His	Leu	Val	Asn
QY	1128	CG	ATG	CCCT	GGAA	AGCT	GAA	1145					
Db	343	Gln	Phe	Met	Thr	Ala	Asp	348					

RESULT 6

A47195

lymphocyte homing receptor isoform CD44 - human

C;Species: Homo sapiens (man)

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994

C;Accession: A47195

R;Screation, G.R.; Bell, M.V.; Jackson, D.G.; Cornelis, F.B.; Gerth, U.; Bell, J.I.

Proc. Natl. Acad. Sci. U.S.A. 89, 12160-12164, 1992

A;Title: Genomic structure of DNA encoding the lymphocyte homing receptor CD44 reveals a

A;Reference number: A47195; MUID:93101687; PMID:1465456

A;Accession: A47195

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-742 <SCR>

A;Note: sequence inconsistent with the nucleotide translation

A;Note: sequence extracted from NCBI backbone (NCBIN:120731, NCBIN:120737, NCBIN:120739,

, NCBIN:120764, NCBIN:120766, NCBIN:120770, NCBIN:120772, NCBIN:120774, NCBIN:120776, NC

Alignment Scores:

Pred. No.: 1.34e-10 Length: 742
Score: 215.50 Matches: 110
Percent Similarity: 34.00% Conservative: 76
Best Local Similarity: 20.11% Mismatches: 178
Query Match: 5.98% Indels: 183
DB: 2 Gaps: 24

US-10-079-111-2 (1-2029) x A47195 (1-742)

QY	255	TT	GCGT	GCAGA	GAGCTT	TCCAT	CCAGG	TGTC	ATGC	AGA	ATTAT	GGGAT	CAC
Db	17	Leu	Ser	Leu	Ala	Gln	Ile	Asp	Leu	Asn	Ile	Thr	Cys
QY	315	AG	CAAA	AAGG	CGGA	ACC	CAG	AGCT	GA	ATTTC	CAGA	AGCTA	374
Db	37	Glu	Lys	Asn	Gly	Arg	Tyr	Ser	Ile	Ser	Arg	Thr	Glu
QY	375	GG	ACTA	AGTT	TGGC	CGCA	AGG	ACCA	AGTT	GAA	CAG	CCCTT	434
Db	57	Asn	Ser	Thr	Leu	Pro	Thr	Met	Ala	Gln	Met	Glu	Lys
QY	435	TG	CAG	CTAT	GCGT	GGTGG	AGAT	TGGAT	TCG	TGTC	ATCT	CTAGG	494
Db	77	Cys	Arg	Tyr	Gly	Phe	Ile---	Glu	Gly	His	Val	Val	Leu
QY	495	AA	GTGT	GGG	AAAA	TGGG	TGGT	GTCT	CTG	ATTG	GGA	AGGTT	554
Db	96	Ile	Cys	Ala	Ala	Asn	Asn	Thr	Gly	Val	Tyr	Ile	Leu
QY	555	GC	AGC	CTAT	TGTT	ACA	ACT	CAT	CTG	ATA	CTT	GGAC	602
Db	115	Asp	Thr	Tyr	Cys	Phe	Asn	Ala	Ser	Ala	Pro	Pro	Glu
QY	602	---	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	602
Db	135	Leu	Pro	Asn	Ala	Phe	Asp	Gly	Pro	Ile	Thr	Ile	Thr
QY	603	---	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	632
Db	155	Tyr	Val	Gln	Lys	Gly	Glu	Tyr	Arg	Thr	Asn	Pro	Glu
QY	633	TT	CAAC	ACTC	AACT	CGA	ACAC	ACAA	CAAC	ACAG	AA-----	-----	665
Db	175	Asp	Asp	Asp	Val	Ser	Ser	Gly	Ser	Ser	Ser	Glu	Arg

Db	185	SerGlySerProSerGluArgSerThrSerGlyGlyTyrSerIlePheHisThrHisLeu	204
		::: :::	
QY	801	-----	ATG 803
Db	205	ProThrValHisProSerArgProArgProTrpSerGlnArgAlaGluAsnThrSer	224
QY	804	GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCATCAAG	863
		::: :::	
Db	225	AspThrArgAspTyrGlySerSerHisAspProSerGlyArgSerTyrThrThrHisAla	244
QY	864	AATGAAGCTGCTGGTTTGGAGGT-----	887
		::: :::	
Db	245	SerGluSerAlaGlyHisSerSerGlySerGluGluHisGlyAlaAsnThrThrSerGly	264
QY	888	-----GTCCCCACGGCTCTGCTAGTAGTCTTGCTCTCCTCTCTCTTCTTGGT	929
		::: :::	
Db	265	ProMetArgLysProGlnIleProGluTrpLeuIleIleLeuAlaSerLeu--LeuAla	283
QY	930	GCTGCAGCTGGTCTTGGATTTTGCTATGTCAAAGGTATGTGAAGGCCTTCCCTTTTACA	989
		::: :::	
Db	284	LeuAlaLeuIleLeuAlaValCys-----IleAlaValAsnSerArgArg	298
QY	990	AACAAGAATCAGCAGAAGCAATGATCGAAACCAAGTAGTAGTAAGGAGGAGAGGCCAAT	1049
		::: :::	
Db	299	ArgCysGlyGlnLysLysLysLeuValIleAsn-----Asn 310	
QY	1050	GATAGCAACCCTAATGAGGAATCAAAGAAAACCTGATAAAAAACCCAGAAGAGTCCAAGAGT	1109
		::: :::	
Db	311	GlyAsnGlyThrMetGluGluArgLysProSerGlyLeuAsnGlyGluAlaSerLysSer	330
RESULT	8		
I37369			
epican - human			
C;Species: Homo sapiens (man)			
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 03-Aug-2001			
C;Accession: I37369; S24631			
R;Kugelman, L.C.; Ganguly, S.; Haggerty, J.G.; Weissman, S.M.; Milstone, L.M.			
J. Invest. Dermatol. 99, 866-891, 1992			
A;Title: The core protein of epican, a heparan sulfate proteoglycan on keratino			
A;Reference number: I37369; PMID:1281868			
A;Note: corrected and republished from J. Invest. Dermatol. 99, 381-385, 1992			
A;Accession: I37369			
A;Status: preliminary; translated from GB/EMBL/DDBJ			
A;Molecule type: mRNA			
A;Residues: 1-699 <RES>			
A;Cross-references: EMBL:X66733; NID:g311190; PID:g311191			

Alignment Scores:	
Pred. No.:	6.15e-10
Score:	208.00
Percent Similarity:	33.98%
Best Local Similarity:	20.19%
Query Match:	5.77%
DB:	2
	Length:
	Matches:
	Conservative:
	Mismatches:
	Indels:
	Gaps:
	699
	104
	71
	178
	162
	23

US-10-079-111-2 (1-2029) x I37369 (1-699)

QY	255	TTGCGTGCAGAA	GAGCTTTCATCC	AGGTGT	CATGC	AGAATTAT	TGGGATCAC	CTTGTG	314
Db	17	LeuSerLeuAla	GlnIleAspLeu	AsnIleThr	CysArgPhe	AlaGlyVal	PheHisVal	36	
QY	315	AGCAAAAAGCG	AACCCAGCAGCT	GAATTTC	CAGAAAGCT	AAGAGGCC	TGTAGGCTGCTG	374	
Db	37	GluLysAsnGly	ArgTyrSerIle	SerArgThr	GluAlaAla	AspLeuCys	LysAlaPhe	56	
QY	375	GGACTAAGTTT	TGGCCGGCAAG	CAAGATTG	AAACAGCCTT	GAAAGCTAG	CTTTGAAACT	434	
Db	57	AsnSerThrLeu	ProThrMetAla	GlnMetGlu	LysAlaLeu	SerIleGly	PheGluThr	76	
QY	435	TGCAGCTATG	GCTGGTTGGAG	ATTCGTGGT	CATCTCTAG	GATTAGCC	CAAAACCC	494	
Db	77	CysArgTyrGly	PheIle---Glu	GlyHisValVal	IleProArgIle	HisProAsnSer	95		

R;Stamenkovic, I.; Aruffo, A.; Amiot, M.; Seed, B.
EMBO J. 10, 343-348, 1991
A;Title: The hematopoietic and epithelial forms of CD44 are distinct polypeptides with
A;Reference number: S13530; MUID:91122041; PMID:1991450
A;Accession: S13530
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-493 <STA>
A;Cross-references: EMBL:X55150; NID:g29800; PIDN:CAA38951.1; PID:g29801
C;Keywords: transmembrane protein

US-10-079-111-2 (1-2029) x S45305 (1-351)

QY 225 TGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGGGTGCAGAAAGAGCTTTCCATCCAGGTG 284
Db 3 TrpGlyLeuCysLeuLeu-----ArgLeuSerLeuAlaGlnIleAspLeuAsnIle 19
QY 285 TCATGCAGAAATTATGGGGATCACCCCTTGTGACGCAAAAAGCGAACCCAGCAGCTGAATTC 344
Db 20 ThrCysArgTyrAlaGlyValPheHisValGluLysAsnGlyArgTyrSerIleSerArg 39
QY 345 ACAGAAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTT 404
Db 40 ThrAlaAlaAspLeuCysLysAlaPheAsnSerThrLeuProThrMetAlaGlnMet 59
QY 405 GAAACAGCCTTGAAAGCTAGCTTTGAAACTGTCAGCTATGGCTGGGTGGAGATGGATTC 464
Db 60 GluArgAlaLeuSerValGlyPheGluThrCysArgTyrGlyPheIle---GluGlyHis 78
QY 465 GTGGTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCCTG 524
Db 79 ValValIleProArgIleGlnProAsnAlaIleCysAlaAlaAsnHisThrGlyValTyr 98
QY 525 ATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAATCATCTGATACT 584
Db 99 Ile---LeuIleSerAsnThrSerGlnTyrAspThrTyrCysPheAsnAlaSerAlaPro 117
QY 585 TGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAGATCCCATATATCAACACTCAA 644
Db 118 ProGluGluAspCys-----ThrSerValThrHisLeuProAsnAlaPhe 132
QY 645 ACTGCAACACAAACACAGAATTTATTGTCACTGACAGTACC---TACTCGGTGGCATCC 701
Db 133 AspGlyProIleThrIleThrIleValAsnArgAspGlyThrArgTyrSerGlnLysGly 152
QY 702 CTTTACTCTACATACCTGCC-----CCTACTACTACTCCTCCTGCTCCAGCTTCC 752
Db 153 GluTyrArgThrAsnProGluAspIleAsnProSerAsnProThrAspAspValSer 172
QY 753 ACTTCTATTCCACGGAGAAAAAATTGATTTGTGTCACAGAGTTTTT-----800
Db 173 SerGlySerSerSerGluArgSerThrSerAlaGlyTyrAsnIlePheHisThrHisLeu 192
QY 801 -----ATGGAACCTAGCACCATGTCTACAGAAACTGAA---833
Db 193 ProThrAlaTyrProThrGluAspGlnAspSerSerArgValSerSerAsnSerAspHis 212
QY 834 -----CCATTTGTTGAAATAAAGCAGCA 857
Db 213 ThrProIleThrLysAspHisAspSerSerValHisProSerGluArgSerHisThrThr 232
QY 858 TTCAAGAATGAAGCTGCTGGGTTT-----GGAGGT-----887
Db 233 HisGlySerGluSerAlaGlyHisSerSerGlySerGlnGluGlyGlyAlaAsnThrThr 252
QY 888 -----GTCCCCACGGCTCTGCTAGTGTGCTTGTGCTTGTCTCTCCTCTTC 923
Db 253 SerGlyProMetArgLysProGlnIleProGluTrpLeuIleIleLeuAlaSerLeu--- 271
QY 924 TTTGGTGTGCAGCTGCTTGGATTTTGTATGTCAAAAAGGTATGTGAAGGCCTTCCT 983
Db 272 LeuAlaLeuAlaLeuIleLeuAlaValCysIleAla-----283
QY 984 TTTACAAACAAGAAATCAGCAGAGGAATGATCGAAACCAAGTAGTAAAGGAGGAGAAG 1043
Db 284 -----ValAsnSerArgArgArgCysGlyGlnLysLysLysLeuValIleAsnAsn 300
QY 1044 GCCAAT-----GATAGCAACCTT-----AATGAGGAATCAAGAAAACT 1082
Db 301 GlyAsnGlyAlaValGlyAspArgLysProSerGlyIleAsnGlyGluAlaSerLysSer 320
QY 1083 GATAAA-----AACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACC 1124
Db 321 GlnGluMetValHisLeuValAsnLysGluProSerGluThrProAspGlnTyrThr 339

RESULT 12

JH0518
lymphocyte homing receptor CD44, splice form CD44R1 - human
N;Alternate names: cell adhesion molecule core protein CD44E, keratinocyte; cell surface
N;Contains: lymphocyte homing receptor CD44, splice form CD44R1; lymphocyte homing recep
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 18-Aug-2000
C;Accession: JH0518; JH0519; PH0859; A39209; A42402; C42402; A53029; S16147
R;Dougherty, G.J.; Lansdorp, P.M.; Cooper, D.L.; Humphries, R.K.
J. Exp. Med. 174, 1-5, 1991
A;Title: Molecular cloning of CD44R1 and CD44R2, two novel isoforms of the human CD44 ly
A;Reference number: JH0518; MUID:91277598; PMID:2056274
A;Accession: JH0518
A;Molecule type: mRNA
A;Residues: 1-426 <DOU>
A;Experimental source: lymphocytes, cell line KGla
A;Accession: JH0519
A;Molecule type: mRNA
A;Residues: 1-223,288-426 <DO2>
A;Experimental source: lymphocyte, cell line KGla
R;Cooper, D.L.; Dougherty, G.; Harn, H.J.; Jackson, S.; Baptist, E.W.; Byers, J.; Datta,
Biochem. Biophys. Res. Commun. 182, 569-578, 1992
A;Title: The complex CD44 transcriptional unit: alternative splicing of three internal e
A;Reference number: PH0859; MUID:92134271; PMID:1734871
A;Accession: PH0859
A;Molecule type: DNA
A;Residues: 223-357 <COO>
R;Brown, T.A.; Bouchard, T.; St. John, T.; Wayne, E.; Carter, W.G.
J. Cell Biol. 113, 207-221, 1991
A;Title: Human keratinocytes express a new CD44 core protein (CD44E) as a heparan-sulfat
A;Reference number: A39209; MUID:91177958; PMID:2007624
A;Accession: A39209
A;Molecule type: mRNA
A;Residues: 184-376 <BRO>
A;Cross-references: GB:X55938; NID:g29802; PIDN:CAA39404.1; PID:g930047
R;Jackson, D.G.; Buckley, J.; Bell, J.I.
J. Biol. Chem. 267, 4732-4739, 1992
A;Title: Multiple variants of the human lymphocyte homing receptor CD44 generated by ins
A;Reference number: A42402; MUID:92165834; PMID:1537855
A;Accession: A42402
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 217-223,288-359 <JAC>
A;Note: sequence extracted from NCBI backbone (NCBIN:83964, NCBIP:83965)
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A;Status: preliminary
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A;Residues: 217-320 <JA2>
A;Note: sequence extracted from NCBI backbone (NCBIN:83968, NCBIP:83969)
A;Note: variant D
R;Shepley, M.P.; Racaniello, V.R.
J. Virol. 68, 1301-1308, 1994
A;Title: A monoclonal antibody that blocks poliovirus attachment recognizes the lymphocy
A;Reference number: A53029; MUID:94149816; PMID:7508992
A;Accession: A53029
A;Status: preliminary
A;Molecule type: protein
A;Residues: 67-76,'X',78-89 <SHE>
C;Genetics:
A;Gene: GDB:CD44; MDU2; MDU3; MI
A;Cross-references: GDB:120739; OMIM:107269
A;Map position: 11pter-11p13
A;Introns: 35/1; 65/1; 133/1
C;Superfamily: human cell adhesion protein CD44
C;Keywords: alternative splicing; cell adhesion; chondroitin sulfate proteoglycan; glyc
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F;1-223,288-426/Product: lymphocyte homing receptor CD44, splice form CD44R2 #status pr
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F;354/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted

Alignment Scores:

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QY	315	AGCAAAAAGCGAACCCAGCAGCTGAATTTCCACAGAAGCTAAGGAGGCCCTGTAGGCTGCTG	374
Db	37	GluLysAsnGlyArgTyrSerIleSerArgThrGluAlaAlaAspLeuCysLysAlaPhe	56
QY	375	GGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCTAGCTTTGAAACT	434
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Db	77	CysArgTyrGlyPheIle---GluGlyHisValValIleProArgIleHisProAsnSer	95
QY	495	AAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTCGAAGGTTCCAGTGAGCCGACAGTTT	554
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QY	633	TTCAACACTCAAACACTGCAACACAAAAACAACAGAA-----TTTATT	671
Db	175	AspAspAspValSerSerGlySerSerSerGluArgSerSerThrSerGlyTyrIle	194
QY	672	-----	680
Db	195	PheTyrThrPheSerThrValHisProIleProAspGluAspSerProTyrIleThrAsp	214
QY	681	AGTACC-----TACTCGGTGGCATCCCTTACTCTACAAATACCTGCCCCT	725
Db	215	SerThrAspArgIleProAlaThrAsnMetAspSerSerHisSerThrThrLeuGlnPro	234
QY	726	ACTACTACTCCTCCTGCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTGT	785
Db	235	ThrAlaAsnProAsnThrGlyLeuValGluAspLeuAspArgThrGlyProLeuSerMet	254
QY	786	GTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAA	845
Db	255	ThrThrGlnGln---SerAsnSerGlnSerPheSerThrSerHisGluGlyLeuGluGlu	273
QY	846	AATAAA-----GCAGCATTCAGAATGAAGCTGCTGGG	878
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QY	981	CCTTTTACAAACAGAATCAGCAGAGGAATGATCGAAACCAAAGTA-----	1028
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C;Species: Homo sapiens (man)			
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000			
C;Accession: I77371			
R;Tanabe, K.K.; Nishi, T.; Sava, H.			
Mol. Carcinog. 7, 212-220, 1993			
A;Title: Novel variants of CD44 arising from alternative splicing: changes in the CD44 a			
A;Reference number: I57483; MUID:93356912; PMID:8352881			
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A;Status: preliminary; translated from GB/EMBL/DDBJ			
A;Molecule type: mRNA			
A;Residues: 1-395 <RES>			
A;Cross-references: GB:S66400; NID:g435697; PIDN:AAB27919.1; PID:g435700			
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A;Map position: 11pter-11p13			
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QY	315	AGCAAAAAGGCGAACCCAGCAGCTGAATTTCCACAGAAGCTAAGGAGGCCCTGTAGGCTGCTG	374
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QY	375	GGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACT	434
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QY	435	TGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCATCTCTAGGATTAGCCCAAAACCCC	494
Db	77	CysArgTyrGlyPheIle---GluGlyHisValValIleProArgIleHisProAsnSer	95
QY	495	AAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTCGAAGGTTCCAGTGAGCCGACAGTTT	554

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QY	633	TTCAACACTCAAACTGCAACACAACAAGAAATTTATTGTCAGTGACAGT-		683
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R:Tavernor, A.S.; Deverson, E.V.; Coadwell, W.J.; Lunn, D.P.; Zhang, C.; Davis, W.; Butc				
Immunogenetics 37, 474-477, 1993				
A>Title: Molecular cloning of equine CD44 cDNA by a COS cell expression system.				
A:Reference number: I46245; MUID:93170897; PMID:8436424				
A:Accession: I46245				
A>Status: preliminary; translated from GB/EMBL/DDBJ				
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A;Cross-references: EMBL:X66862; NID:g1059; PIDN:CAA47331.1; PID:g1060				
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A47171
chondroitin sulfate proteoglycan PG-M core protein - chicken
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C/Accession: A47171
R/Shinomura, T.; Nishida, Y.; Ito, K.; Kimata, K.
J. Biol. Chem. 268, 14461-14469, 1993
A/Title: cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed during
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US-10-079-111-2 (1-2029) x A47171 (1-3562)
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QY 207 TTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAA 266
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Job time : 97.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 13, 2004, 10:03:01 ; Search time 40.5 Seconds
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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 283362

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO spoel_p/US10079111/runat 13092004 102125 1816/app query.fasta_1.2183
-DB=SwissProt_42 -QFMT=fastan -SUFFIX=rsp -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10079111@cgn_1_1_56@runat 13092004 102125 1816 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	233.5	6.5	362	1 CD44_CRIGR	P20944 cricetulus
2	228.5	6.3	503	1 CD44_RAT	P26051 rattus norv
3	222.5	6.2	362	1 CD44_PAPHA	P14745 papio hamad
4	221	6.1	742	1 CD44_HUMAN	P16070 h cd44 anti
5	212.5	5.9	431	1 CD44_MESAU	Q60522 m cd44 anti
6	211	5.9	778	1 CD44_MOUSE	P15379 mus musculu
7	208.5	5.8	366	1 CD44_BOVIN	Q29423 bos taurus
8	202.5	5.6	351	1 CD44_CANFA	Q28284 canis famil
9	186	5.2	359	1 CD44_HORSE	Q05078 equus cabal
10	152.5	4.2	3562	1 PGCV_CHICK	Q90953 gallus gall
11	150	4.2	537	1 PGCA_PIG	Q29011 sus scrofa
12	148.5	4.1	2109	1 PGCA_CHICK	P07898 gallus gall
13	145	4.0	277	1 TSG6_HUMAN	P98066 homo sapien
14	144	4.0	275	1 TSG6_MOUSE	O08859 mus musculu
15	143	4.0	2364	1 PGCA_BOVIN	P13608 bos taurus
16	139.5	3.9	2333	1 PGCA_CANFA	Q28343 canis famil
17	138.5	3.8	2415	1 PGCA_HUMAN	P16112 homo sapien
18	137	3.8	276	1 TSG6_RABIT	P98065 oryctolagus

19	136.5	3.8	2124	1 PGCA_RAT	P07897 rattus norv
20	132.5	3.7	2132	1 PGCA_MOUSE	Q61282 mus musculu
21	131.5	3.6	912	1 PGCB_BOVIN	Q28062 bos taurus
22	130.5	3.6	883	1 PGCB_MOUSE	Q61361 mus musculu
23	130.5	3.6	883	1 PGCB_RAT	P55068 rattus norv
24	128	3.6	2738	1 PGCV_RAT	Q9erb4 rattus norv
25	127.5	3.5	1321	1 PGCN_HUMAN	O14594 homo sapien
26	127.5	3.5	3358	1 PGCV_MOUSE	Q62059 mus musculu
27	126	3.5	1257	1 PGCN_RAT	P55067 rattus norv
28	122	3.4	394	1 PGCN_RABIT	Q28670 oryctolagus
29	120	3.3	3396	1 PGCV_HUMAN	P13611 homo sapien
30	118	3.3	341	1 BRA1_MOUSE	Q9esm3 mus musculu
31	117	3.2	340	1 BRA1_HUMAN	Q9gzv7 homo sapien
32	115	3.2	3381	1 PGCV_BOVIN	P81282 bos taurus
33	113	3.1	341	1 BRA1_RAT	Q9esm2 rattus norv
34	113	3.1	892	1 LDL2_XENLA	Q99088 xenopus lae
35	112.5	3.1	417	1 PGCB_FELCA	P41725 felis silve
36	112	3.1	390	1 VGLI_HSV11	P06487 herpes simp
37	112	3.1	1268	1 PGCN_MOUSE	P55066 mus musculu
38	111.5	3.1	402	1 ODP2_MYCPN	P75392 mycoplasma
39	110	3.1	354	1 PLK_HUMAN	P10915 homo sapien
40	109.5	3.0	355	1 PLK_CHICK	P07354 gallus gall
41	109	3.0	354	1 PLK_RAT	P03994 rattus norv
42	109	3.0	356	1 PLK_MOUSE	Q9gup5 mus musculu
43	109	3.0	1609	1 FIG2_YEAST	P25653 saccharomyc
44	107	3.0	354	1 PLK_BOVIN	P55252 bos taurus
45	106.5	3.0	1169	1 YK82_YEAST	P36170 saccharomyc

ALIGNMENTS

RESULT 1

CD44_CRIGR	ID	CD44_CRIGR	STANDARD;	PRT;	362 AA.
AC	P20944;				
DT	01-FEB-1991 (Rel. 17, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	15-MAR-2004 (Rel. 43, Last annotation update)				
DE	CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)				
DE	(Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte				
DE	homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor).				
GN	CD44.				
OS	Cricetulus griseus (Chinese hamster).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;				
OC	Cricetulus.				
OX	NCBI_TaxID=10029;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90304889; PubMed=1694723;				
RA	Aruffo A., Stamenkovic I., Melnick M., Underhill C.B., Seed B.;				
RT	"CD44 is the principal cell surface receptor for hyaluronate.";				
RL	Cell 61:1303-1313(1990).				
CC	-!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to				
CC	mucosal high endothelial venule and to types I and VI collagen.				
CC	Probably involved in matrix adhesion, lymphocyte activation and				
CC	lymph node homing.				
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-!- INDUCTION: By EBV.				
CC	-!- PTM: Extensively modified including N- and O-linked glycosylation,				
CC	addition of the glycosaminoglycan chondroitin sulfate, of sulfate,				
CC	of phosphate to cytoplasmic domain serine residues.				
CC	-!- SIMILARITY: Contains 1 link domain.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
CC	EMBL; M33827; AAA36967.1; --				

QY	987	ACAAACAAGAATCAGCAGAAGGAA-----	-----ATGATC	1016
Db	284	AsnAsnHisGluTyrGlnAspGluGluThrProHisAlaThrSerThrThrTrpAla	303	
QY	1017	GAAACCAAGTAGTAAGGAGGAGAGGCAATGATAGCAACCCCTAATGAGGAATCAAAG	1076	
Db	304	AspProAsnSerThrThrGluGluAlaAlaThrGlnLysGluLysTrpPheGluAsnGlu	323	
QY	1077	AAACTGTAAAAACCCA-----GAAGAGTCCAAGAGTCCAAGCAAAACTACC	1124	
Db	324	TrpGlnGlyAsnProProThrProSerGluAspSerHisValThrGluGlyThrThr	343	
QY	1125	GTGGGATGCTGGAAGCTGAAGTTTAGATGAGA-----CAGAAATGAGGAGACACA	1175	
Db	344	AlaSerAlaHisAsnAsnHisProSerGlnArgMetThrThrGlnSerGlnGluAspVal	363	
QY	1176	CCTGAGGCTGGTTTCTTTTCATGCTCCTTACCTGCCCTGCCAGCTGGGGAAATCAAAAGGGCC	1235	
Db	364	SerTrpThrAspPhePheAsp---ProIleSerHisProMetGlyGln-----Gly	379	
QY	1236	AAAGAACCAAGAAAGAAAGTCCACCTCTGGTTCCTAACTGGAATCAGTCCAGGACTGCCA	1295	
Db	380	HisGlnThrGluSerLysGlyHis-----SerSerGly---Asn	391	
QY	1296	TTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCT-----CCTTATTGTAACCTGTC	1349	
Db	392	GlnAspSerGlyValThrThrThrSerGlyProAlaArgArgProGlnIle---ProGlu	410	
QY	1350	TGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCCTTTCTAGCCTGGCTATGTCTA	1409	
Db	411	TrpLeu--IleIleLeuAlaSerLeuLeuAlaLeuAlaLeuIleLeuAlaValCys---	428	
QY	1410	ATAATATCCACTGGGAGAAAGGAGTTTGCAAAAGTGCAAGGACCTTAAACATCTCATCA	1469	
Db	429	-----IleAlaValAsnSerArgArgCysGlyGlnLysLysLysLeuVal-	444	
QY	1470	GTATCCAGTGGTAAA-----	-----AAGGCC	1490
Db	445	IleAsnSerGlyAsnGlyThrValGluAspArgLysProSerGluLeuAsnGlyGluAla	464	
QY	1491	TCCTGGCTGTCTGAGGCTAGTGGTTGAAAGCCAAAGGAGTCACTGAGACC---	AAGGCT	1547
Db	465	SerLysSerGlnGluMetValHisLeuValAsnLysGluProThrGluThrProAspGln	484	
QY	1548	TTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCTCA	1583	
Db	485	PheMetThrAlaAspGluThrArgAsnLeuGlnSer	496	
RESULT 3				
CD44_PAPHA				
ID	CD44_PAPHA	STANDARD;	PRT;	362 AA.
AC	P14745;			
DT	01-APR-1990	(Rel. 14, Created)		
DT	01-APR-1990	(Rel. 14, Last sequence update)		
DT	15-MAR-2004	(Rel. 43, Last annotation update)		
DE	CD44	antigen precursor (phagocytic glycoprotein I) (PGP-I) (HUTCH-I)		
DE	(Extracellular matrix receptor-III) (ECWR-III) (GP90 lymphocyte			
DE	homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor).			
GN	CD44.			
OS	Papio hamadryas	(Hamadryas baboon).		
OC	Eukaryota;	Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia;	Eutheria; Primates; Catarrhini; Cercopithecidae;		
OC	Cercopithecinae;	Papio.		
OX	NCBI_TaxID=9557;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 66-74.			
RX	MEDLINE=89282830;	PubMed=2471974;		
RA	Idzerda R.L., Carter W.G., Nottenburg C., Wayne E.A.,			
RA	Gallatin W.M., St John T.;			
RT	"Isolation and DNA sequence of a cDNA clone encoding a lymphocyte			
RT	adhesion receptor for high endothelium."			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:4659-4663 (1989).			
CC	-!	FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to		
CC		mucosal high endothelial venule and to types I and VI collagen.		
CC		Probably involved in matrix adhesion, lymphocyte activation and		
CC		lymph node homing.		
CC	-!	SUBCELLULAR LOCATION: Type I membrane protein.		
CC	-!	PTM: Extensively modified including N- and O-linked glycosylation,		
CC		addition of the glycosaminoglycan chondroitin sulfate, of sulfate,		
CC		of phosphate to cytoplasmic domain serine residues.		
CC	-!	SIMILARITY: Contains 1 link domain.		
CC		-----		
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC		between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC		the European Bioinformatics Institute. There are no restrictions on its		
CC		use by non-profit institutions as long as its content is in no way		
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CC		entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC		or send an email to license@isb-sib.ch).		
CC		-----		
DR	EMBL;	M22452; AAA35385.1; -.		
DR	HSSP;	P98066; 1TSG.		
DR	InterPro;	IPR001231; CD44_antigen.		
DR	InterPro;	IPR000538; Link.		
DR	Pfam;	PF00193; Xlink; 1.		
DR	PRINTS;	PR00658; CD44.		
DR	PRINTS;	PR01265; LINKMODULE.		
DR	ProDom;	PD000918; Link; 1.		
DR	SMART;	SM00445; LINK; 1.		
DR	PROSITE;	PS01241; LINK; 1.		
KW		Cell adhesion; Transmembrane; Glycoprotein; Phosphorylation; Receptor;		
KW		Proteoglycan; Signal; Alternative splicing;		
KW		Pyrrolidone carboxylic acid.		
FT	SIGNAL	1 20	BY SIMILARITY.	
FT	CHAIN	21 362	CD44 ANTIGEN.	
FT	DOMAIN	21 269	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	270 290	POTENTIAL.	
FT	DOMAIN	291 362	CYTOPLASMIC (POTENTIAL).	
FT	DOMAIN	48 119	LINK.	
FT	DOMAIN	150 158	ARG/LYS-RICH (BASIC).	
FT	DOMAIN	225 269	STEM.	
FT	MOD RES	21 21	PYRROLIDONE CARBOXYLIC ACID (PROBABLE).	
FT	DISULFID	53 118	BY SIMILARITY.	
FT	DISULFID	77 97	BY SIMILARITY.	
FT	MOD_RES	292 292	PHOSPHORYLATION (BY PKC) (PARTIAL) (BY	
FT			SIMILARITY).	
FT	MOD_RES	326 326	PHOSPHORYLATION (PARTIAL) (BY	
FT			SIMILARITY).	
FT	CARBOHYD	25 25	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	57 57	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	100 100	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	110 110	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	120 120	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	256 256	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CONFLICT	67 67	E -> V (IN REF. 1; AA SEQUENCE).	
SQ	SEQUENCE	362 AA;	39378 MW; 578BFCE7C3D52FFF CRC64;	
Alignment Scores:				
Pred. No.:		2.71e-11	Length:	362
Score:		222.50	Matches:	92
Percent Similarity:		37.40%	Conservative:	43
Best local Similarity:		25.48%	Mismatches:	127
Query Match:		6.17%	Indels:	99
DB:		1	Gaps:	16
US-10-079-111-2 (1-2029) x CD44_PAPHA (1-362)				
QY	240	CTGGTCCAAGGCTCTTTGCGTGCAGAGAGCTTTCCATCCAGGTGTCAGAAATTATG	299	
Db	14	LeuValGlnLeuSerLeu-----AlaGlnIleAspLeuAsnIleThrCysArgPheGlu	31	
QY	300	GGGATCACCCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTCACAGAAGCTAAGGAG	359	
Db	32	GlyIleTyrHisValGluLysAsnGlyArgTyrSerIleSerArgThrGluAlaAlaAsp	51	

RX MEDLINE=89168435; PubMed=2466576;
RA Goldstein L.A., Zhou D.F.H., Picker L.J., Minty C.N., Bargatze R.F.,
RA Ding J.F., Butcher E.C.;
RT "A human lymphocyte homing receptor, the hermes antigen, is related
RT to cartilage proteoglycan core and link proteins.";
RL Cell 56:1063-1072(1989).
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM WITHOUT EXON 6).
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [10]
RP SEQUENCE OF 184-222 AND 473-625 FROM N.A. (ISOFORM KERATINOCYTE).
RC TISSUE=Foreskin;
RX MEDLINE=91177958; PubMed=2007624;
RA Brown T.A., Bouchard T., St John T., Wayner E., Carter W.G.;
RT "Human keratinocytes express a new CD44 core protein (CD44E) as a
RT heparan-sulfate intrinsic membrane proteoglycan with additional
RT exons.";
RL J. Cell Biol. 113:207-221(1991).
RN [11]
RP SEQUENCE FROM N.A.
RC TISSUE=Articular cartilage;
RA Bosch P.P., Stevens J.W., Buckwalter J.A., Midura R.J.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE OF 267-603 FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=92005448; PubMed=1717145;
RA Hofmann M., Rudy W., Zoeller M., Toelg C., Ponta H., Herrlich P.,
RA Guenther U.;
RT "CD44 splice variants confer metastatic behavior in rats: homologous
RT sequences are expressed in human tumor cell lines.";
RL Cancer Res. 51:5292-5297(1991).
RN [13]
RP SEQUENCE OF 223-265 FROM N.A.
RX MEDLINE=94198700; PubMed=8148709;
RA Matsumura Y., Harbury D., Smith J., Tarin D.;
RT "Non-invasive detection of malignancy by identification of unusual
RT CD44 gene activity in exfoliated cancer cells.";
RL BMJ 308:619-624(1994).
RN [14]
RP SEQUENCE OF 1-22 FROM N.A.
RC TISSUE=Lymphoblast;
RX MEDLINE=92017823; PubMed=1922057;
RA Shtivelman E., Bishop J.M.;
RT "Expression of CD44 is repressed in neuroblastoma cells.";
RL Mol. Cell. Biol. 11:5446-5453(1991).
RN [15]
RP REVIEW ON FUNCTION AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=22399881; PubMed=12511867;
RA Ponta H., Sherman L., Herrlich P.A.;
RT "CD44: from adhesion molecules to signalling regulators.";
RL Nat. Rev. Mol. Cell Biol. 4:33-45(2003).

RN [16]
RP PHOSPHORYLATION OF SER-706.
RX MEDLINE=98248445; PubMed=9580567;
RA Peck D., Isacke C.M.;
RT "Hyaluronan-dependent cell migration can be blocked by a CD44
RT cytoplasmic domain peptide containing a phosphoserine at position
RT 325.";
RL J. Cell Sci. 111:1595-1601(1998).
RN [17]
RP PHOSPHORYLATION OF SER-672.
RX MEDLINE=22038351; PubMed=12032545;
RA Legg J.W., Lewis C.A., Parsons M., Ng T., Isacke C.M.;
RT "A novel PKC-regulated mechanism controls CD44 ezrin association and
RT directional cell motility.";
RL Nat. Cell Biol. 4:399-407(2002).
RN [18]
RP GLYCOSYLATION AND PROCESSING.
RX MEDLINE=22766015; PubMed=12883358;
RA Bartolazzi A.;
RT "CD44s adhesive function spontaneous and PMA-inducible CD44 cleavage
RT are regulated at post-translational level in cells of melanocytic
RL lineage.";
RL Melanoma Res. 13:325-337(2003).
RN [19]
RP VARIANT BLOOD GROUP INDIAN PRO-46.
RX MEDLINE=96215152; PubMed=8636151;
RA Telen M.J., Udani M., Washington M.K., Levesque M.C., Lloyd E.,
RA Rao N.;
RT "A blood group-related polymorphism of CD44 abolishes a hyaluronan-
RT binding consensus sequence without preventing hyaluronan binding.";
RL J. Biol. Chem. 271:7147-7153(1996).
CC -!- FUNCTION: Receptor for hyaluronic acid (HA). Mediates cell-cell
CC and cell-matrix interactions through its affinity for HA, and
CC possibly also through its affinity for other ligands such as
CC osteopontin, collagens, and matrix metalloproteinases (MMPs).
CC Adhesion with HA plays an important role in cell migration, tumor
CC growth and progression. Also involved in lymphocyte activation,
CC recirculation and homing, and in hematopoiesis. Altered expression
CC or dysfunction causes numerous pathogenic phenotypes. Great
CC protein heterogeneity due to numerous alternative splicing and
CC post-translational modification events.
CC -!- SUBUNIT: Interacts with HA, as well as other glycosaminoglycans,
CC collagen, laminin, and fibronectin via its N-terminal segment.
CC Interacts with ANK, the ERM proteins (VIL2, RDX and
CC MSN), and NF2 via its C-terminal segment.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist. Additional isoforms
CC are produced by alternative splicing of 10 out of 19 exons
CC within the extracellular domain. Additional diversity is

Alignment Scores:
Pred. No.: 4.45e-11 Length: 742
Score: 221.00 Matches: 116
Percent Similarity: 32.08% Conservative: 63
Best Local Similarity: 20.79% Mismatches: 176
Query Match: 6.13% Indels: 203
DB: 1 Gaps: 23

US-10-079-111-2 (1-2029) x CD44_HUMAN (1-742)

QY 255 TTGCGTGCAGAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGATCACCCTTGTG 314
||| :::: :: :::::||||| ::::: |||
Db 17 LeuSerLeuAlaGlnIleAspLeuAsnIleThrCysArgPheAlaGlyValPheHisVal 36
QY 315 AGCAAAAGCGGAACCAGCAGCTGATTTTCACAGAAGCTAAGGAGCCCTGTAGGCTGCTG 374
||| ::::: ||||| ::::: |||
Db 37 GluLysAsnGlyArgTyrSerIleSerArgThrGluAlaAlaspLeuCysLysAlaPhe 56
QY 375 GGACTAAGTTGGCCGCAAGGACCACCAAGTTGAAACAGCCCTTGAAGCTAGCTTTGAAACT 434
::: ||| ::::: |||||
Db 57 AsnSerThrLeuProThrMetAlaGlnMetGluLysAlaLeuSerIleGlyPheGluThr 76

QY	435	TGCAGCTATGGCTGGTGGAGATGGATTTCGTGGTCACTCTAGGATTAGCCCAACCC	494
Db	77	CysArgTyrGlyPheIle---GluGlyHisValIleProArgIleHisProAsnSer	95
QY	495	AAGTGTGGGAAAAATGGGTGGTGTCTCTGATTGGAGGTTCAGTGAGCCGACAGTTT	554
Db	96	IleCysAlaAlaAsnAsnThrGlyValTyrIleLeuThrSerAsnThrSer---GlnTyr	114
QY	555	GCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTCATT-----	602
Db	115	AspThrTyrCysPheAsnAlaSerAlaProProGluGluAspCysThrSerValThrAsp	134
QY	602	-----	602
Db	135	LeuProAsnAlaPheAspGlyProIleThrIleThrIleValAsnArgAspGlyThrArg	154
QY	603	-----CCAGAAATATACACCACCAAGATCCCAT	632
Db	155	TyrValGlnLysGlyGluTyrArgThrAsnProGluAspIleTyrProSerAsnProThr	174
QY	633	TTCAAACACTCAAACACTGCAACACAAACACAGAATTTATTGTCAGTGACAGTACCTACG	692
Db	175	AspAspValSerSerGlySerSerGluArgSerSerThrSerGlyGlyTyr---	193
QY	693	GTGGCATCCCTTACTCTACAATA---CCTGCCCTTACTACTCTCCT-----	740
Db	194	IlePheTyrThrPheSerThrValHisProIleProAspGluAspSerProTyrIleThr	213
QY	741	-----GCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTGT	785
Db	214	AspSerThrAspArgIleProAlaThrThr-----	223
QY	786	GTCACAGAAGTTTTTATGGAACACTAGCACCATGTCTACAGAAACTGAACCATTTGTGAA	845
Db	224	-----LeuMetSerThrSerAlaThrAlaThrGluThr-----	234
QY	846	AATAAAGCAGCATTCAAGAATGAAGCTGTGGTTTGGAGGTGTCCCCACGGCTCTGCTA	905
Db	235	-----AlaThrLysArgGlnGluThr---TrpAspTrp-----	244
QY	906	GTGCTGTCTCTCTCTTTTGGTGTGCTGAGCTGGTCTGGATTGTGCTATGTCAAAAGG	965
Db	245	-----PheSerTrpLeuPheLeuProSerGluS	254
QY	966	TATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAATGATCGAAACAAA	1025
Db	254	erLysAsnHisLeu-----HisThrThrThrGlnMetAlaGlyThrSerSerAsnThrI	272
QY	1026	GTAATAAGGAGGAGAGGCAATGATAGCAACCCCTAATGAGGAATCAAAGAAA-----	1079
Db	272	leSerAlaGlyTrpGlu-ProAsnGluGluAsnGluAspGluArgAspArgHisLeuSer	291
QY	1079	-----	1079
Db	292	PheSerGlySerGlyIleAspAspAspGluAspPheIleSerSerThrIleSerThrThr	311
QY	1080	-----ACTGATAAAACCCAGAAAGAG	1100
Db	312	ProArgAlaPheAspHisThrLysGlnAsnGlnAspTrpThrGlnTrpAsnProSerHis	331
QY	1101	TCCAAGAGTCCAAGC-----AAAACCTACCGTGCATGCTGGAAGCTGAAGTTTAG	1151
Db	332	Ser---AsnProGluValLeuLeuGlnThrThrThrArgMetThrAspValAsp-----	348
QY	1152	ATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCTCATGCTCCTTACCCCTGCC	1211
Db	349	-----ArgAsnGlyThrThrAlaTyrGluGlyAsnTrpAsn-----	360
QY	1212	CCAGCTGGGGAATCAAAAGGCCCAAGAACCAAGAAAGTCCACCTTGGTTCCTA	1271
Db	361	-----ProGluAlaHisPro-----	365
QY	1272	ACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCT	1331
Db	366	-----ProLeuIleHisHisGluHisGluGluGluThr	378
QY	1332	CCTTATTGTAAACCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGCGCTTTC	1391
Db	379	ProHisSer-----ThrSerThrIleGlnAlaThrProSer-----	390
QY	1392	TAGCCTGGCTATGTCCTAATAATATCCCACCTGGGAGAAAGAGTTTTCAAAGTGCAAG	1451
Db	390	-----	390
QY	1452	ACCTAAACATCTCATCAGTATCCAGTGGTAAAGGCTCCTCGCTGTCTGAGGCTAGG	1511
Db	391	-----SerThrThrGluGluThrAlaThrGlnLysGluGlnTrpPheGlyAsn---Arg	407
QY	1512	TGGGTTGAAAGCCAGGAGTCACTGAGACCAAGGCTTCTCTACTGATCCCGCAGCTCAG	1571
Db	408	TrpHisGlu-----GlyTyrArgGlnThr-----ProArgGluAspSerHisSer	422
QY	1572	ACCCTTTCTTCAGCTCTGAAAGAGAAACACGATATCCCAC-----CTGACATGT	1619
Db	423	ThrThrGlyThrAlaAlaAlaSerAlaHisThrSerHisProMetGlnGlyArgThrThr	442
QY	1620	CCTTCTGAGCCCGGTAAAGCAAAAGAATGGCAGAAAGTTTAGCCCC	1667
Db	443	ProSerProGluAspSerSer-----TrpThrAspPheAsnPro	456
RESULT 5			
CD44_MESAU			
ID	CD44_MESAU	STANDARD;	PRT; 431 AA.
AC	Q60522; Q60523;		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	01-NOV-1997 (Rel. 35, Last annotation update)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)		
DE	(Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte		
DE	homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor)		
DE	(Heparan sulfate proteoglycan) (HAM1 antigen).		
GN	CD44.		
OS	Mesocricetus auratus (Golden hamster).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;		
OC	Mesocricetus.		
OX	NCBI_TaxID=10036;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).		
RC	STRAIN=LVG; TISSUE=Alveolar macrophage;		
RA	Paulauskis J.D., Kobzik L., Gerard C., Katler M., Godleski J.J.;		
RL	Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.		
CC	-!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to		
CC	mucosal high endothelial venule and to types I and VI collagen.		
CC	Probably involved in matrix adhesion, lymphocyte activation and		
CC	lymph node homing.		
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.		
CC	-!- ALTERNATIVE PRODUCTS:		
CC	Event=Alternative splicing; Named isoforms=2;		
CC	Comment=Additional isoforms seem to exist;		
CC	Name=1;		
CC	isoId=Q60522-1; Sequence=Displayed;		
CC	Name=2;		
CC	isoId=Q60522-2; Sequence=VSP_005322;		
CC	-!- PTM: N-glycosylated (By similarity).		
CC	-!- PTM: O-glycosylated; contains chondroitin sulfate glycans which		
CC	can be more or less sulfated (By similarity).		
CC	-!- PTM: Phosphorylated; activation of PKC results in the		
CC	dephosphorylation of Ser-395 (constitutive phosphorylation site),		
CC	and the phosphorylation of Ser-361 (By similarity).		
CC	-!- SIMILARITY: Contains 1 link domain.		

CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC	the European Bioinformatics Institute. There are no restrictions on its		

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CC -----

DR EMBL; U10880; AAC13767.1; -.
DR EMBL; U10881; AAA19316.1; -.
DR HSSP; P98066; 1TSG.
DR InterPro; IPR001231; CD44_antigen.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK; 1.
KW Cell adhesion; Transmembrane; Glycoprotein; Phosphorylation; Receptor;
KW Proteoglycan; Signal; Alternative splicing;
KW Pyrrolidone carboxylic acid.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 431 CD44 ANTIGEN.
FT DOMAIN 23 338 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 339 359 POTENTIAL.
FT DOMAIN 360 431 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 50 121 LINK.
FT DOMAIN 152 160 ARG/LYS-RICH (BASIC).
FT DOMAIN 226 338 STEM.
FT MOD_RES 23 23 PYRROLIDONE CARBOXYLIC ACID (BY
SIMILARITY).
FT DISULFID 55 120 BY SIMILARITY.
FT DISULFID 79 99 BY SIMILARITY.
FT MOD_RES 361 361 PHOSPHORYLATION (BY PKC) (PARTIAL) (BY
SIMILARITY).
FT MOD_RES 395 395 PHOSPHORYLATION (PARTIAL) (BY
SIMILARITY).
FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 222 291 TRSGKDKRRGGGLPKDATTSLGYTHYPETMENGTLTPV
TPAKTGVFGETEVTVAEDSNFNVDSLPG -> R (in
isoform 2).
FT /FTid=VSP 005322.
SQ SEQUENCE 431 AA; 46807 MW; 4300262E0C6BEA6A CRC64;

Alignment Scores:
Pred. No.: 2.13e-10 Length: 431
Score: 212.50 Matches: 80
Percent Similarity: 38.59% Conservative: 40
Best local Similarity: 25.72% Mismatches: 128
Query Match: 5.90% Indels: 63
DB: 1 Gaps: 12

US-10-079-111-2 (1-2029) x CD44_MESAU (1-431)
QY 252 TCCTTGCTGCAGAAAGAGCTTCCATCCAGGTGTCATGCAGATTATGGGATCACCCCTT 311
||||| ::::: :: ::::: ||||| ||:::
Db 18 SerLeuAlaGlnGlnIleAspLeuAsnIleThrCysArgTyrAlaGlyValPheHis 37
312 GTGAGCAAAAAGCGCAACAGCAGCTGAATTCACAGAAGCTAAGGAGCCCTGTAGGCTG 371
||| ||| ::::: ||||| ||:::
Db ValGluLysAsnGlyArgTyrSerIleSerArgThrGluAlaAlaAspLeuCysGlnAla 57
372 CTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAA 431
::: ||| ||||| ::::: |||||
Db PheAsnSerThrLeuProThrMetAspGlnMetValMetAlaLeuSerLysGlyPheGlu 77
432 ACTTGCAGCTATGGCTGGGTTGGAGATCGATTCATCTCTAGGATTAGCCCAAC 491
||||| ||||| ::::: ::::: ||||| |||||

Db 78 ThrCysArgTyrGlyPheIle---GluGlyHisValIleProArgIleGlnProAsn 96
QY 492 CCCAAGTGTGGAAAAAATGGGGTGGTGTCTCTGATTGTGGAAGTTCCAGTGAGCCGACAG 551
||| ||| ||||| ||||| |||||
Db 97 AlaIleCysAlaAlaAsnHisThrGlyValTyrIleLeuThrSerAsnThrSer---His 115
552 TTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTCGATTCAGAAAATT 611
::: ||||| ::::: ||||| |||||
Db TyrAspThrTyrCysPheAsnAlaSerAlaProLeuGluGluAspCys----- 131
QY 612 ATCACCACCAAGATCCCATATTCAACACTCAACTCAACTCCCTTACTCTACA-----ATA 716
||| ::::: ::: ||||| ||||| |||||
Db 132 ---ThrSerValThrAspLeuProAsnSerPheGluGlyProValThrIleThrIleVal 150
QY 672 GTCAGTGACAGTACC---TACTCGGTGGCATCCCCTTACTCTACA-----ATA 716
||| ||| ||||| ||||| ||||| |||||
Db 151 AsnArgAspGlyThrArgTyrSerLysLysGlyGluTyrArgThrHisGlnGluAspIle 170
QY 717 CCTGCCCTTACTACTCTCTCTCTCCAGCTTCC----- 752
||| ||||| ::::: |||||
Db 171 AspAlaSerAsnThrThrAspAspValSerSerGlySerSerGluLysSerThr 190
QY 753 -----ACITCTATTCCACGGAGAAAAAATTGATTGTGTCACA 791
||| ::::: |||||
Db 191 SerGlyGlyTyrValPheHisThrTyrLeuProThrIleHisSerThrAlaAspGlnAsp 210
QY 792 GAAGTTTATGGAACTAGCACCATGCTCTACAGAACTGAACCATTTGTTGAAAAATAAA 851
::: ::: ||||| ::::: |||||
Db 211 AspProTyrPheIleGlySerThrMetAlaThr-----ThrArg 223
QY 852 GCAGCATCAAGAATGAAGCTGTGGGTTTGGAGGTGTCCCACGGCTCTGCTAGTGCTT 911
::: ||::: ||| ||||| ::::: |||||
Db 224 SerGlyGlyLysAspGlyArgArgGly---GlyGlyLeuProLys----- 237
QY 912 GCTCTCCTCTTCTTTGGTGTGCAGCTGGTCTTGGATTTTGTATGTCAAAAGGTATGTG 971
||| ||||| ||||| |||||
Db 238 -----AspAlaThrThrSerLeu-----GluGlyTyrThr 247
QY 972 AAGGCCCTCCCTTTTACAAACAAGAATCAGCAGAGGAATGATC----- 1016
::: ||||| ||| ::::: |||||
Db 248 ThrHisTyrProGluThrMetGluAsnGlyThrLeuThrProValThrProAlaLysThr 267
QY 1017 -----GAAACCAAGTAGTAAAGGAGGAGGAGGCAAT-----GAT 1052
||||| ::::: ||||| |||||
Db 268 GlyValPheGlyGluThrGluValThrValAlaGluAspSerAsnPheAsnValAspGly 287
QY 1053 AGCAACCCCTAATGAGGAATCAAGAAAACTGAT 1085
||| ||| ::::: |||||
Db 288 SerLeuProGlyAspGlnAspSerSerMetAsp 298
RESULT 6
CD44_MOUSE
ID CD44_MOUSE STANDARD; PRT; 778 AA.
AC P15379; Q05732; Q61395; Q62060; Q62061; Q62062; Q62063; Q62408;
AC Q62409; Q64296; Q99J14; Q9QYX8;
DT 01-APR-1990 (Rel. 14, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
DE (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor)
DE (LY-24).
GN CD44.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 4; 6; 7 AND 12).
RC STRAIN=DBA/2; TISSUE=Lung;
RX MEDLINE=93107170; PubMed=1469058;
RA He Q., Lesley J., Hyman R., Ishihara K., Kincade P.W.;
RT "Molecular isoforms of murine CD44 and evidence that the membrane

RT proximal domain is not critical for hyaluronate recognition.";

RL J. Cell Biol. 119:1711-1719(1992).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 13).

RX MEDLINE=90038499; PubMed=2681416;

RA Zhou D.F.H., Ding J.F., Picker L.J., Bargatze R.F., Butcher E.C.,

RA Goeddel D.V.;

RT "Molecular cloning and expression of Pgp-1. The mouse homolog of the

RT human H-CAM (Hermes) lymphocyte homing receptor.";

RL J. Immunol. 143:3390-3395(1989).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 13).

RX MEDLINE=90046829; PubMed=2682651;

RA Nottenburg C., Rees G., St John T.;

RT "Isolation of mouse CD44 cDNA: structural features are distinct from

RT the primate cDNA.";

RL Proc. Natl. Acad. Sci. U.S.A. 86:8521-8525(1989).

RN [4]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RX MEDLINE=20318634; PubMed=10859330;

RA Wittig B.M., Johansson B., Zoeller M., Schwaerzler C., Guenther U.;

RT "Abrogation of experimental colitis correlates with increased

RT apoptosis in mice deficient for CD44 variant exon 7 (CD44v7).";

RL J. Exp. Med. 191:2053-2064(2000).

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 13).

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters K.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnersch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [6]

RP SEQUENCE FROM N.A. (ISOFORM 13).

RC STRAIN=C57BL/6J; TISSUE=Embryo;

RX MEDLINE=22354683; PubMed=12466851;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaïdo I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Baldarelli R., Hilli D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RN [7]

RP SEQUENCE OF 8-778 FROM N.A. (ISOFORM 13).

RX MEDLINE=90094420; PubMed=2403559;

RA Wolffe E.J., Gause W.C., Pelfrey C.M., Holland S.M., Steinberg A.D.,

RA August J.T.;

RT "The cDNA sequence of mouse Pgp-1 and homology to human CD44 cell

RT surface antigen and proteoglycan core/link proteins.";

RL J. Biol. Chem. 265:341-347(1990).

RN [8]

RP SEQUENCE OF 224-637 FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7 AND 8).

RC STRAIN=GR;

RX MEDLINE=93219085; PubMed=8464707;

RA Toelg C., Hofmann M., Herrlich P., Ponta H.;

RT "Splicing choice from ten variant exons establishes CD44

RT variability.";

RL Nucleic Acids Res. 21:1225-1229(1993).

RN [9]

RP SEQUENCE OF 224-637 FROM N.A. (ISOFORM 9).

RC STRAIN=BALB/c;

RX MEDLINE=93286043; PubMed=8509359;

RA Screaton G.R., Bell M.V., Bell J.I., Jackson D.G.;

RT "The identification of a new alternative exon with highly restricted

RT tissue expression in transcripts encoding the mouse Pgp-1 (CD44)

RT homing receptor. Comparison of all 10 variable exons between mouse,

RT human, and rat.";

RL J. Biol. Chem. 268:12235-12238(1993).

RN [10]

RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 10 AND 11).

RC STRAIN=Swiss Webster;

RX MEDLINE=96355396; PubMed=8702806;

RA Yu Q., Toole B.P.;

RT "A new alternatively spliced exon between v9 and v10 provides a

RT molecular basis for synthesis of soluble CD44.";

RL J. Biol. Chem. 271:20603-20607(1996).

CC -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to

CC mucosal high endothelial venule and to types I and VI collagen.

CC Probably involved in matrix adhesion, lymphocyte activation and

CC lymph node homing.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=13;

CC Name=1;

CC IsoId=P15379-14; Sequence=Displayed;

CC Name=2;

CC IsoId=P15379-7; Sequence=VSP_007329;

CC Name=3;

CC IsoId=P15379-8; Sequence=VSP_007330;

CC Name=4; Synonyms=M2;

CC IsoId=P15379-4; Sequence=VSP_007331;

CC Name=5;

CC IsoId=P15379-9; Sequence=VSP_007332;

CC Name=6; Synonyms=M3;

CC IsoId=P15379-5; Sequence=VSP_005326;

CC Name=7; Synonyms=M4;

CC IsoId=P15379-6; Sequence=VSP_005327;

CC Name=8;

CC IsoId=P15379-10; Sequence=VSP_007330, VSP_007334;

CC Name=9;

CC IsoId=P15379-11; Sequence=VSP_007332, VSP_007335;

CC Name=10;

CC IsoId=P15379-12; Sequence=VSP_007336, VSP_007337;

CC Name=11;

CC IsoId=P15379-13; Sequence=VSP_007338, VSP_007339;

CC Name=12; Synonyms=M1;

CC IsoId=P15379-3; Sequence=VSP_005328;

CC Name=13; Synonyms=M0;

QY 1083 GATAAA-----AACCCAGAAGAGTCCAAAGAGTCCAAGCAAAACTACC 1124
::: ||| ||| |||::: ||| :::
Db 321 GlnGluMetValHisLeuValAsnLysGluProSerGluThrProAspGlnTyrThr 339

RESULT 9
CD44_HORSE
ID CD44_HORSE STANDARD; PRT; 359 AA.
AC Q05078;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
DE (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor).
GN CD44.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93170897; PubMed=8436424;
RA Tavernor A.S., Deverson E.V., Coadwell W.J., Lunn D.P., Zhang C.,
RA Davis W., Butcher G.W.;
RT "Molecular cloning of equine CD44 cDNA by a COS cell expression
RT system.";
RL Immunogenetics 37:474-477(1993).
CC -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
CC mucosal high endothelial venule and to types I and VI collagen.
CC Probably involved in matrix adhesion, lymphocyte activation and
CC lymph node homing.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- PTM: Extensively modified including N- and O-linked glycosylation,
CC addition of the glycosaminoglycan chondroitin sulfate, of sulfate,
CC of phosphate to cytoplasmic domain serine residues.
CC -!- SIMILARITY: Contains 1 link domain.
CC -----
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CC -----
DR EMBL; X66862; CAA47331.1; -.
DR PIR; I46245; S24240.
DR HSSP; P98066; LTSG.
DR InterPro; IPR001231; CD44_antigen.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK; 1.
KW Cell adhesion; Transmembrane; Glycoprotein; Phosphorylation; Receptor;
KW Proteoglycan; Signal; Alternative splicing;
KW Pyrrolidone carboxylic acid.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 359 CD44 ANTIGEN.
FT DOMAIN 21 266 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 267 287 POTENTIAL.
FT DOMAIN 288 359 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 48 119 LINK.
FT DOMAIN 150 158 ARG/LYS-RICH (BASIC).
FT DOMAIN 225 266 STEM.
FT MOD_RES 21 21 PYRROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT DISULFID 53 118 BY SIMILARITY.
FT DISULFID 77 97 BY SIMILARITY.
FT MOD_RES 289 289 PHOSPHORYLATION (BY PKC) (PARTIAL) (BY
FT SIMILARITY).

FT MOD_RES 323 323 PHOSPHORYLATION (PARTIAL) (BY
FT SIMILARITY).
FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 359 AA; 38990 MW; BE20461C587AA34B CRC64;

Alignment Scores:
Pred. No.: 4.21e-08 Length: 359
Score: 186.00 Matches: 84
Percent Similarity: 36.95% Conservative: 42
Best Local Similarity: 24.63% Mismatches: 159
Query Match: 5.16% Indels: 56
DB: 1 Gaps: 11

US-10-079-111-2 (1-2029) x CD44_HORSE (1-359)

QY 255 TTGCGTGCAGAAGAGCTTTCATCCAGGTGTCTATGCAGAAATTATGGGATCACCCTTGTG 314
||| ::::: ::::: ||||| ||::: |||
Db 17 LeuSerLeuAlaGlnIleAspLeuAsnIleThrCysArgTyrAlaGlyValPheHisVal 36

QY 315 AGCAAAAAGGCGAACCAAGCAGCTGAATTTCACAGAAGCTAAGAGGCCTGTAGGCTGCTG 374
||| ::::: ||||| ||::: |||
Db 37 GluLysAsnGlyArgTyrSerIleSerArgThrGluAlaAlaAspLeuCysLysAlaPhe 56

QY 375 GGACTAAGTTTGGCCGCAAGCACCAAGTTGAAACAGCCCTGAAAGCTAGCTTTGAAACT 434
::: ||| ::::: ||||| |||||
Db 57 AsnSerThrLeuProThrMetAlaGlnMetGlnLysAlaLeuAsnIleGlyPheGluThr 76

QY 435 TGCAGCTATGGCTGGTGGAGATGGATTTCGTGGTCACTCTCTAGGATTAGCCCAACCCC 494
||| ||::: ::::: ||||| |||||
Db 77 CysArgIleGlyPheIle---GluGlyHisValValIleProProIleHisProAsnSer 95

QY 495 AAGTGTGGGAAAAATGGGGTGGTGTCTGATTGGAAGGTTCCAGTGAGCCGACAGTTT 554
||| ||| ||||| ||| |||||
Db 96 IleCysAlaAlaAsnAsnThrGlyValTyrIleLeuThrSerAsnThrSer---GlnTyr 114

QY 555 GCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT----- 602
||| ||::: ||::: ||||| |||||
Db 115 AspThrTyrCysPheAsnAlaSerAlaProProGluGluAspCysThrSerValThrAsp 134

QY 603 -----CCAGAAATTATCACC----- 617
||| ||| |||||
Db 135 LeuProAsnAlaPheGluGlyProIleThrIleThrIleValAsnArgAspGlyThrArg 154

QY 618 -----ACCAAGATCCCATATTCAACACACTCAAACACTGCAACA 653
||| ||| |||||
Db 155 TyrThrLysLysGlyGluTyrArgThrAsnProGluAspIleAsnProSerThrProAla 174

QY 654 CAAACAACAGAAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACA 713
||| ||| ||| :::
Db 175 AspAspValSerSerGlySerSerSerGluArgSerThrSerGlyTyrSerIle 194

QY 714 ATACCTGCC-----CCTACTACTCTCCT----- 737
||| ||||| |||
Db 195 PheHisThrHisLeuProThrThrArgProThrGlnAspGlnSerSerProTrpValSer 214

QY 738 -----CCTGCTCCAGCTTCCACTTCTATTCCACGAGAGAAAAAATGATTGTGTGCACA 791
||| ||| ||::: ||| |||
Db 215 AspSerProGluLysThrProThrThrLysAspArgAlaSerGlyGlyArgAlaGlnThr 234

QY 792 GAAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAATAAA 851
||| ||||| ||||| :::::
Db 235 ThrHisGlySerGluThrSerGlyHisSerThrGlySerGln-----GluGlyGly 251

QY 852 GCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCCGCTCTGTAGTGCTT 911
||| :::
Db 252 AlaSerThrThrSerGlyProIleArgArgProGlnIleProGluTrpLeuIleLeu 271

QY 912 GCTCTCCTCTTCTTTGGTGTGCAGCTGGTCTTGATTTTGTATGTCAAAAGGTATGTG 971
||| ||| ||| ||| ||| :::

Db 272 AlaSerLeu---LeuAlaLeuAlaLeuIleLeuAlaValCys-----Ile 285
QY 972 AAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAAATGATCGAAACCAA 1025
Db 286 AlaValAsnSerArgArgCysGlyGlnLysLysLysLeuValIleAsnAsnGlyAsn 305
QY 1026 ---GTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAAACT 1082
Db 306 GlyAlaValAspArgLysAlaSerGlyLeuAsn---GlyGluAlaSerArgSerGln 324
QY 1083 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAGCAACTACCGTGCATGCTGGAAGCT 1142
Db 325 GluMetValHisLeuValAsnLysGluSerSerGluThrGlnAspGlnPheMetThrAla 344
QY 1143 GAA 1145
Db 345 Asp 345
RESULT 10
PGCV_CHICK
ID PGCV_CHICK STANDARD; PRT; 3562 AA.
AC Q90953; Q90945;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Versican core protein precursor (Large fibroblast proteoglycan)
DE (Chondroitin sulfate proteoglycan core protein 2) (PG-M).
GN CPBG2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS V0 AND V1).
RC STRAIN=White leghorn; TISSUE=Limb bud;
RX MEDLINE=93300846; PubMed=8314802;
RA Shinomura T., Nishida Y., Ito K., Kimata K.;
RT "cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan
RT expressed during chondrogenesis in chick limb buds. Alternative
RT spliced multiforms of PG-M and their relationships to versican";
RL J. Biol. Chem. 268:14461-14469(1993).
CC -!- FUNCTION: May play a role in intercellular signaling and in
CC connecting cells with the extracellular matrix. May take part in
CC the regulation of cell motility, growth and differentiation. Binds
CC hyaluronic acid.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=V0;
CC IsoId=Q90953-1; Sequence=Displayed;
CC Name=V1;
CC IsoId=Q90953-2; Sequence=VSP_003093;
CC -!- TISSUE SPECIFICITY: Prechondrogenic condensation area of
CC developing limb buds.
CC -!- DEVELOPMENTAL STAGE: Disappears after the cartilage development
CC (By similarity).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 link domains.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.

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CC or send an email to license@isb-sib.ch).

DR EMBL; X60226; CAA42787.1; --.

DR EMBL; D13542; BAA02742.1; --.
DR PIR; A47171; A47171.
DR HSSP; P00740; 1EDM.
DR InterPro; IPR000152; Asx hydroxyl_s.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR000538; Link.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00059; lectin_c; 1.
DR Pfam; PF00084; sushi; 1.
DR Pfam; PF00193; Xlink; 2.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 2.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00409; IG_1.
DR SMART; SM00445; LINK; 2.
DR PROSITE; PS00010; ASX HYDROXYL; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1_2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS50835; IG_LINK; 1.
DR PROSITE; PS01241; LINK; 2.
KW Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;
KW Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
KW Hyaluronic acid; Alternative splicing.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 3562 VERSICAN CORE PROTEIN.
FT DOMAIN 27 143 IG-LIKE V-TYPE.
FT DOMAIN 166 243 LINK 1.
FT DOMAIN 264 345 LINK 2.
FT DOMAIN 3254 3290 EGF-LIKE 1.
FT DOMAIN 3292 3328 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3341 3455 C-TYPE LECTIN.
FT DOMAIN 3460 3518 SUSHI.
FT DISULFID 44 129 BY SIMILARITY.
FT DISULFID 171 242 BY SIMILARITY.
FT DISULFID 195 216 BY SIMILARITY.
FT DISULFID 269 344 BY SIMILARITY.
FT DISULFID 293 314 BY SIMILARITY.
FT DISULFID 3258 3269 BY SIMILARITY.
FT DISULFID 3263 3278 BY SIMILARITY.
FT DISULFID 3280 3289 BY SIMILARITY.
FT DISULFID 3296 3307 BY SIMILARITY.
FT DISULFID 3301 3316 BY SIMILARITY.
FT DISULFID 3318 3327 BY SIMILARITY.
FT DISULFID 3334 3345 BY SIMILARITY.
FT DISULFID 3362 3454 BY SIMILARITY.
FT DISULFID 3430 3446 BY SIMILARITY.
FT DISULFID 3461 3504 BY SIMILARITY.
FT DISULFID 3490 3517 BY SIMILARITY.
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 529 529 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 709 709 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 948 948 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1409 1409 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1479 1479 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1523 1523 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1530 1530 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1625 1625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1751 1751 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	1988	1988	N-LINKED	(GLCNAC. . .)	(POTENTIAL) .
FT	CARBOHYD	2088	2088	N-LINKED	(GLCNAC. . .)	(POTENTIAL) .
FT	CARBOHYD	2089	2089	N-LINKED	(GLCNAC. . .)	(POTENTIAL) .
FT	CARBOHYD	2507	2507	N-LINKED	(GLCNAC. . .)	(POTENTIAL) .
FT	CARBOHYD	2642	2642	N-LINKED	(GLCNAC. . .)	(POTENTIAL) .
FT	CARBOHYD	2679	2679	N-LINKED	(GLCNAC. . .)	(POTENTIAL) .
FT	CARBOHYD	2748	2748	N-LINKED	(GLCNAC. . .)	(POTENTIAL) .
FT	CARBOHYD	2762	2762	N-LINKED	(GLCNAC. . .)	(POTENTIAL) .
FT	CARBOHYD	3069	3069	N-LINKED	(GLCNAC. . .)	(POTENTIAL) .
FT	CARBOHYD	3194	3194	N-LINKED	(GLCNAC. . .)	(POTENTIAL) .
FT	CARBOHYD	3232	3232	N-LINKED	(GLCNAC. . .)	(POTENTIAL) .
FT	CARBOHYD	3545	3545	N-LINKED	(GLCNAC. . .)	(POTENTIAL) .
FT	VARSP LIC	485	1411	Missing (in isoform V1) .		
FT	/FTid=VSP 003093.					
SQ	SEQUENCE	3562 AA; 388078 MW; 9BC566E88C1602D2 CRC64;				
Alignment Scores:						
Pred. No.:		6.62e-05	Length:	3562		
Score:		152.50	Matches:	126		
Percent Similarity:		35.02%	Conservative:	68		
Best Local Similarity:		22.74%	Mismatches:	217		
Query Match:		4.23%	Indels:	143		
DB:		1	Gaps:	24		
US-10-079-111-2 (1-2029) x PGCV_CHICK (1-3562)						
QY	18	CTTGAAAGCAGGGAATCCGGATGTCGCGTTATGAAGTGGAGCAGTGAGTGAGCCTC	77			
Db	162	LeuAsnPheThrGlnAlaGlnGlnThrCysLeuAspAsnGlyAlaValIleAlaSer---	180			
QY	78	AACATAGTTCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACC	137			
Db	181	-----ProGlu---GlnLeuLysAlaAlaTyrGluAspGlyPheGluGlnCysAsp	196			
QY	138	AGTGGCCATCTGAGG-----	155			
Db	197	AlaGlyTrpLeuSerAspGlnThrValArgTyrProIleArgHisProArgIleGlyCys	216			
QY	156	TTC-----CCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTG	206			
Db	217	PheGlyAspLysMetGlyLysLysGlyValArgThrTyrGlyArg-----	231			
QY	207	TTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAA	266			
Db	232	-----ArgPhePro	234			
QY	267	GAGCTTTCATCCAGGTGTCATGCAGAATT-----ATGGGGATCACCCCTTGTGAGCAAA	320			
Db	235	AsnGluThrTyrAspValTyrCysTyrValGluHisMetGlnAspGluValHisVal	254			
QY	321	AAGCGAAACACGACGCTGAATTCACAGAAGCTAAGGAGGCCCTGTAGGCTGTGGGACTA	380			
Db	255	SerValProGluLysLeuThrPheGluGluAlaLysGluLeuCysArgLysArgAspGly	274			
QY	381	AGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGC	440			
Db	275	ValLeuAlaSerValGlyAsnMetTyrValAlaTrpArgAsnGlyPheAspGlnCysAsp	294			
QY	441	TATGGCTGGGTGGAGATGGATTTCGTGGTCATCTCTAGGATTAGCCCAACCCCAAGTGT	500			
Db	295	TyrGlyTrpLeuAlaAspGlySerValArgTyrProAlaSerValAlaArgProGlnCys	314			
QY	501	GGGAAAAAATGGGTGGGTGTCCTGATT-----	533			
Db	315	GlyGlyGlyLeuLeuGlyValArgThrLeuTyrArgTyrGluAsnGlnThrGlyPhePro	334			
QY	534	GTTCCAGTCAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAAC	593			
Db	335	TyrProAspSerLys---PheAspAlaTyrCysTyrGluArgLysLysIleValSerGlu	353			
QY	594	TCGTGCATTCCAGAAATTATCACCACC-----AAAGATCCCATATTCAACACTCAAAC	647			
Db	354	ProThrThrValLysLeuValThrThrLeuLysThrAspSerValGluLeuSerSerAla	373			

QY	648	GCAACACAAACAGAAATTTATTGTCTAGTGACAGTACCTACTCGGTGGCATCCCCTTAC	707
Db	374	LysValThrLeuLysProSerValPheGluSerSerValThrGluValAlaValThrLys	393
QY	708	TCTACAATACCT-----GCCCTACTACTACTCTCTCTCTGCTCCAGCTTCCACT	755
Db	394	ThrLysValProAlaTrpGluAlaThrLeuGluThrGluAspThrLysMetThrThr	413
QY	756	TCTATTCCACGGAGAAAAAATTGATTGTGTACAGAAAGTTTTTATGAAACT-----	809
Db	414	GluValAlaGluGluLysArgGluMet-----GluValLeuMetGluAsnIleLys	430
QY	810	---AGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCATTCAGAAT	866
Db	431	LeuThrThrLeuLeuProGlnThrValThrAspGlyGlu-IleSerProTyrAspThrLe	450
QY	867	GAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTGCTAGTGTCTCTCTCTCTTT	926
Db	450	uGlyArgThrGluTyrAspValSerProArgLeu-----ThrGluSerThrSerAl	467
QY	927	GGTGTGCAGCTGGTCTTGGATTGCTATGTCAAAGGTATGTGAAGGCCTTCCCTTTT	986
Db	467	aAlaLeuGluValGluHisThrTyrSerGluAla-GluLeuSerGluGluGlnGly----	485
QY	987	ACAAACAAGAATCAGCAGAAAGGAATGATCGAAACCAAAGTAGTAAAGGAGAGAAG---	1043
Db	486	--ArgSerGluSerThrGlu-AspAlaPheLeuThrSerValValPheGlnAspSerThr	504
QY	1044	-----GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACTGATAAAACCCAGAA	1097
Db	505	AlaValAlaLysSerSerThrGlySerTrpGluAspIleGluThrGly-AspThrGlnLy	524
QY	1098	GAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCTGGAAGCTGAAAGTTTAGATGAGA	1157
Db	524	sHisAsp-----	527
QY	1158	CAGAAATGAGGAGACACACACTGAGGCTGGTTTCTTTTCATGCTCTTACCTGCCCCAGCT	1217
Db	527	yAspAsnGlnThrGluGlnIleGluValGlyProValMetThrAlaThr-----	543
QY	1218	GGGGAATCAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACCTTGGTTCTTAAGTGA	1277
Db	544	----AspSerLeuValProAlaSerGlnArgGluLeuProArgThrGlySer-----	559
QY	1278	ATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCACCAAGAGAATGCCCTTCTCCTTAT	1337
Db	560	-----SerValSerLeuThrLysGluAsnLeuTyrLeu-----	570
QY	1338	TGTAACCTGTCTGGATCCTAT-----CCTCCTACCTCCAAAGCTTCCCACGGCCT	1388
Db	571	-----GlySerHisSerThrLysGluProThrLysLysSerMetGluAlaLy	586
QY	1389	TTCTAGCCTGGCTATGTCCTAATAATATCCCACCTGGGAGAAAGAGTTTTTGCAAAGTGCA	1448
Db	586	sSerAsp-----LysLysLeuThrThrValVa	595
QY	1449	AGGACCTAAAAACA-----TCTCATCAGTATCCAGTGGTAAAAAAGGCCTCCTGGCTGTCT	1502
Db	595	IleProLysAlaLeuPheThrAspGlnTyrAsp-----	607
QY	1503	GAGCTAGGTGGGTTGAAAGCCCAAGGAGTGCACTG	1536
Db	607	uThrThrGlyGly---GluGlyArgGluSerMet	617
RESULT 11			
PGCA_PIG			
ID	PGCA_PIG	STANDARD;	PRT; 537 AA.
AC	Q29011; O18833;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	10-OCT-2003 (Rel. 42, Last sequence update)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	Aggrecan core protein (Cartilage-specific proteoglycan core protein)		

DE (CSPCP) (Fragments).

GN AGCl.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE OF 1-370.

RC TISSUE=Cartilage;

RX MEDLINE=93038505; PubMed=1417734;

RA Barry F.P., Gaw J.U., Young C.N., Neame P.J.;

RT "Hyaluronan-binding region of aggrecan from pig laryngeal cartilage.

RT Amino acid sequence, analysis of N-linked oligosaccharides and

RT location of the keratan sulphate.";

RL Biochem. J. 286:761-769(1992).

RN [2]

RP SEQUENCE OF 324-453 FROM N.A.

RC TISSUE=Chondrocytes;

RX MEDLINE=98209637; PubMed=9550267;

RA Flannery C.R., Little C.B., Caterson B.;

RT "Molecular cloning and sequence analysis of the aggrecan interglobular

RT domain from porcine, equine, bovine and ovine cartilage: comparison of

RT proteinase-susceptible regions and sites of keratan sulfate

RT substitution.";

RL Matrix Biol. 16:507-511(1998).

RN [3]

RP SEQUENCE OF 454-537 FROM N.A.

RC TISSUE=Cartilage;

RX MEDLINE=95128522; PubMed=7827755;

RA Barry F.P., Neame P.J., Sasse J., Pearson D.;

RT "Length variation in the keratan sulfate domain of mammalian

RT aggrecan.";

RL Matrix Biol. 14:323-328(1994).

CC -!- FUNCTION: This proteoglycan is a major component of extracellular

CC matrix of cartilaginous tissues. A major function of this protein

CC is to resist compression in cartilage. It binds avidly to

CC hyaluronic acid via an amino-terminal globular region. May play a

CC regulatory role in the matrix assembly of the cartilage.

CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By

CC similarity).

CC -!- DOMAIN: Two globular domains, G1 and G2, comprise the amino

CC terminus of the proteoglycan, while another globular region, G3,

CC makes up the COOH terminus. G1 contains link domains and thus

CC consists of three disulfide-bonded loop structures designated as

CC the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS)

CC and the chondroitin sulfate (CS) attachment domains lie between G2

CC and G3.

CC -!- PTM: Contains mostly chondroitin sulfate, but also keratan sulfate

CC chains, N-linked and O-linked oligosaccharides (By similarity).

CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; AF019757; AAC48799.1; -.

DR EMBL; S74664; AAC60528.2; -.

DR PIR; S78009; S78009.

DR InterPro; IPR001304; Lectin_C.

DR InterPro; IPR000538; Link.

DR ProDcm; PD000918; Link; 2.

DR PROSITE; PS01241; LINK; 2.

DR PROSITE; PS00615; C_TYPE_LLECTIN_1; PARTIAL.

DR PROSITE; PS50041; C_TYPE_LLECTIN_2; PARTIAL.

DR PROSITE; PS50835; IG_LIKE; 1.

DR PROSITE; PS00290; IG_MHC; 1.

DR Glycoprotein; Proteoglycan; Repeat; Immunoglobulin domain.

FT NON TER 1 1

FT DOMAIN 28 124 IG-LIKE V-TYPE DOMAIN.

FT	DOMAIN	154	231	LINK 1.
FT	DOMAIN	252	333	LINK 2.
FT	DOMAIN	32	124	G1-A.
FT	DOMAIN	136	231	G1-B.
FT	DOMAIN	237	333	G1-B'.
FT	DISULFID	35	117	BY SIMILARITY.
FT	DISULFID	159	230	BY SIMILARITY.
FT	DISULFID	183	204	BY SIMILARITY.
FT	DISULFID	257	332	BY SIMILARITY.
FT	DISULFID	281	302	BY SIMILARITY.
FT	NON CONS	453	454	
FT	DOMAIN	<454	520	KS.
FT	DOMAIN	523	>537	CS-1.
FT	CARBOHYD	110	110	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	223	223	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	317	317	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	371	371	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	418	418	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	NON TER	537	537	
SQ	SEQUENCE	537 AA;	58708 MW;	9A4C23CCA5422F0D CRC64;

Alignment Scores:

Pred. NO.:	6.58e-05	Length:	537
Score:	150.00	Matches:	63
Percent Similarity:	35.98%	Conservative:	23
Best Local Similarity:	26.36%	Mismatches:	85
Query Match:	4.16%	Indels:	68
DB:	1	Gaps:	11

US-10-079-111-2 (1-2029) x PGCA_PIG (1-537)

QY	330	CAGCAGCTGAATTTACAGAACTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCC	389
Db	246	GlulysPheThrPheGlnGluAlaAlaAsnGluCysArgArgLeuGlyAlaArgLeuAla	265
QY	390	GGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGACGCTATGGCTGG	449
Db	266	ThrThrGlyGlnLeuTyrLeuAlaTrpArgGlyGlyMetAspMetCysSerAlaGlyTrp	285
QY	450	GTTGGAGATGGATTCGTG-----GTCACTCTCTAGGATTAGCCCAAAACCCCAAGTGTGGG	503
Db	286	LeuAlaAspArgSerValArgTyrProIleSerLysAlaArgProAsn-----CysGly	303
QY	504	AAAAATGGGTGGGTCTCTGATT-----TGGAAGGTT	536
Db	304	GlyAsnLeuLeuglyValArgThrValTyrLeuHisAlaAsnGlnThrGlyTyrProAsp	323
QY	537	CCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGAT-----ACTTGGACT	581
Db	324	ProSerSerArg---TyrAspAlaIleCysTyrThrGlyGluAspPheValAspIlePro	342
QY	582	-----ACTTGGACT	590
Db	343	GluAsnPhePheGlyValGlyGlyGluGluAspIleThrIleGlnThrValThrTrpPro	362
QY	591	AACTCGTGCATTCCA-----GAAATTATC	614
Db	363	AspValGluLeuProLeuProArgAsnIleThrGluGlyGluAlaArgGlyThrValIle	382
QY	615	ACCACCAAAGATCCCATATTCAAC---ACTCAAACCTGCAACACAAACACAGAA---TTT	668
Db	383	LeuThrValIysProValPheGluPheSerProThrAlaProGluProGluGluProphe	402
QY	669	ATTGTCAGTGACAGTACCTACTCGGTGGCATCCCT-----TAC	707
Db	403	ThrPheAlaProGlyThrGlyAlaThrAlaPheProGluAlaGluAsnArgThrGlyGlu	422
QY	708	TCTACAATACCT-----GCCCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCT	758
Db	423	AlaThrArgProTrpAlaPheProGluGluSerThrProGlyLeuGlyAlaProThrAla	442
QY	759	ATTCCACGGAGAAAAAATTGATTTGTGTGCACAGAAAGTTTATGGAA-----	806

Db 443 PheThrSerGluAspLeuValGlnValThrSerAlaAlaThrGluGluGlyThrGlu 462

QY 807 -----ACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAATAAA 851
||| ||||| ||||| ||||| |||||

Db 463 GlyProSerAlaThrGluAlaProSerThrSerGluGluProPheProSerGluLys 481

RESULT 12

PGCA_CHICK

ID PGCA_CHICK STANDARD; PRT; 2109 AA.

AC P07898; Q90810; Q90820; Q90991; Q91047;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Aggrecan core protein precursor (Cartilage-specific proteoglycan core

DE protein) (CSPCP).

GN AGC1.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RP [1]

RC SEQUENCE FROM N.A.

RC STRAIN=White leghorn; TISSUE=Embryo;

RX MEDLINE=94043149; PubMed=8226878;

RA Li H., Schwartz N.B., Vertel B.M.;

RT "cDNA cloning of chick cartilage chondroitin sulfate (aggrecan) core

RT protein and identification of a stop codon in the aggrecan gene

RT associated with the chondrodystrophy, nanomelia.";

RL J. Biol. Chem. 268:23504-23511(1993).

RN [2]

RP SEQUENCE OF 1042-1559 FROM N.A.

RC TISSUE=Embryo;

RX MEDLINE=90307744; PubMed=1694853;

RA Krueger R.C. Jr., Fields T.A., Mensch J.R. Jr., Schwartz N.B.;

RT "Chick cartilage chondroitin sulfate proteoglycan core protein. II.

RT Nucleotide sequence of cDNA clone and localization of the S103L

RT epitope";

RL J. Biol. Chem. 265:12088-12097(1990).

RN [3]

RP SEQUENCE OF 1-1855 AND 1893-2109 FROM N.A.

RC TISSUE=Cartilage;

RX MEDLINE=93111968; PubMed=1339285;

RA Chandrasekaran L., Tanzer M.L.;

RT "Molecular cloning of chicken aggrecan. Structural analyses.";

RL Biochem. J. 288:903-910(1992).

RN [4]

RP ERRATUM.

RX MEDLINE=94107258; PubMed=8280087;

RA Chandrasekaran L., Tanzer M.L.;

RL Biochem. J. 296:885-887(1993).

RN [5]

RP SEQUENCE OF 1492-1610 FROM N.A.

RC STRAIN=White leghorn; TISSUE=Chondrocytes;

RX MEDLINE=95128519; PubMed=7827752;

RA Primorac D., Stover M.L., Clark S.H., Rowe D.W.;

RT "Molecular basis of nanomelia, a heritable chondrodystrophy of

RT chicken.";

RL Matrix Biol. 14:297-305(1994).

RN [6]

RP SEQUENCE OF 1894-2109 FROM N.A.

RX MEDLINE=89008500; PubMed=3170613;

RA Tanaka T., Har-El R., Tanzer M.L.;

RT "Partial structure of the gene for chicken cartilage proteoglycan

RT core protein.";

RL J. Biol. Chem. 263:15831-15835(1988).

RN [7]

RP SEQUENCE OF 1693-1855 AND 1893-2109 FROM N.A.

RX MEDLINE=86259736; PubMed=3460082;

RA Sai S., Tanaka T., Kosher R.A., Tanzer M.L.;

RT "Cloning and sequence analysis of a partial cDNA for chicken

RT cartilage proteoglycan core protein.";

RL Proc. Natl. Acad. Sci. U.S.A. 83:5081-5085(1986).

CC -!- FUNCTION: This proteoglycan is a major component of extracellular

CC matrix of cartilagenous tissues. A major function of this protein

CC is to resist compression in cartilage. It binds avidly to

CC hyaluronic acid via an amino-terminal globular region. May play a

CC regulatory role in the matrix assembly of the cartilage.

CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By

CC similarity).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=P07898-1; Sequence=Displayed;

CC Name=2;

CC IsoId=P07898-2; Sequence=VSP_003073;

CC -!- DOMAIN: Two globular domains, G1 and G2, comprise the amino

CC terminus of the proteoglycan, while another globular region, G3,

CC makes up the COOH terminus. G1 contains link domains and thus

CC consists of three disulfide-bonded loop structures designated as

CC the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS)

CC and the chondroitin sulfate (CS) attachment domains lie between G2

CC and G3.

CC -!- PTM: Contains mostly chondroitin sulfate, but also keratan sulfate

CC chains, N-linked and O-linked oligosaccharides.

CC -!- DISEASE: DEFECTS IN AGC1 ARE THE CAUSE OF NANOMELIA, A LETHAL

CC CONNECTIVE TISSUE DISORDER AFFECTING CARTILAGE DEVELOPMENT

CC (CHONDRODYSTROPHY) CHARACTERIZED BY SHORTENED AND MALFORMED LIMBS.

CC AGGECAN IS TRUNCATED AT ITS C-TERMINAL IN THE CS-2 BINDING DOMAIN

CC AND IS NOT ANYMORE SECRETED FROM THE CHONDROCYTES.

CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

CC -!- SIMILARITY: Contains 4 link domains.

CC -!- SIMILARITY: Contains 1 EGF-like domain.

CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; L21913; AAB19128.1; -.

CC EMBL; M38187; AAA48731.1; -.

CC EMBL; M88101; -; NOT ANNOTATED_CDS.

CC EMBL; S74657; AAC60751.1; -.

CC EMBL; S74656; AAC60751.1; JOINED.

CC EMBL; J04028; AAA48719.1; -.

CC EMBL; M13993; AAA48720.1; -.

CC PIR; I50421; I50421.

CC HSSP; P08709; 1BF9.

CC InterPro; IPR002353; Antifreeze1.

CC InterPro; IPR00152; Asx_hydroxyl_s.

CC InterPro; IPR000742; EGF_2.

CC InterPro; IPR001881; EGF_Ca.

CC InterPro; IPR006209; EGF_like.

CC InterPro; IPR007110; Ig-like.

CC InterPro; IPR003599; Ig.

CC InterPro; IPR001304; Lectin_C.

CC InterPro; IPR000538; Link.

CC InterPro; IPR003324; SGXXSG.

CC InterPro; IPR000436; Sushi_SCR_CCP.

CC Pfam; PF00008; EGF; 1.

CC Pfam; PF00047; ig; 1.

CC Pfam; PF00059; lectin_c; 1.

CC Pfam; PF02339; SGXXSG; 56.

CC Pfam; PF00084; sushi; 1.

CC Pfam; PF00193; Xlink; 4.

CC PRINTS; PR00356; ANTIFREEZE1.

CC PRINTS; PR01265; LINKMODULE.

CC ProDom; PD000918; Link; 4.

CC SMART; SM00032; CCP; 1.

CC SMART; SM00034; CLECT; 1.

DR	SMART; SM00179; EGF_CA; 1.				
DR	SMART; SM00409; IG; 1.				
DR	SMART; SM00445; LINK; 4.				
DR	PROSITE; PS00010; ASX_HYDROXYL; 1.				
DR	PROSITE; PS00615; C_TYPE_LECTIN_1; 1.				
DR	PROSITE; PS50041; C_TYPE_LECTIN_2; 1.				
DR	PROSITE; PS00022; EGF_1; 1.				
DR	PROSITE; PS50026; EGF_3; 1.				
DR	PROSITE; PS01187; EGF_CA; 1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
DR	PROSITE; PS01241; LINK; 4.				
KW	Glycoprotein; Proteoglycan; Lectin; Signal; Sushi; EGF-like domain;				
KW	Alternative splicing; Repeat; Immunoglobulin domain.				
FT	SIGNAL 1 16				
FT	CHAIN 17 2109				
FT	DOMAIN 34 143				
FT	DOMAIN 166 243				
FT	DOMAIN 264 346				
FT	DOMAIN 537 614				
FT	DOMAIN 635 716				
FT	DOMAIN 1363 1742				
FT	DOMAIN 1855 1892				
FT	DOMAIN 1901 2019				
FT	DOMAIN 2023 2081				
FT	DOMAIN 48 137				
FT	DOMAIN 148 243				
FT	DOMAIN 249 346				
FT	DOMAIN 519 613				
FT	DOMAIN 620 715				
FT	DOMAIN 718 803				
FT	DOMAIN 805 1264				
FT	DOMAIN 1265 1742				
FT	DOMAIN 1893 2109				
FT	DISULFID 51 129				
FT	DISULFID 171 242				
FT	DISULFID 195 216				
FT	DISULFID 269 345				
FT	DISULFID 293 314				
FT	DISULFID 542 613				
FT	DISULFID 566 587				
FT	DISULFID 640 715				
FT	DISULFID 664 685				
FT	DISULFID 1859 1870				
FT	DISULFID 1864 1879				
FT	DISULFID 1881 1890				
FT	DISULFID 1897 1908				
FT	DISULFID 1925 2017				
FT	DISULFID 1993 2009				
FT	DISULFID 2024 2067				
FT	DISULFID 2053 2080				
FT	CARBOHYD 76 76				
FT	CARBOHYD 122 122				
FT	CARBOHYD 330 330				
FT	CARBOHYD 388 388				
FT	CARBOHYD 439 439				
FT	CARBOHYD 644 644				
FT	CARBOHYD 700 700				
FT	CARBOHYD 765 765				
FT	CARBOHYD 801 801				
FT	VARSPLIC 1856 1892				
FT	CONFLICT 362 362				
Alignment Scores:					
Pred. No.:	0.000129	Length:	2109		
Score:	148.50	Matches:	74		
Percent Similarity:	36.86%	Conservative:	27		
Best Local Similarity:	27.01%	Mismatches:	104		
Query Match:	4.12%	Indels:	69		
DB:	1	Gaps:	13		
US-10-079-111-2 (1-2029) x PGCA_CHICK (1-2109)					

QY	330	CAGCAGCTGAATTTACAGAGAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTTGGCC	389
Db	258	GluLysPheThrPheGlnGluAlaPheAspLysCysHisSerLeuGlyAlaArgLeuAla	277
QY	390	GGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGG	449
Db	278	ThrThrGlyGluLeuTyrLeuAlaTrpLysAspGlyMetAspMetCysSerAlaGlyTrp	297
QY	450	GTTGGAGATGGATTCGTG-----GTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGG	503
Db	298	LeuAlaAspArgSerValArgTyrProIleSerArgAlaArgProAsn-----CysGly	315
QY	504	AAAAATGGGTGGGTGTC---CTGATTTGGAAGGTTCCAGTG-----	542
Db	316	GlyAsnLeuValGlyValArgThrValTyrLeuAsnProAlaAsnGlnThrGlyTyrPro	335
QY	543	-----AGCCGACAGTTTGCAGCCCTATTGTTACAACTCATCTGATACTTGGACTAACTCG	596
Db	336	HisProSerSerArgTyrAspAlaIleCysTyrSerGlyAspAsp-----PheGluAla	353
QY	597	TGCATTCCA-----GAAATTATCACCCACCAAGATCCCATATTCACAACT	641
Db	354	LeuValProGlyLeuPheThrAspGluValGlyThrGluLeuGlySerAlaPheThrIle	373
QY	642	CAAACTGCAACACAAACA-----ACAGAATTTATT	671
Db	374	GlnThrValThrGlnThrGluValGluLeuProLeuProArgAsnValThrGlu-----	391
QY	672	GTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACT	731
Db	392	--GluGluAlaArgGlySerIleAlaThrLeuGluProMetGluIleThrAlaThrAla	410
QY	732	ACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTTGTTGTGCACA	791
Db	411	ThrGluLeuTyrGluAlaPheThrValLeuProAsp-----LeuPheAlaThr	426
QY	792	GAAGTTTTTATGGAAGCTAGCACCATTGCTACAGAAACTGAACCAATTTGTTGAAAAATAA	851
Db	427	SerValThrValGluThrAlaSer-----ProArgGluGluAsn---	439
QY	852	GCAGCATTTCAAGAAATGAAGCTGTGGGTTTGGAGGTGTCCTCCACGGCTCTGCTAGTCTT	911
Db	440	---ValThrArgGluGluIleThrGlyIleTrpAlaValProGluGlu-----	454
QY	912	GCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAAGGTATGTG	971
Db	455	-----ValThrThrSerVal	459
QY	972	AAGGCCTTCCCTTTTACAAACAGAAATCAGCAGAGGAAATGATCGAAACCAAGTAGTA	1031
Db	460	SerGlyThrAlaPheThrThr-----GlyMetAlaGluValSerSerVal	474
QY	1032	AAGGAGGAGAGGCCCAATGATAGCAACCCCTAATGAGGAATCA	1073
Db	475	GluGluAlaIleAlaValThrAlaThrProGlyLeuGluSer	488
RESULT 13			
TSG6_HUMAN			
ID	TSG6_HUMAN	STANDARD;	PRT; 277 AA.
AC	P98066; Q8WWI9;		
DT	01-FEB-1996 (Rel. 33, Created)		
DT	01-FEB-1996 (Rel. 33, Last sequence update)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	Tumor necrosis factor-inducible protein TSG-6 precursor (TNF-		
DE	stimulated gene 6 protein) (Hyaluronate-binding protein).		
GN	TNFAIP6 OR TSG6.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Fibroblast;		

DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor-inducible protein TSG-6 precursor (TNF-
stimulated gene 6 protein).
GN TNFAIP6 OR TNFIP6 OR TSG6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE.
RC STRAIN=CD-1; TISSUE=Cumulus cell, Embryo, and Oocyte;
RX MEDLINE=98087423; PubMed=9427551;
RA Fueloep C., Kamath R.V., Li Y., Otto J.M., Salustri A., Olsen B.R.,
RA Glant T.T., Hascall V.C.;
RT "Coding sequence, exon-intron structure and chromosomal localization
of murine TNF-stimulated gene 6 that is specifically expressed by
expanding cumulus cell-oocyte complexes.";
RL Gene 202:95-102(1997).
CC -!- FUNCTION: Possibly involved in cell-cell and cell-matrix
interactions during inflammation and tumorigenesis (By
similarity).
CC -!- DEVELOPMENTAL STAGE: Expressed in cumulus cell-oocyte complexes
during expansion in vivo.
CC -!- SIMILARITY: Contains 1 link domain.
CC -!- SIMILARITY: Contains 1 CUB domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U83903; AAC53527.1; -.
DR PIR; JC6506; JC6506.
DR HSSP; P98066; 1TSG.
DR MGD; MGI:1195266; Tnfaip6.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000538; Link.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01241; LINK; 1.
KW Cell adhesion; Signal; Glycoprotein.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 275 TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN
FT LINK.
FT DOMAIN 35 128 TSG-6.
FT DOMAIN 135 247 CUB.
FT DISULFID 58 127 BY SIMILARITY.
FT DISULFID 82 103 BY SIMILARITY.
FT DISULFID 135 161 BY SIMILARITY.
FT DISULFID 188 210 BY SIMILARITY.
FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 275 AA; 30924 MW; 1CD247228260B8F9 CRC64;

Alignment Scores:
Pred. No.: 0.000184 Length: 275
Score: 144.00 Matches: 29
Percent Similarity: 51.14% Conservative: 16
Best Local Similarity: 32.95% Mismatches: 41
Query Match: 4.00% Indels: 2
DB: 1 Gaps: 1

US-10-079-111-2 (1-2029) x TSG6_MOUSE (1-275)

QY 315 AGCAAAAGGCGAACACAGCAGCTGAATTTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTG 374
Db 42 AlaArgAlaGlyArgTyrLysLeuThrTyrAlaGluAlaLysAlaValCysGluPheGlu 61
QY 375 GGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACT 434
Db 62 GlyGlyArgLeuAlaThrTyrLysGlnLeuGluAlaAlaArgLysIleGlyPheHisVal 81
QY 435 TGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGTCATCTCTAGGATTAGCCCAACCC 494
Db 82 CysAlaAlaGlyTrpMetAlaLysGlyArgValGlyTyrProIleValLysProGlyPro 101
QY 495 AAGTGTGGGAAATGGGGTGGTCTCCTGATTGGAAGGTTCCAGTGAGCCGA----- 548
Db 102 AsnCysGlyPheGlyLysThrGlyIleIleAspTyrGlyIleArgLeuAsnArgSerGlu 121
QY 549 CAGTTTGCAGCCTATTGTTACAAC 572
Db 122 ArgTrpAspAlaTyrCysTyrAsn 129
RESULT 15
PGCA_BOVIN STANDARD; PRT; 2364 AA.
ID PGCA_BOVIN STANDARD; PRT; 2364 AA.
AC P13608; P79117; Q28159;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE AggreCAN core protein precursor (Cartilage-specific proteoglycan core
protein) (CSPCP).
GN AGC1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovioidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Hering T.M., Kollar J., Huynh T.D.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 563-1056 FROM N.A.
RX MEDLINE=89380219; PubMed=2528543;
RA Antonsson P., Heinegaard D., Oldberg A.;
RT "The keratan sulfate-enriched region of bovine cartilage proteoglycan
consists of a consecutively repeated hexapeptide motif.";
RL J. Biol. Chem. 264:16170-16173(1989).
RN [3]
RP SEQUENCE OF 1609-2113 AND 2151-2364 FROM N.A.
RX MEDLINE=87270630; PubMed=3111460;
RA Oldberg A., Antonsson P., Heinegaard D.;
RT "The partial amino acid sequence of bovine cartilage proteoglycan,
deduced from a cDNA clone, contains numerous Ser-Gly sequences
arranged in homologous repeats.";
RL Biochem. J. 243:255-259(1987).
RN [4]
RP SEQUENCE OF 2114-2150 FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=93352525; PubMed=8349621;
RA Fueloep C., Walcz E., Valyon M., Glant T.T.;
RT "Expression of alternatively spliced epidermal growth factor-like
domains in aggregans of different species. Evidence for a novel
module.";
RL J. Biol. Chem. 268:17377-17383(1993).
RN [5]
RP PARTIAL SEQUENCE.
RX MEDLINE=85027710; PubMed=6489519;
RA Perin J.-P., Bonnet F., Jolles J., Jolles P.;
RT "Sequence data concerning the protein core of the cartilage
proteoglycan monomers. Characterization of a sequence allowing the
synthesis of an oligonucleotide probe.";
RL FEBS Lett. 176:37-42(1984).
RN [6]


```

Db      320 GlyAsnLeuLeuGlyValArgThrValTyrLeuHisAlaAsnGlnThrGlyTyrProAsp 339
QY      537 CCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCG 596
Db      340 ProSerSerArg--TyrAspAlaIleCysTyrThrGlyGluAspPheValAsp----- 356
QY      597 TGCATTCCAGAA-----ATTATCACCACC 620
Db      357 ---IleProGluSerPhePheGlyValGlyGlyGluGluAspIleThrIleGlnThrVal 375
QY      621 AAAGATCCCATATTCAACACTCAAACCTGCAACACAAACACAGAAATTTATTGTCAGTGAC 680
Db      376 ThrTrpProAspValGluLeuProLeuProArgAsnIleThrGlyGluAlaArgGly 395
QY      681 AGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTACTCCTCCT 740
Db      396 SerValIleLeuThrAlaLysProAspPheGluVal---SerProThrAlaProGluPro 414
QY      741 GCTCCAGCTTCCACTTCTATTCCACGGAGAGAAAAAATTGATTGTGTGCACAGAAGTTTTT 800
Db      415 GluGluProPheThrPheValProGluValArg-----AlaThrAlaPhe 429
QY      801 ATGGAACACTAGCACCATGTCTACAGAA---ACTGAACCATTTGTTGAAAAATAAAGCAGCA 857
Db      430 ProGluValGluAsnArgThrGluGluAlaThrArgProTrp-----Ala 444
QY      858 TTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCACGGCT-----CTG 902
Db      445 PheProArgGluSerThrProGlyLeuGlyAlaProThrAlaPheThrSerGluAspLeu 464
QY      903 CTAGTGCTTGCTCTCCTCTTCTTTTGGTGCTGCA 935
Db      465 ValValGlnValThrLeuAlaProGlyAlaAla 475
```

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model
Run on: September 13, 2004, 10:01:56 ; Search time 235.5 Seconds
(without alignments)
5436.827 Million cell updates/sec

Title: US-10-079-111-2
Perfect score: 3604
Sequence: 1 ccttgacaagtcagaagctt.....aaacattttaaaaaaaaaa 2029

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 2034082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+n2p:model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10079111/runat_13092004_102126_1826/app_query.fasta_1.2183
-DB=SPTREMBL_25 -QFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosu62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10079111 @CGN 1 1 344 @runat_13092004_102126_1826 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SPTREMBL_25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_rvirus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	1657	46.0 322 4 Q9UNF4	Q9unf4 homo sapien

2	1643	45.6	322	4	Q8TC18	Q8tc18 homo sapien
3	1638	45.4	322	4	Q9YSY7	Q9ysy7 homo sapien
4	1103	30.6	318	11	Q8BHC0	Q8bhc0 mus musculu
5	1095	30.4	318	11	Q99NE4	Q99ne4 mus musculu
6	726.5	20.2	201	6	Q7YS22	Q7ys22 sus scrofa
7	231.5	6.4	780	11	O08779	O08779 rattus norv
8	227	6.3	364	11	O70509	O70509 rattus norv
9	226	6.3	742	4	Q9UJ36	Q9uj36 homo sapien
10	219	6.1	265	13	Q98SR5	Q98sr5 anas platyr
11	217.5	6.0	398	13	Q90ZL8	Q90zl8 anas platyr
12	216	6.0	719	4	Q9H5A5	Q9h5a5 homo sapien
13	213	5.9	699	4	Q96J24	Q96j24 homo sapien
14	208	5.8	676	4	Q9H5A7	Q9h5a7 homo sapien
15	206.5	5.7	168	13	Q90ZL6	Q90zl6 anas platyr
16	205	5.7	493	4	Q86Z27	Q86z27 homo sapien
17	204	5.7	361	4	Q86T72	Q86t72 homo sapien
18	203.5	5.6	364	6	O97569	O97569 ceratotheri
19	203.5	5.6	396	13	Q9W6S4	Q9w6s4 gallus gall
20	202	5.6	361	4	Q8N694	Q8n694 homo sapien
21	201	5.6	580	11	Q80X37	Q80x37 mus musculu
22	199	5.5	338	4	Q9H5A4	Q9h5a4 homo sapien
23	196	5.4	294	4	Q92493	Q92493 homo sapien
24	195	5.4	470	4	Q9H5A6	Q9h5a6 homo sapien
25	191	5.3	271	4	Q9H5A3	Q9h5a3 homo sapien
26	149.5	4.1	2109	13	P79787	P79787 gallus gall
27	146.5	4.1	1238	11	Q8K0K6	Q8k0k6 mus musculu
28	146.5	4.1	2571	11	Q8R4Y4	Q8r4y4 mus musculu
29	145.5	4.0	494	6	Q9BGH3	Q9bgh3 sus scrofa
30	145	4.0	1069	4	Q9UF98	Q9uf98 homo sapien
31	141.5	3.9	911	4	Q96FP7	Q96fp7 homo sapien
32	141.5	3.9	911	4	Q96GW7	Q96gw7 homo sapien
33	139	3.9	961	3	Q92223	Q92223 emericecella
34	138.5	3.8	671	4	Q9HBK1	Q9hbk1 homo sapien
35	138.5	3.8	911	4	Q9HBK4	Q9hbk4 homo sapien
36	138.5	3.8	911	4	Q8TBB9	Q8tbb9 homo sapien
37	136	3.8	894	11	Q8BM87	Q8bm87 mus musculu
38	136	3.8	2559	11	Q8R4U0	Q8r4u0 mus musculu
39	134	3.7	897	4	Q9NRY3	Q9nry3 homo sapien
40	133	3.7	514	11	Q62913	Q62913 rattus norv
41	133	3.7	1192	4	Q9H7H7	Q9h7h7 homo sapien
42	133	3.7	1416	4	Q86UR4	Q86ur4 homo sapien
43	133	3.7	1431	11	Q8CFM6	Q8cfm6 rattus norv
44	133	3.7	1736	4	Q8TES1	Q8tes1 homo sapien
45	133	3.7	2551	4	Q8WWQ8	Q8wwq8 homo sapien

ALIGNMENTS

RESULT 1			
Q9UNF4	ID	Q9UNF4	PRELIMINARY; PRT; 322 AA.
AC	Q9UNF4;		
DT	01-MAY-2000	(TREMBlrel. 13, Created)	
DT	01-MAR-2001	(TREMBlrel. 16, Last sequence update)	
DT	01-OCT-2003	(TREMBlrel. 25, Last annotation update)	
DE	Hyaluronic acid receptor.		
GN	HAR.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Winkelman J.C., Basu S., Ozdemir E., Blough R.I.;		
RT	"HAR: a novel homolog of CD44 and putative hyaluronic acid receptor encoded by a gene on human chromosome 11p15.";		
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF127670; AAD49220.2; -		
DR	HSSP; P98066; ITSG.		
DR	GO; GO:0005540; F:hyaluronic acid binding; IEA.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	GO; GO:0007155; P:cell adhesion; IEA.		
DR	InterPro; IPR000538; Link.		

DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35213 MW; 8B4D6D623F52D559 CRC64;

Alignment Scores:
Pred. No.: 9.12e-156 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0
DB: 4 Gaps: 0

US-10-079-111-2 (1-2029) x Q9UNF4 (1-322)

QY 183 ATGCCAGGTGCTTCAGCCTGGTGGTTGCTTCTCACTTCATCTGGACCACGAGGCTCCTG 242
Db |||||
1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 20

QY 243 GTCCAAGGCTCTTTCGGTGCAGAAGAGCTTTCATCCAGGTGCATGCAGAATTATGGG 302
Db |||||
21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

QY 303 ATCACCCCTTGTAGCAAAAAGCGAACCAGCAGCTGAATTCACAGAAGCTAAAGGAGCC 362
Db |||||
41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60

QY 363 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 422
Db |||||
61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

QY 423 AGCTTTGAACTTGCAGCTATGGCTGGTGGAGATGGATTTCGTGGTCATCTCTAGGATT 482
Db |||||
81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

QY 483 AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCCTGATTTGGAAGGTTCCAGTG 542
Db |||||
101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

QY 543 AGCCGACAGTTTGCAGCCTATTGTTTACAACTCATCTGATACTTGGACTAACTCGTGCAAT 602
Db |||||
121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

QY 603 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACAACA 662
Db |||||
141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

QY 663 GAATTTATGTGAGTACAGTACTACTCGGTGGCATCCCTTACTCTACATACTACCTGCC 722
Db |||||
161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

QY 723 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 782
Db |||||
181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

QY 783 TGTGTACAGAAAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 842
Db |||||
201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

QY 843 GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 902
Db |||||
221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240

QY 903 CTAGTGCTTGTCTCCTCTTCTTTGGTGTGCAGCTGGTGTGGATTTTGCTATGTCAAA 962
Db |||||
241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260

QY 963 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACC 1022
Db |||||
261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280

QY 1023 AAAGTAGTAAAGGAGAGCCCAATGATAGCAACCCCTAATGAGGAATCAAAAGAAACT 1082
Db |||||
281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300

QY 1083 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAAGCT 1142
Db |||||
301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320

QY 1143 GAAAGTT 1148
Db |||||
321 GluVal 322

RESULT 2
Q8TC18
ID Q8TC18 PRELIMINARY; PRT; 322 AA.
AC Q8TC18;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Extracellular link domain-containing 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026231; AAH26231.1; -.
DR Genew; HGNC:14687; XLKD1.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
SQ SEQUENCE 322 AA; 35183 MW; 0B1EDBD76CE4610A CRC64;

Alignment Scores:
Pred. No.: 2.26e-154 Length: 322
Score: 1643.00 Matches: 321
Percent Similarity: 99.69% Conservative: 0
Best Local Similarity: 99.69% Mismatches: 1
Query Match: 45.59% Indels: 0
DB: 4 Gaps: 0

US-10-079-111-2 (1-2029) x Q8TC18 (1-322)

QY 183 ATGCCAGGTGCTTCAGCCTGGTGGTTGCTTCTCACTTCATCTGGACCACGAGGCTCCTG 242
Db |||||
1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 20

QY 243 GTCCAAGGCTCTTTCGGTGCAGAAGAGCTTTCATCCAGGTGTCTATCCAGAATTATGGGG 302
Db |||||
21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

QY 303 ATCACCCCTTGTAGCAAAAAGCGAACCAGCAGCTGAATTCACAGAAGCTAAGGAGGCC 362
Db |||||
41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60

QY 363 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 422
Db |||||
61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

QY 423 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTTCGTGGTCATCTCTAGGATT 482
Db |||||
81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

QY 483 AGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCCTGATTTGGAAGGTTCCAGTG 542
Db |||||
101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

Db 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
QY 1023 AAAGTAGTAAAGGAGAGAGCCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACT 1082
Db 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
QY 1083 GATAAAACCCAGAGAGTCCAAAGAGTCCAAAGCAAAACTACCGTGGATGCTGGAAGCT 1142
Db 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
QY 1143 GAAGTT 1148
Db 321 GluVal 322

RESULT 4
Q8BHC0 PRELIMINARY; PRT; 318 AA.
AC Q8BHC0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Extra cellular link domain-containing 1.
GN XLKD1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Lung, and Mammary gland;
RA Strausberg R.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; BC038653; AAH38653.1; -.
DR EMBL; BC038892; AAH38892.1; -.
DR EMBL; AK004726; BAC25094.1; -.
DR MGD; MGI:2136348; Xlkd1.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0005540; F:hyaluronic acid binding; IDA.
DR GO; GO:0004888; F:transmembrane receptor activity; IDA.
DR GO; GO:0006027; P:glycosaminoglycan catabolism; IDA.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK; 1.
SQ SEQUENCE 318 AA; 34573 MW; 34AA31AEF5430B08 CRC64;

Alignment Scores:
Pred. No.: 1.4e-100 Length: 318
Score: 1103.00 Matches: 221
Percent Similarity: 79.18% Conservative: 30
Best Local Similarity: 69.72% Mismatches: 62
Query Match: 30.60% Indels: 4
DB: 11 Gaps: 3

US-10-079-111-2 (1-2029) x Q8BHC0 (1-318)
QY 198 AGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTG 257
Db 6 SerLeuValLeuLeuAlaSerIleTrpThrArgHisProValGlnGlyAlaAsp 25
QY 258 CGTGCAAGAGAGCTTCCATCCAGGTGCATGCAGAATTATGGGGATCACCCCTTGTGAGC 317
Db 26 LeuValGlnAspLeuSerIleSer---ThrCysArgIleMetGlyValAlaLeuValGly 44

QY 318 AAAAAAGCGCAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCCTGTAGGCTGTGGGA 377
Db 45 ArgAsnLysAsnProGlnMetAsnPheThrGluAlaAsnGluAlaCysLysMetLeuGly 64
QY 378 CTAAGTTTGGCCGCAAGGACCAAGTTGAACAGCCCTTGAAGCTAGCTTTGAAACTTGC 437
Db 65 LeuThrLeuAlaSerArgAspGlnValGluSerAlaGlnLysSerGlyPheGluThrCys 84
QY 438 AGCTATGGCTGGTTGGAGATGGATTTCGTGGTCATCTCTAGGATTAGCCCAACCCCAAG 497
Db 85 SerTyrGlyTrpValGlyGluGlnPheSerValIleProArgIlePheSerAsnProArg 104
QY 498 TGTGGAAAAATGGGGTGGTGTCTCTGATTGGAAAGGTTCCAGTGAGCCGACAGTTTGCA 557
Db 105 CysGlyLysAsnGlyLysGlyValLeuIleTrpAsnAlaProSerSerGlnLysPheLys 124
QY 558 GCCTATTGTACAACTCATCTGATACTTGGACTAACTCGTGCAATCCAGAAATATCACC 617
Db 125 AlaTyrCysHisAsnSerSerAspThrTrpValAsnSerCysIleProGluIleValThr 144
QY 618 ACCAAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACAGAAATTTATGTTCAGT 677
Db 145 ThrPheTyrProValLeuAspThrGln-----ThrProAlaThrGluPheSerValSer 162
QY 678 GACAGTACCTACTCGGTGGCATCCCTTACTCTACAAATACCTGCCCTACTACTACTCCT 737
Db 163 SerSerAlaTyrLeuAlaSerSerProAspSerThrThrProValSerAlaThrThr--- 181
QY 738 CCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAAGTT 797
Db 182 ArgAlaProProLeuThrSerMetAlaArgLysThrLysLysIleCysIleThrGluVal 201
QY 798 TTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCAATTTGTTGAAAAATAAGCAGCA 857
Db 202 TyrThrGluProIleThrMetAlaThrGluThrGluAlaPheValAlaSerGlyAlaAla 221
QY 858 TTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGTGCTCTC 917
Db 222 PheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeuLeuValLeuAlaLeu 241
QY 918 CTCCTTCTTGGTGTGCTGAGCTGGTCTTGGATTTTGTATGTCAAAAGGTATGTGAAGCC 977
Db 242 LeuPhePheGlyAlaAlaAlaValLeuAlaValCysTyrValLysArgTyrValLysAla 261
QY 978 TTCCCTTTTACAAACAAGAATCAGCAGAAAGAAATGATCGAAACCAAGTAGTAAAGGAG 1037
Db 262 PheProPheThrThrLysAsnGlnGlnLysGluMetIleGluThrLysValValLysGlu 281
QY 1038 GAGAAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACTGATAAAACCCAGAA 1097
Db 282 GluLysAlaAspAspValAsnAlaAsnGluGluSerLysLysThrIleLysAsnProGlu 301
QY 1098 GAGTCCAAGAGTCCAAGCAAACTACCGTCCGATGCCCTGGAGCTGAAGTT 1148
Db 302 GluAlaLysSerProProLysThrThrValArgCysLeuGluAlaGluVal 318

RESULT 5
Q99NE4
ID Q99NE4 PRELIMINARY; PRT; 318 AA.
AC Q99NE4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hyaluronan receptor precursor.
GN XLKD1 OR LYVE-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c; TISSUE=Digestive tract;


```
RX MEDLINE=99156989; PubMed=10037799;
RA Banerji S.;
RT "LYVE-1, a new homologue of the CD44 glycoprotein is a lymph-specific
RT receptor for hyaluronan.";
RL J. Cell Biol. 144:789-801(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c; TISSUE=Digestive tract;
RX MEDLINE=21276443; PubMed=11278811;
RA Prevo R., Banerji S., Ferguson D.J.P., Clasper S., Jackson D.G.;
RT "Mouse LYVE-1 is an endocytic receptor for hyaluronan in lymphatic
RT endothelium.";
RL J. Biol. Chem. 276:19420-19430(2001).
DR EMBL; AJ311501; CAC33082.1; -.
DR HSSP; P98066; 1TSG.
DR MGD; MGI:2136348; Xlkd1.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0005540; F:hyaluronic acid binding; IDA.
DR GO; GO:0004888; F:transmembrane receptor activity; IDA.
DR GO; GO:0006027; P:glycosaminoglycan catabolism; IDA.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK; 1.
KW Receptor; Signal.
FT SIGNAL 1 23
FT CHAIN 24 318 LYVE-1.
SQ SEQUENCE 318 AA; 34641 MW; 1248974A16113330 CRC64;

Alignment Scores:
Pred. No.: 8.8e-100 Length: 318
Score: 1095.00 Matches: 219
Percent Similarity: 78.55% Conservative: 30
Best Local Similarity: 69.09% Mismatches: 64
Query Match: 30.38% Indels: 4
DB: 11 Gaps: 3

US-10-079-111-2 (1-2029) x Q99NE4 (1-318)

QY 198 AGCCTGGTGTGCTTCTCAGCTTCCATCTGGACCGAGGCTCTGGTCCAGGCTCTTTG 257
|||||
6 SerLeuValPhePheLeuAlaSerIleTrpThrArgHisProValGlnGlyAlaAap 25

QY 258 CGTGCAGAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGATCACCCTTGTGAGC 317
|||||
26 LeuValGlnAspLeuSerIleSer---ThrCysArgIleMetGlyValAlaLeuValGly 44

QY 318 AAAAAGCGCAACGACGAGCTGAATTTACAGAAGCTAAGGAGCGCTGTAGGCTGTGGGA 377
:::
45 ArgAsnLysAsnProGlnMetAsnPheThrGluAlaAsnGluAlaCysLysMetLeuGly 64

QY 378 CTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGC 437
|||||
65 LeuThrLeuAlaSerArgAspGlnValGluSerAlaGlnLysSerGlyPheGluThrCys 84

QY 438 AGCTATGGCTGGTTGGAGATGGATTGCTGGTCACTCTAGGATTAGCCCAACCCCAAG 497
|||||
85 SerTyrGlyTrpValGlyGluGlnPheSerValIleProArgIlePheSerAsnProArg 104

QY 498 TGTGGGAAAAATGGGGTGCTCTGATTTTGGAAAGTTTCCAGTGAGCCGACAGTTTGCA 557
|||||
105 CysGlyLysAsnGlyLysGlyValIleLeuLeuTrpAsnAlaProSerSerGlnLysPheLys 124

QY 558 GCCTATTGTTACAACACTCATCTGATACTTGGACTAACTCGTGCATTCCAGAAATTATCACC 617
|||||
125 AlaTyrCysHisAsnSerSerAspThrTrpValAsnSerCysIleProGluIleValThr 144

QY 618 ACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACACAGAAATTTATTGTCAGT 677
|||
145 ThrPheTyrProValLeuAspThrGln-----ThrProAlaThrGluPheSerValSer 162

QY 678 GACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCCCTACTACTCCT 737
```

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Db 163 SerSerAlaTyrLeuAlaSerSerProAspSerThrThrProValSerAlaThrThr--- 181
QY 738 CCTGCTCCAGCTTCCACACTTCTATTCCACGAGAGAAAAAATTGATTGTGTACAGAAAGTT 797
|||||
Db 182 ArgAlaProProLeuThrSerMetAlaArgLysThrLysLysIleCysIleThrGluVal 201
QY 798 TTTATGGAACACTAGCACCATGCTGTACAGAAACTGAACCATTTGTGAAAAATAAGCAGCA 857
:::
Db 202 TyrThrGluProIleThrMetAlaThrGluThrGluAlaPheValAlaSerGlyAlaAla 221
QY 858 TTCAACAATGAAGCTGCTGGGTTGGAGGTGTCCCCACGGCTCTGCTAGTGTGCTCTC 917
|||||
Db 222 PheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeuValLeuAlaLeu 241
QY 918 CTCTTCTTTGGTGTGCAGCTGGTCTTGGATTTTGTCTATGTCAAAAGGTATGTGAAGGCC 977
|||||
Db 242 LeuPhePheGlyAlaAlaValLeuAlaValCysTyrValLysArgTyrValLysAla 261
QY 978 TTCCCTTTTACAAACAAGAAATCAGCAGAGAAGAAATGATCGAAACCAAAGTAGTAAAGGAG 1037
|||||
Db 262 PheProPheThrThrLysAsnGlnLysGluMetIleGluThrLysValValLysGlu 281
QY 1038 GAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACATGATAAAACCCAGAA 1097
|||||
Db 282 GluLysAlaAspValAsnAlaAsnGluGluSerLysLysThrIleLysAsnProGlu 301
QY 1098 GAGTCCAAGAGTCCAAGCAAACTACCGTGCAGTGCCTGGAAGCTGAAGTT 1148
|||||
Db 302 GluAlaLysSerProProLysThrThrValArgCysLeuGluAlaGluVal 318

RESULT 6
Q7YS22
ID Q7YS22 PRELIMINARY; PRT; 201 AA.
AC Q7YS22;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Lymphatic endothelial hyaluronan receptor LYVE-1 (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Michael K.W., Xu S.-H., Voisine P., Khan T.A., Feng J., Li J.,
RA Sellke F.W., Bianchi C.;
RT "Identification of pig LYVE-1.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY304537; AAP69946.1; -.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 201 201
SQ SEQUENCE 201 AA; 22219 MW; BAAF34E7EACBBAE3 CRC64;

Alignment Scores:
Pred. No.: 3.85e-63 Length: 201
Score: 726.50 Matches: 141
Percent Similarity: 80.60% Conservative: 21
Best Local Similarity: 70.15% Mismatches: 36
Query Match: 20.16% Indels: 3
DB: 6 Gaps: 2

US-10-079-111-2 (1-2029) x Q7YS22 (1-201)

QY 423 AGCTTTGAAACCTTGCAGCTATGGCTGGTGGAGATGGATTGCTGCATCTCTAGGATT 482
|||||
Db 1 SerPheGluThrCysSerTyrGlyTrpValLysAspGlnPheLeuValIleProArgIle 20
QY 483 AGCCCAAAACCCCAAGTGTGGGAAAAAATGGGGTGGGTGCTCTGATTGGAAGGTTCCAGTG 542
|||||
Db 21 TyrProAsnProLysCysGlyLysAsnGlyLysGlyValLeuValTrpArgHisSerLeu 40
```

QY	543	AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACCTTGGACTAACTCGTGCATT	602
Db	41	SerGlnLysPheGluAlaTyrCysHisAsnSerSerAspThrArgThrAsnSerCysIle	60
QY	603	CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACA	662
Db	61	ProGluIleIleProThrAsnAspProThrPheAsnThrAsnThrAlaProTyrThrThr	80
QY	663	GAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCC-----CCTTACTCTACAATA	716
Db	81	GluMetThrValAsnAspArgThrSerSerSerSerSerThrAsnGlyProSerSerVal	100
QY	717	---CCTGCCCTACTACTACTCCTCCTCGTCCAGCTTCCACTTCTATTCCACGGAGAAAA	773
Db	101	MetProThrValThrThrSerLeuProLeuAlaThrThrSerThrProArgLysArg	120
QY	774	AAATTGATTGTGCACAGAAAGTTTTTTATGGAACTAGCACCATGTCTACAGAAACTGAA	833
Db	121	LysLeuIleCysIleThrGluAlaPheMetGluThrSerThrIleSerThrGluThrGlu	140
QY	834	CCATTTGTTGAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGTGTCCCC	893
Db	141	LeuTyrIleGluAsnArgThrAlaPheLysAsnGluAlaIleGlyPheGlyGlyIlePro	160
QY	894	ACGGCTCTGCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	953
Db	161	ThrAlaLeuLeuValLeuAlaLeuLeuPhePheAlaAlaAlaGlyLeuAlaValCys	180
QY	954	TATGTCAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAATCAGCAGGAAATG	1013
Db	181	TyrValLysArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMet	200
QY	1014	ATC 1016	
Db	201	Ile 201	
RESULT 7			
ID	O08779	PRELIMINARY; PRT; 780 AA.	
AC	O08779;		
DT	01-JUL-1997 (TrEMBLrel. 04, Created)		
DT	01-JUL-1997 (TrEMBLrel. 04, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	CD44 protein.		
GN	CD44.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BDX; TISSUE=Pancreas;		
RA	Hofmann M.;		
RT	"Rattus norvegicus CD44 protein sequence.";		
RL	Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; U96138; AAB54002.1; -.		
DR	HSSP; P98066; 1TSG.		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0004895; F:cell adhesion receptor activity; IEA.		
DR	GO; GO:0005540; F:hyaluronic acid binding; IEA.		
DR	GO; GO:0007155; P:cell adhesion; IEA.		
DR	InterPro; IPR001231; CD44 antigen.		
DR	InterPro; IPR000538; Link.		
DR	Pfam; PF00193; Xlink; 1.		
DR	PRINTS; PR00658; CD44.		
DR	PRINTS; PR01265; LINKMODULE.		
DR	ProDcm; PD000918; Link; 1.		
DR	SMART; SM00445; LINK; 1.		
DR	PROSITE; PS01241; LINK; 1.		
SQ	SEQUENCE 780 AA; 85917 MW; CC4D35AB1EA7377C CRC64;		

Alignment Scores:

Pred. No.: 1.26e-13 Length: 780

Score:	231.50	Matches:	138
Percent Similarity:	34.29%	Conservative:	77
Best Local Similarity:	22.01%	Mismatches:	254
Query Match:	6.42%	Indels:	160
DB:	11	Gaps:	23
US-10-079-111-2 (1-2029) x O08779 (1-780)			
QY	225	TGGACCACGAGGCTCCTGGTCCAAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTG	284
Db	10	TrpGlyLeuLeuCysLeuLeuGlnLeuSerLeuAlaGlnGlnIleAspLeuAsnIle	29
QY	285	TCATGCAGAAATTATGGGGGATCACCCCTTGTGAGCAAAAAGCGAACCAGCAGCTGAATTTC	344
Db	30	ThrCysArgTyrAlaGlyValPheHisValGluLysAsnGlyArgTyrSerIleSerArg	49
QY	345	ACAGAAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAAGTTTGGCCGGCAGGACCAAGTT	404
Db	50	ThrGluAlaAlaAspLeuCysGluAlaPheAsnThrThrLeuProThrMetAlaGlnMet	69
QY	405	GAACACAGCCTTGAAGCTAGCTTTGAAACTTGACGCTATGGCTGGTTGGAGATGGATTTC	464
Db	70	GluLeuAlaLeuArgLysGlyPheGluThrCysArgTyrGlyPheIle---GluGlyHis	88
QY	465	GTGTCATCTCTAGGATTAGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGTCTCCTG	524
Db	89	ValValIleProArgIleHisProAsnAlaIleCysAlaAlaAsnAsnThrGlyValTyr	108
QY	525	ATTTGGAAGGTTCCAGTGAGCCGACAGTTTTGACGCTATTGTTACAACTCATCTGATACT	584
Db	109	IleLeuLeuAlaSerAsnThrSerHisTyrAspThrTyrCysPheAsnAlaSerAlaPro	128
QY	585	TGGACTAACTCGTGCATTCAGAAAATTATCACACCAAAAGATCCCATATTCAACACTCAA	644
Db	129	LeuGluGluAspCys-----ThrSerValThrAspLeuProAsnSerPhe	143
QY	645	ACTGCAACACAAACAACAGAATTTATTGTGCTAGTGACAGTACC--TACTCGGTGGCATCC	701
Db	144	AspGlyProValThrIleThrIleValAsnArgAspGlyThrArgTyrSerLysLysGly	163
QY	702	CCTTACTCTACA-----ATACCTGCCCTACTACTCTCTCTCTCTCTCTCTCTCTCT	749
Db	164	GluTyrArgThrHisGlnGluAspIleAspAlaSerAsnIleIleAspGluAspValSer	183
QY	750	TCCACTTCTATTCCACGGAGAAAAAATTGATTGTGTACAGAAAGTTTTTATGGAAACT	809
Db	184	SerGlySerThrIleGluLysSer-----ThrProGluGlyTyrIleLeuHis	199
QY	810	AGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCATCAAGAAATGAA	869
Db	200	ThrAspLeuProThr---SerGlnProThrGlyAspArgAspAlaPhe-----	215
QY	870	GCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGTCTCTCTCTCTCTCTCTCT	929
Db	216	-----PheIleGlySerThrLeuAlaThrIleAlaSerThrVal-----	228
QY	930	GCTGCAGCTGGTCTGGATTTTTGCTATGTCAAAAGGTATGTGAAGGCCTTCCCT-----	983
Db	229	-----TyrSerLysSerHisAlaThrAlaGlnLysGlnAsn	240
QY	984	-----TTTCAAAACAAGAAATCAGCAGAGGAAATGATCGAAACCAA	1025
Db	241	AsnTrpIleTrpSerTrpPheGlyAsnSerGlnSerThrThrGlnThrGlnAspSerPro	260
QY	1026	GTAGTAAAGGAGAGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACTGAT	1085
Db	261	ThrThrThrAlaThrAlaLeuMetThrThrProGluThrProLysArgGlnGlu	280
QY	1086	AAA-----AACCCAGAAGAGTCCCAAGAGTCCCAAGCAAAACT	1121
Db	281	AlaGlnAsnTrpPheSerTrpPheGlnProSerGluSerLysSerHisLeuHisThr	300
QY	1122	ACCGTGCG-ATGCTGGAAAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGA	1180

Db 272 leSerAlaGlyTrpGlu-ProAsnGluGluAsnGluAspGluArgAspArgHisLeuSer 291
QY 1079 -----
Db 292 PheSerGlySerGlyIleAspAspAspGluAspPheIleSerSerThrIleSerThrThr 311
QY 1080 -----ACTGATAAAACCCAGAGAG 1100
Db 312 ProArgAlaPheAspHisThrLysGlnAsnGlnAspTrpThrGlnTrpAsnProSerHis 331
QY 1101 TCCAAGAGTCCAAGC-----AAAACACTACCGTGCATGCCTGGAAGCTGAAGTTTAG 1151
Db 332 Ser---AsnProGluValLeuLeuGlnThrThrThrArgMetThrAspValAsp----- 348
QY 1152 ATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCCTTACCCCTGCC 1211
Db 349 -----ArgAsnGlyThrThrAlaTyrGluGlyAsnTrpAsn----- 360
QY 1212 CCAGCTGGGGAATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCCCTTGGTTCCTA 1271
Db 361 -----ProGluAlaHisPro----- 365
QY 1272 ACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCT 1331
Db 366 -----ProLeuIleHisHisGluHisGluGluGluThr 378
QY 1332 CCTATTGTAAACCCTGTCTGGATCCTATCCTACCTCCAAAGCTTCCCACGGCCTTTC 1391
Db 379 ProHisSer-----ThrSerThrIleGlnAlaThrProSer----- 390
QY 1392 TAGCCTGGCTATGTCCTAATAATATCCCACTGGGAGAAAGGAGTTTGCAAAGTGCAAGG 1451
Db 390 ----- 390
QY 1452 ACCTAAACATCTCATCAGTATCCAGTGGTAAAGGCCCTCTGGCTGTCTGAGGCTAGG 1511
Db 391 -----SerThrThrGluThrAlaThrGlnLysGluGlnTrpPheGlyAsn---Arg 407
QY 1512 TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGCAGCTCAG 1571
Db 408 TrpHisGlu-----GlyTyrArgGlnThr-----ProArgGluAspSerHisSer 422
QY 1572 ACCCTTTCTTCAGCTCTGAAAGAGAGAAACACGTATCCCAC-----CTGACATGT 1619
Db 423 ThrThrGlyThrAlaAlaAlaSerAlaHisThrSerHisProMetGlnGlyArgThrThr 442
QY 1620 CCTTCTGAGCCCGGTAAAGAGCAAAAGAATGGCAGAAAAGTTTAGCCCC 1667
Db 443 ProSerProGluAspSerSer-----TrpThrAspPhePheAsnPro 456

RESULT 10
Q98SR5
ID Q98SR5 PRELIMINARY; PRT; 265 AA.
AC Q98SR5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE T cell antigen CD44 isoform b.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White Pekin;
RA Chan S.W.S., Warr G.W., Middleton D.L., Higgins D.A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332869; AAK18277.1; -.
DR HSSP; P98066; 1TSG.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004895; F:cell adhesion receptor activity; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.

DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR001231; CD44 antigen.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRINTS; PRO1265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK; 1.
SQ SEQUENCE 265 AA; 29215 MW; 77C176E0A898D081 CRC64;

Alignment Scores: 1.53e-12 Length: 265
Pred. No.: 219.00 Matches: 66
Score: 42.06% Conservative: 32
Percent Similarity: 28.33% Mismatches: 103
Best Local Similarity: 6.08% Indels: 32
Query Match: 13 Gaps: 5
DB;

US-10-079-111-2 (1-2029) x Q98SR5 (1-265)

QY 222 ATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCTGCAGAAAGAGCTTTCATCCAG 281
Db 6 ValTrpAlaThrPheGlyLeuCysLeuLeuLysLeuCysLeuThrGlnPheAsn 25
QY 282 GTGTCATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAGCGCAACGACGCTGAAT 341
Db 26 ValSerCysArgTyrArgGlyValPheHisValGluLysAsnGlyArgTyrSerLeuThr 45
QY 342 TTCACAGAAAGCTAAGGAGGCTGTAGGCTGTGGGACTAAGTTTGGCCGGCAAGGACCAA 401
Db 46 ArgThrGluAlaAlaAspLeuCysArgAlaLeuAsnSerThrLeuSerThrLeuGluGln 65
QY 402 GTTGAACACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGA 461
Db 66 LeuGluLysAlaHisGluLeuGlyPheGluThrCysArgTyrGlyPheVal---ValGly 84
QY 462 TTCGTGGTCATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGAAAAAATGGGTGGGTGTC 521
Db 85 TyrIleValIleProArgIleAsnProTyrHisLeuCysAlaAlaAsnHisThrGlyIle 104
QY 522 CTGATTTGGAAGTTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGAT 581
Db 105 TyrLysLeuSerAlaAsnThrThrGlyArgTyrAspAlaTyrCysTyrAsnAlaThrGlu 124
QY 582 ACTTGGACTAACTCGTGCATTCCA----- 605
Db 125 ThrArgAspLysAlaCysGluProIleGluArgIleAspThrSerPheLeuSerAsnGln 144
QY 606 ---GAAATTATCACCACCAAGATCCC-----ATATTCACACACTCAAACT 647
Db 145 GlyGluIleValIleAspAsnGluAspGlySerArgTyrAsnAlaAspGlyThrArgHis 164
QY 648 GCAACACAAACACAGAAATTATTGTCAGTGACAGTACTACTCGGTGGCATCCCTTAC 707
Db 165 SerGlyAspSerSerThrSerGlyValAspAspGluAsnValGlySerGlySerSerHis 184
QY 708 TCTACAATACCTGCCCTACTACTACTCTCTCTGCTCCAGCTTCC----- 752
Db 185 AspThrThrProValAspThrSerIleArgArgSerSerProSerTyrTyrGlySerVal 204
QY 753 ACTTCTATTCCACGG-----AGAAAAAATTTGATTTGTGTC 788
Db 205 ThrProValProHisLeuSerAspHisSerSerGlyGlyGluLysGluPheProVal 224
QY 789 ACAGAAGTTTTTATGGAACCTAGCACCATTGCTACAGAA 827
Db 225 ThrAsnSerAspAspGluIleSerProThrSerThrAsp 237

RESULT 11
Q90ZL8
ID Q90ZL8 PRELIMINARY; PRT; 398 AA.
AC Q90ZL8;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE T cell antigen CD44 isoform a.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White Pekin;
RA Chan S.W.S.; Middleton D.L.; Warr G.W.; Higgins D.A.;
RT "Anas platyrhynchos T cell antigens.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029553; AAK40246.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004895; F:cell adhesion receptor activity; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR001231; CD44 antigen.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK; 1.
SQ SEQUENCE 398 AA; 43673 MW; 25A944EE2F4AED6D CRC64;

Alignment Scores:
Pred. No.: 2.48e-12 Length: 398
Score: 217.50 Matches: 56
Percent Similarity: 44.68% Conservative: 28
Best Local Similarity: 29.79% Mismatches: 85
Query Match: 6.03% Indels: 19
DB: 13 Gaps: 3

US-10-079-111-2 (1-2029) x Q90ZL8 (1-398)

QY 222 ATCTGGACCACGAGGCTCCTGGTCCAGGCTTTGGGTGCAGAGAGCTTTCCATCCAG 281
Db 6 ValTrpAlaThrPheGlyLeuCysLeuLeuLysLeuCysLeuThrGluThrGlnPheAsn 25

QY 282 GTGTCATGCAGAATTATGGGGATCACCCCTGTGAGCAAAAAGCGAACCCAGAGCTGAAT 341
Db 26 ValSerCysArgTyrArgGlyValPheHisValGluLysAsnGlyArgTyrSerLeuThr 45

QY 342 TTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAAGTTTGGCGGCAAGGACCAA 401
Db 46 ArgThrGluAlaAlaAspLeuCysArgAlaLeuAsnSerThrLeuSerThrLeuGluGln 65

QY 402 GTTGAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGA 461
Db 66 LeuGluLysAlaHisGluLeuGlyPheGluThrCysArgTyrGlyPheVal---ValGly 84

QY 462 TTCGTGTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGTC 521
Db 85 TyrIleValIleProArgIleAsnProTyrHisLeuCysAlaAlaAsnHisThrGlyIle 104

QY 522 CTGATTTGGAGGTTCCAGTGAGCCGACAGTTTGCAGCCCTATTGTTACAACTCATCTGAT 581
Db 105 TyrLysLeuSerAlaAsnThrThrGlyArgTyrAspAlaTyrCysTyrAsnAlaThrGlu 124

QY 582 ACTTGGACTAACTCGTGCATTCCA----- 605
Db 125 ThrArgAspLysAlaCysGluProIleGluArgIleAspThrSerPheLeuSerAsnGln 144

QY 606 ---GAAATTATACCACCAAGATCCC-----ATATTCAACACTCAAACT 647
Db 145 GlyGluIleValIleAspAsnGluAspGlySerArgTyrAsnAlaAspGlyThrArgHis 164

QY 648 GCAACACAAACACAGAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTAC 707
Db 648 GCAACACAAACACAGAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTAC 707

Db 165 SerGlyAspSerSerThrSerGlyValAspAspGluAsnValGlySerGlySerSerHis 184
QY 708 TCTACAAATACCTGCCCTACTACT 731
Db 185 AspThrThrProValAspThrSer 192

RESULT 12
Q9H5A5
ID Q9H5A5 PRELIMINARY; PRT; 719 AA.
AC Q9H5A5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DJ68D18.2.3 (CD44 antigen (Homing function and indian blood group system)) (Fragment).
DE system)) (Fragment).
GN CD44.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Cobley V.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL133330; CAC10347.1; -.
DR HSSP; P98066; 1TSG.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004895; F:cell adhesion receptor activity; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR001231; CD44 antigen.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK; 1.
FT NON TER 1
SQ SEQUENCE 719 AA; 78854 MW; 36B747A896AD7380 CRC64;

Alignment Scores:
Pred. No.: 4.3e-12 Length: 719
Score: 216.00 Matches: 115
Percent Similarity: 31.94% Conservative: 61
Best Local Similarity: 20.87% Mismatches: 172
Query Match: 5.99% Indels: 203
DB: 4 Gaps: 23

US-10-079-111-2 (1-2029) x Q9H5A5 (1-719)

QY 276 ATCCAGGTGTCATGCAGAATTATGGGGATCACCCCTTGTGAGCAAAAAGCGAACCCAGCAG 335
Db 1 LeuAsnIleThrCysArgPheAlaGlyValPheHisValGluLysAsnGlyArgTyrSer 20

QY 336 CTGAATTTACAGAAGCTAAGGAGGCCTGTAGGCTGTGGGACTAAGTTTGGCCGCAAG 395
Db 21 IleSerArgThrGluAlaAlaAspLeuCysLysAlaPheAsnSerThrLeuProThrMet 40

QY 396 GACCAAGTTGAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAAGCTATGGCTGGTTGGA 455
Db 41 AlaGlnMetGluLysAlaLeuSerIleGlyPheGluThrCysArgTyrGlyPheIle--- 59

QY 456 GATGATTGCTGGTTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGGTG 515
Db 60 GluGlyHisValValIleProArgIleHisProAsnSerIleCysAlaAlaAsnAsnThr 79

QY 516 GGTGTCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACACTCA 575
Db 80 GlyValTyrIleLeuThrSerAsnThrSer---GlnTyrAspThrTyrCysPheAsnAla 98

QY 576 TCTGATACTTGGACTAACTCGTGCATT----- 602

Db 99 SerAlaProProGluGluAspCysThrSerValThrAspLeuProAsnAlaPheAspGly 118
QY 602 ----- 602
Db 119 ProIleThrIleThrIleValAsnArgAspGlyThrArgTyrValGlnLysGlyGluTyr 138
QY 603 -----CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACA 653
Db 139 ArgThrAsnProGluAspIleTyrProSerAsnProThrAspAspValSerSerGly 158
QY 654 CAAACAACAGAAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACA 713
Db 159 SerSerSerGluArgSerSerThrSerGlyGlyTyr---IlePheTyrThrPheSerThr 177
QY 714 ATA---CCTGCCCTACTACTACTCTCCT-----GCTCCA 746
Db 178 ValHisProIleProAspGluAspSerProTrpIleThrAspSerThrAspArgIlePro 197
QY 747 GCTTCCACTTCTATTCCACGGAGAAAAAATTGATTGTGTCACAGAAGTTTATGGAA 806
Db 198 AlaThrThr-----LeuMetSer 203
QY 807 ACTAGCACCATGTCTACAGAAACTGACCATTTGTTGAAAAATAAGCAGCATTCAGAAT 866
Db 204 ThrSerAlaThrAlaThrGluThr-----AlaThrLysArgGln 216
QY 867 GAAGCTGCTGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGCTTGCTCTCTCTTT 926
Db 217 GluThr--TrpAspTrp----- 221
QY 927 GGTGCTGCAGCTGGTCTTGGATTTTGTCTATGTCAAAGGTATGTGAAGCCCTTCCCTTT 986
Db 222 -----PheSerTrpLeupheLeuProSerGluSerLysAsnHisLeu-----H 236
QY 987 ACAACAAGAATCAGCAGAGGAATATGATCGAAACCAAGTAGTAAGGAGGAGGCC 1046
Db 236 isThrThrThrGlnMetAlaGlyThrSerSerAsnThrIleSerAlaGlyTrpGlu-Pro 255
QY 1047 AATGATAGCAACCTTAATGAGGAATCAAAGAA----- 1079
Db 256 AsnGluGluAsnGluAspGluArgAspArgHisLeuSerPheSerGlySerGlyIleAsp 275
QY 1079 ----- 1079
Db 276 AspAspGluAspPheIleSerSerThrIleSerThrThrProArgAlaPheAspHisThr 295
QY 1080 -----ACTGATAAAACCCAGAAAGATCCAGAGTCCAAGATCCAAGC----- 1115
Db 296 LysGlnAsnGlnAspTrpThrGlnTrpAsnProSerHisSer---AsnProGluValLeu 314
QY 1116 ---AAAACACTACCGTGCATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAATGAGGAGAC 1172
Db 315 LeuGlnThrThrThrArgMetThrAspValAsp-----ArgAsnGlyThr 329
QY 1173 ACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCCTGCCCCAGCTGGGGAAATCAAAGG 1232
Db 330 ThrAlaTyrGluGlyAsnTrpAsn----- 337
QY 1233 GCCAAAGAACCAAGAAGAAAGTCCACCCTTGGTTCTCTAACTGGAATCAGCTCAGGACTG 1292
Db 338 -----ProGluAlaHisPro----- 342
QY 1293 CCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATGTAAACCCTGTCTGG 1352
Db 343 ProLeuIleHisHisGluHisGluGluGluGluThrProHisSer----- 358
QY 1353 ATCCTATCCTCCTACCTCCAAGCTTCCACGGCCTTTCTAGCCTGGCTATGTCCTAATA 1412
Db 359 -----ThrSerThrIleGlnAlaThrProSer----- 367
QY 1413 ATATCCCACCTGGGAGAAAGGAGTTTTGCAAAAGTGCAAGGACCTAAAACATCTCATCAGTA 1472
Db 368 -----SerThrThrGluGlu 372

QY 1473 TCCAGTGTFAAAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGTTGAAAGCCAAGGAGTC 1532
Db 373 ThrAlaThrGlnLysGluGlnTrpPheGlyAsn---ArgTrpHisGlu-----GlyTyr 389
QY 1533 ACTGAGACCAAGGCTTTCTCTACTGATTCCGCGAGCTCAGACCCCTTCTTCAGCTCTGAAA 1592
Db 390 ArgGlnThr-----ProLysGluAspSerHisSerThrThrGlyThrAlaAlaAa 406
QY 1593 GAGAAACACGTATCCAC-----CTGACATGTCCTCTGAGCCCGGTAAGAGC 1640
Db 407 SerAlaHisThrSerHisProMetGlnGlyArgThrThrProSerProGluAspSerSer 426
QY 1641 AAAAGATGGCAGAAAAAGTTTAGCCCC 1667
Db 427 -----TrpThrAspPheAsnPro 433
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AC Q96J24;
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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to CD44 antigen (Homing function and indian blood group system).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBDJ databases.
DR EMBL; BC004372; AAH04372.1; -.
DR PIR; I37369; I37369.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004895; F:cell adhesion receptor activity; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR001231; CD44_antigen.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK; 1.
SQ SEQUENCE 699 AA; 76628 MW; 68AC366A392DBC7C CRC64;
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Best Local Similarity: 20.39% Mismatches: 177
Query Match: 5.91% Indels: 162
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QY 315 AGCAAAAAGGGAACCAACGACGCTGAATTCACAGAAGCTAAGGAGGCCCTGTAGGCTGCTG 374
Db 37 GluLysAsnGlyArgTyrSerIleSerArgThrGluAlaAlaAspLeuCysLysAlaPhe 56
QY 375 GGACTAAGTTTGGCCCGCAAGACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACT 434
Db 57 AsnSerThrLeuProThrMetAlaGlnMetGluLysAlaLeuSerIleGlyPheGluThr 76


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Db      41 AlaGlnMetGluLysAlaLeuSerIleGlyPheGluThrCysArgTyrGlyPheIle--- 59
      456 GATGGATTGCGTGGTCATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTG 515
Db      60 GluGlyHisValValIleProArgIleHisProAsnSerIleCysAlaAlaAsnAsnThr 79
      516 GGTGTCCTGATTGTGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCA 575
Db      80 GlyValTyrIleLeuThrSerAsnThrSer---GlnTyrAspThrTyrCysPheAsnAla 98
      576 TCTGATACTTGGACTAACTCGTGCATT----- 602
Db      99 SerAlaProProGluGluAspCysThrSerValThrAspLeuProAsnAlaPheAspGly 118
      602 ----- 602
Db     119 ProIleThrIleThrIleValAsnArgAspGlyThrArgTyrValGlnLysGlyGluTyr 138
      603 -----CCAGAAATTATCACCACCACCAAGATCCCATATTCAAACACTCAAACTGCAACA 653
Db     139 ArgThrAsnProGluAspIleTyrProSerAsnProThrAspAspAspValSerSerGly 158
      654 CAAACAACAGAAATTATTGTGTCAGTGACAGTACCTACTCGTGGCATCCCTTACTCTACACA 713
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      714 ATA---CCTGCCCTACTACTCTCCTCCT-----GCTCCAGCTTCCACTTCTATTCCA 764
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Db     198 AlaThrSer-----ThrSerSerAsnThrIleSerAla 208
      825 GAAACTGAACCATTTGTTGAAATPAAAGCAGCATTCAGAAATGAAGCTGCTGGTTTGGGA 884
Db     209 GlyTrpGluProAsnGluAsnGluAspGlu---ArgAspArgHisLeuSerPheSer 227
      885 GGTGTCCTCCACGGCTCTGCTAGTGTGCTGTCTCTCTCTCTTTGGTGTGCAGCTGGTCTT 944
Db     228 Gly-----SerGlyIle 231
      945 GGATTTTGCTATGTCAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAG 1004
Db     232 -----AspAspAsp 234
      1005 AAGGAAATGATCGAAACCAAGTAGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1064
Db     235 GluAspPheIleSerSerThrIleSerThrThrProArgAlaPheAsp---HisThrLys 253
      1065 GAGGAATCAAAGAAAACTGATAAAACCCAGAGAGTCCAGAGTCCCAAGC----- 1115
Db     254 GlnAsnGlnAspTrpThrGlnTrpAsnProSerHisSer---AsnProGluValLeuLeu 272
      1116 AAAACTACCGTGCATGCGCTGGAAGCTGAAGTTTAGATGAGACAGAAAAATGAGGAGACACA 1175
Db     273 GlnThrThrThrArgMetThrAspValAsp-----ArgAsnGlyThrThr 287
      1176 CCTGAGGCTGTTTCTTTTCATGCTCTTACCCTTACCCTGCCCCAGCTGGGAAATCAAAAGGCC 1235
Db     288 AlaTyrGluGlyAsnTrpAsn----- 294
      1236 AAAGAACCAAGAAGAAAGTCCACCCTTGGTTCCCTTAAGTGAATCAGCTCAGGACTGCCA 1295
Db     295 -----ProGluAlaHisPro-----Pro 300
      1296 TTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCCTTATTGTAACCCCTGTCTGGATC 1355
Db     301 LeuIleHisHisGluHisGluGluGluGluThrProHisSer----- 315
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      1476 AGTGGTAAAAAGCCCTCCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGCCCAAGGAGTCACT 1535
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      1536 GAGACCAAGGCTTCTCTACTGATTCCGACGCTCAGACCCCTTTCTTCAGCTCTGAAAGAG 1595
Db     348 GlnThr-----ProLysGluAspSerHisSerThrThrGlyThrAlaAlaAlaSer 364
      1596 AAACACGATATCCAC-----CTGACATGTCCTTCTGAGCCCGGTAAAGAGCAAA 1643
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      1644 AGAATGGCAGAAAAAGTTTAGCCCC 1667
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      DT 01-DEC-2001 (TrEMBLrel. 19, Created)
      DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
      DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
      DE T-cell antigen CD44 isoform C.
      OS Anas platyrhynchos (Domestic duck).
      OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
      OX NCBI_TaxID=8839;
      RN [1]
      RP SEQUENCE FROM N.A.
      RA Chan S.W.S., Middleton D.L., Lundqvist M., Warr G.W., Higgins D.A.;
      RT "Anas platyrhynchos T-cell antigens.";
      RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
      DR EMBL; AY032667; AAK52086.1; -.
      DR GO; GO:0016020; C:membrane; IEA.
      DR GO; GO:0004895; F:cell adhesion receptor activity; IEA.
      DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
      DR GO; GO:0007155; P:cell adhesion; IEA.
      DR InterPro; IPR001231; CD44_antigen.
      DR InterPro; IPR000538; Link.
      DR Pfam; PF00193; Xlink; 1.
      DR PRINTS; PR00658; CD44.
      DR PRINTS; PR01265; LINKMODULE.
      DR ProDom; PD000918; Link; 1.
      DR SMART; SM00445; Link; 1.
      DR PROSITE; PS01241; LINK; 1.
      SQ SEQUENCE 168 AA; 18964 MW; 122EFE727977056E CRC64;

Alignment Scores:
Pred. No.:      2.29e-11      Length:      168
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      282 GTGTCATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAGCGCAACGACGCTGAAT 341
Db      26 ValSerCysLysTyrArgGlyValPheHisValGluLysAsnGlyArgTyrSerLeuThr 45
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Db      46 ArgThrGluAlaAlaAspLeuCysArgAlaLeuAsnSerThrLeuSerThrLeuGln 65
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Db      66 LeuGluLysAlaHisGluLeuGlyPheGluThrCysArgTyrGlyPheVal---ValGly 84
QY      462 TTCGTGGTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAAATGGGGTGGGTGTC 521
Db      85 TyrIleValIleProArgIleAsnProTyrHisLeuCysAlaAlaAsnHisThrGlyIle 104
QY      522 CTGATTGTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCCTATTGTTACAACCTCATCTGAT 581
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Search completed: September 13, 2004, 10:21:24
Job time : 255.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 13, 2004, 10:13:27 ; Search time 36.5 Seconds
(without alignments)
5739.676 Million cell updates/sec

Title: US-10-079-111-2
Perfect score: 3604
Sequence: 1 ccttgacaagtcagaagctt.....aaacatttaaaaaaaaaa 2029

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 778828

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA: *
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1657	46.0	322	4	US-09-232-160-21
2	1657	46.0	322	4	US-09-907-794A-201
3	1657	46.0	322	4	US-09-905-125A-201
4	1657	46.0	322	4	US-09-902-775A-201
5	1651	45.8	322	2	US-08-892-880-2
6	1103	30.6	318	4	US-09-724-864-60
7	231.5	6.4	363	1	US-07-946-497-7
8	231.5	6.4	363	1	US-08-483-322-7
9	231.5	6.4	363	2	US-08-478-882-7
10	228.5	6.3	503	1	US-07-946-497-2
11	228.5	6.3	503	1	US-08-483-322-2
12	228.5	6.3	503	2	US-08-478-882-2

13	224.5	6.2	339	2	US-08-892-880-3	Sequence 3, Appli
14	222.5	6.2	362	6	5504194-2	Patent No. 5504194
15	207	5.7	361	1	US-07-946-497-6	Sequence 6, Appli
16	207	5.7	361	1	US-08-483-322-6	Sequence 6, Appli
17	207	5.7	361	2	US-08-478-882-6	Sequence 6, Appli
18	161	4.5	90	2	US-08-242-097-3	Sequence 3, Appli
19	161	4.5	90	3	US-09-206-695-3	Sequence 3, Appli
20	161	4.5	90	4	US-09-799-118-3	Sequence 3, Appli
21	145	4.0	277	1	US-08-024-868-2	Sequence 2, Appli
22	145	4.0	277	2	US-08-242-097-2	Sequence 2, Appli
23	145	4.0	277	3	US-09-206-695-2	Sequence 2, Appli
24	145	4.0	277	4	US-09-000-179-1	Sequence 1, Appli
25	145	4.0	277	4	US-09-799-118-2	Sequence 2, Appli
26	145	4.0	277	5	PCT-US96-11995-1	Sequence 1, Appli
27	131.5	3.6	912	5	PCT-US95-03747-2	Sequence 2, Appli
28	130.5	3.6	528	4	US-09-010-147B-20	Sequence 20, Appl
29	126	3.5	1257	1	US-08-340-428B-49	Sequence 49, Appl
30	123.5	3.4	360	4	US-09-907-794A-213	Sequence 213, App
31	123.5	3.4	360	4	US-09-905-125A-213	Sequence 213, App
32	123.5	3.4	360	4	US-09-902-775A-213	Sequence 213, App
33	115	3.2	908	5	PCT-US95-03747-3	Sequence 3, Appli
34	113.5	3.1	97	2	US-08-242-097-5	Sequence 5, Appli
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36	113.5	3.1	97	4	US-09-799-118-5	Sequence 5, Appli
37	111	3.1	328	1	US-08-225-477B-5	Sequence 5, Appli
38	111	3.1	328	5	PCT-US95-04353-5	Sequence 5, Appli
39	111	3.1	2409	6	5180808-2	Patent No. 5180808
40	107	3.0	371	1	US-08-225-477B-8	Sequence 8, Appli
41	107	3.0	371	5	PCT-US95-04353-8	Sequence 8, Appli
42	106	2.9	329	1	US-08-225-477B-3	Sequence 3, Appli
43	106	2.9	329	5	PCT-US95-04353-3	Sequence 3, Appli
44	105	2.9	333	1	US-08-225-477B-4	Sequence 4, Appli
45	105	2.9	333	5	PCT-US95-04353-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-232-160-21
; Sequence 21, Application US/09232160
; Patent No. 6368794
; GENERAL INFORMATION:
; APPLICANT: Steve Daniel
; APPLICANT: James Gilmore
; APPLICANT: Susan G. Stuart
; APPLICANT: Laura Stuve
; TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: PA-0003 US
; CURRENT APPLICATION NUMBER: US/09/232,160
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PERL Program
; SEQ ID NO 21
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 3044710
US-09-232-160-21

Alignment Scores:
Pred. No.: 5.42e-174 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0
DB: 4 Gaps: 0

US-10-079-111-2 (1-2029) x US-09-232-160-21 (1-322)

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Db 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
QY 303 ATACCCCTTGTGAGCAAAAAGCGCAACCAGCAGCTGAATTCACAGAAGCTAAGGAGGCC 362
Db 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
QY 363 TGTAGGCTGTGGGACTAAGTTTGGCGGCAAGGACCAAGTTGAACAGCCTTGAAAAGCT 422
Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
QY 723 CCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATTGATT 782
Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
QY 783 TGTGTCAAGAGTTTTATGGAACCTAGCACCATGTCTACAGAACTGAACCATTTGTT 842
Db 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
QY 843 GAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 902
Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
QY 903 CTAGTGTCTGCTCTCTCTCTCTTTGTCGTGCAGCTGGTCTTGGATTTTGCTATGTCAA 962
Db 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
QY 963 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAATGATCGAAACC 1022
Db 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
QY 1023 AAAGTAGTAAAGGAGGAGAGGCAATCATAGCAACCCCTAATGAGGAATCAAAGAAAACT 1082
Db 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluSerLysLysThr 300
QY 1083 GATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAAGCT 1142
Db 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
QY 1143 GAAGTT 1148
Db 321 GluVal 322

RESULT 2

US-09-907-794A-201
; Sequence 201, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
US-09-907-794A-201

Alignment Scores: 5.42e-174 Length: 322
Pred. No.:

Score:	1657.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	45.98%	Indels:	0
DB:	4	Gaps:	0
US-10-079-111-2 (1-2029) x US-09-907-794A-201 (1-322)			
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QY	243	GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG	302
Db	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
QY	303	ATCACCCCTTGTCAGCAAAAAGGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAAGGAGCC	362
Db	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
QY	363	TGTAGGCTGCTGGACTAAGTTTGGCCGCGCAAGGACCAAGTTTGAACAGCCTTGAAAGCT	422
Db	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
QY	423	AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGGTCACTCTAGGATT	482
Db	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
QY	483	AGCCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCTGATTGGAAGGTTCCAGTG	542
Db	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
QY	543	AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT	602
Db	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
QY	603	CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACCTCAAACACAAACA	662
Db	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
QY	663	GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	722
Db	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
QY	723	CCTACTACTCTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	782
Db	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
QY	783	TGTGTACAGAAAGTTTATGGAAACTAGCACATGTCTACAGAAACTGAACCATTTGTT	842
Db	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
QY	843	GAATAATAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCGCCACGGCTCTG	902
Db	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
QY	903	CTAGTGCTTCTCTCCTCTTCTTTGGTGTGCAGCTGGTCTTGGATTTTGTATGTCAA	962
Db	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
QY	963	AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAATCAGCAGAGGAATGATCGAAACC	1022
Db	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr	280
QY	1023	AAAGTAGTAAAGGAGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACT	1082
Db	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
QY	1083	GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAAACCTACCGTGCATGCTGGAAGCT	1142
Db	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
QY	1143	GAAGTT	1148

Db	321	GluVal	322
RESULT 3			
US-09-905-125A-201			
; Sequence 201, Application US/09905125A			
; Patent No. 6664376			
; GENERAL INFORMATION:			
; APPLICANT: Genentech, Inc.			
; APPLICANT: Ashkenazi, Avi			
; APPLICANT: Botstein, David			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Eaton, Dan L.			
; APPLICANT: Ferrara, Napoleone			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Fong, Sherman			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Gerber, Hanspeter			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, A.			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, Christopher J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Hillan, Kenneth, J.			
; APPLICANT: Kljavin, Ivar J.			
; APPLICANT: Mather, Jennie P.			
; APPLICANT: Pan, James			
; APPLICANT: Paoni, Nicholas F.			
; APPLICANT: Roy, Margaret Ann			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Williams, P. Mickey			
; APPLICANT: Wood, William, I.			
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
; TITLE OF INVENTION: Acids Encoding the Same			
; FILE REFERENCE: 10466-14			
; CURRENT APPLICATION NUMBER: US/09/905.125A			
; CURRENT FILING DATE: 2001-07-12			
; PRIOR APPLICATION NUMBER: PCT/US00/04414			
; PRIOR FILING DATE: 2000-02-22			
; PRIOR APPLICATION NUMBER: US 60/143,048			
; PRIOR FILING DATE: 1999-07-07			
; PRIOR APPLICATION NUMBER: US 60/145,698			
; PRIOR FILING DATE: 1999-07-26			
; PRIOR APPLICATION NUMBER: US 60/146,222			
; PRIOR FILING DATE: 1999-07-28			
; PRIOR APPLICATION NUMBER: PCT/US99/20594			
; PRIOR FILING DATE: 1999-09-08			
; PRIOR APPLICATION NUMBER: PCT/US99/20944			
; PRIOR FILING DATE: 1999-09-13			
; PRIOR APPLICATION NUMBER: PCT/US99/21090			
; PRIOR FILING DATE: 1999-09-15			
; PRIOR APPLICATION NUMBER: PCT/US99/21547			
; PRIOR FILING DATE: 1999-09-15			
; PRIOR APPLICATION NUMBER: PCT/US99/23089			
; PRIOR FILING DATE: 1999-10-05			
; PRIOR APPLICATION NUMBER: PCT/US99/28214			
; PRIOR FILING DATE: 1999-11-29			
; PRIOR APPLICATION NUMBER: PCT/US99/28313			
; PRIOR FILING DATE: 1999-11-30			
; PRIOR APPLICATION NUMBER: PCT/US99/28564			
; PRIOR FILING DATE: 1999-12-02			
; PRIOR APPLICATION NUMBER: PCT/US99/28565			
; PRIOR FILING DATE: 1999-12-02			
; PRIOR APPLICATION NUMBER: PCT/US99/30095			
; PRIOR FILING DATE: 1999-12-16			
; PRIOR APPLICATION NUMBER: PCT/US99/30911			
; PRIOR FILING DATE: 1999-12-20			
; PRIOR APPLICATION NUMBER: PCT/US99/30999			
; PRIOR FILING DATE: 1999-12-20			
; PRIOR APPLICATION NUMBER: PCT/US00/00219			
; PRIOR FILING DATE: 2000-01-05			
; NUMBER OF SEQ ID NOS: 423			

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; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
US-09-905-125A-201

Alignment Scores:
Pred. No.:      5.42e-174      Length:      322
Score:          1657.00      Matches:      322
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      45.98%      Indels:      0
DB:              4      Gaps:      0

US-10-079-111-2 (1-2029) x US-09-905-125A-201 (1-322)

QY 183 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGTCCTG 242
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QY 243 GTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGG 302
Db 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

QY 303 ATCAACCTTGTGAGCAAAAAGGCGAACACGACGAGCTGAATTTACAGAAGCTAAGGAGGCC 362
Db 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60

QY 363 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 422
Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

QY 423 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTGCTGGTCATCTCTAGGATT 482
Db 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100

QY 483 AGCCCAAAACCCCAAGTGTGGGAAAAAATGGGTGGTGTCTCGATTGGAAGGTTCCAGTG 542
Db 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValIleLeuTrpLysValProVal 120

QY 543 AGCGACAGTTTGCAGCCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATT 602
Db 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

QY 603 CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 662
Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

QY 663 GAATTTATTGTCAGTGACGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 722
Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

QY 723 CCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 782
Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

QY 783 TGTGTACAGAAAGTTTTATGGAAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 842
Db 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

QY 843 GAAAAATAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 902
Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240

QY 903 CTAGTGCTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 962
Db 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260

QY 963 AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCACAGAAGGAAATGATCGAAACC 1022
Db 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
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QY 1023 AAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCTAATGAGGAATCAAGAAACT 1082
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QY 1083 GATAAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTCCGATGCCTGGAAGCT 1142
Db 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320

QY 1143 GAAGTT 1148
Db 321 GluVal 322

RESULT 4
US-09-902-775A-201
; Sequence 201, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
US-09-902-775A-201

Alignment Scores:
Pred. No.: 5.42e-174 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0
DB: 4 Gaps: 0

US-10-079-111-2 (1-2029) x US-09-902-775A-201 (1-322)

QY 183 ATGGCCAGGTGCTTCAGCCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 242
Db 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20

QY 243 GTCCAAAGCTCTTTGGGTGCAGAAGAGCTTTCCATCCAGGTGTCAATGCAGAAATTATGGGG 302
Db 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40

QY 303 ATCACCCCTTGTAGCAAAAAGGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAAGGAGGCC 362
Db 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60

QY 363 TGTAGGCTGCTGGGACTAAGTTTGGCCGCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 422
Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

QY 423 AGCTTTGAAACITTGACGCTATGGCTGGGTGGAGATGGATTGCTGGTCACTCTAGGATT 482
Db 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

QY 483 AGCCCCAAACCCCAAGTGTGGGAAAAATGGGTGGTGTCTGATTTGGAAAGTTCAGTG 542
Db 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

QY 543 AGCCGACAGTTTGACGCTATTGTTACAACCTCACTGATACTTGGACTAATCGTGCAATT 602
Db 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

QY 603 CCAGAAATTATCACCAACCAAAAGATCCCATATTTCAACACTCAAACCTGCAACACAAACA 662
Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

QY 663 GAATTTATTGTGACGTACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCC 722
Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

QY 723 CCTACTACTACTCTCTGCTCCAGCTTCCACTTCTATTCACGGAGAAAAAATTGATT 782
Db 181 ProThrThrThrProAlaProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

QY 783 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCAATGTCTACAGAAACTGAACCATTTGTT 842
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Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
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QY 1143 GAAGTT 1148
Db 321 GluVal 322

RESULT 5
US-08-892-880-2
; Sequence 2, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HERewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 322 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-892-880-2

Alignment Scores:
Pred. No.: 2.5e-173 Length: 322
Score: 1651.00 Matches: 321
Percent Similarity: 99.69% Conservative: 0
Best Local Similarity: 99.69% Mismatches: 1
Query Match: 45.81% Indels: 0

DB:	2	Gaps:	0
US-10-079-111-2 (1-2029) x US-08-892-880-2 (1-322)			
QY	183	ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG	242
Db	1	MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu	20
QY	243	GTCCAAAGGCTCTTTGCGTGCAGAAAGCTTCCATCCAGGTGTCAATGAGAATTATGGGG	302
Db	21	ValGlnGlySerLeuArgAlaGluGluSerIleGlnValSerCysArgIleMetGly	40
QY	303	ATCACCTTGTGAGCAAAAAGGCAACACGACGCTGAATTCACAGAAGCTAAGGAGGCC	362
Db	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
QY	363	TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT	422
Db	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
QY	423	AGCTTTGAAAACCTTGCAGCTATGGCTGGTGGATGGAGATGGATTCGTTGTCATCTCTAGGATT	482
Db	81	SerPheAlaThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
QY	483	AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTG	542
Db	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
QY	543	AGCCGCAGAGTTTGCAGCCTATTGTTTACAACTCATCTGATACCTTGGACTAACTCGTGCATT	602
Db	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
QY	603	CCAGAAATTATCACCAACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACAACA	662
Db	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
QY	663	GAATTTATTTGTCAGTACACTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	722
Db	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
QY	723	CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATTGATT	782
Db	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
QY	783	TGTGTCACAGAAGTTTTTATGGAACACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	842
Db	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
QY	843	GAAATAAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTTGAGGTGTCCCCACGGCTCTG	902
Db	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
QY	903	CTAGTGCTTGCTCTCCTCTTCTTTGGTGTGTCAGCTGGTCTTGGATTTTGCTATGTCAA	962
Db	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
QY	963	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAAATGATCGAAACC	1022
Db	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
QY	1023	AAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAAC	1082
Db	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
QY	1083	GATAAAACCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTCGATGCCTGGAAGCT	1142
Db	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
QY	1143	GAAGTT 1148	
Db	321	GluVal 322	
RESULT 6			

US-09-724-864-60			
; Sequence 60, Application US/09724864			
; Patent No. 6380362			
; GENERAL INFORMATION:			
; APPLICANT: Watson, James D			
; APPLICANT: Murison, James G.			
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed			
; TITLE OF INVENTION: by the polynucleotides and methods for their use.			
; FILE REFERENCE: 11000.1050U1			
; CURRENT APPLICATION NUMBER: US/09/724,864			
; CURRENT FILING DATE: 2000-11-28			
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678			
; PRIOR FILING DATE: 1999-12-23			
; NUMBER OF SEQ ID NOS: 72			
; SOFTWARE: FastSEQ for Windows Version 4.0			
; SEQ ID NO 60			
; LENGTH: 318			
; TYPE: PRT			
; ORGANISM: Mouse			
US-09-724-864-60			
Alignment Scores:			
Pred. No.:	8.65e-113	Length:	318
Score:	1103.00	Matches:	221
Percent Similarity:	79.18%	Conservative:	30
Best Local Similarity:	69.72%	Mismatches:	62
Query Match:	30.60%	Indels:	4
DB:	4	Gaps:	3
US-10-079-111-2 (1-2029) x US-09-724-864-60 (1-318)			
QY	198	AGCCTGGTGTGCTTCTCACITTCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTG	257
Db	6	SerLeuValLeuLeuLeuAlaSerIleTrpThrThrArgHisProValGlnGlyAlaAsp	25
QY	258	CGTGCAAGAGACTTTCCATCCAGGTGTCATGCAGAAATTATGGGGATCACCCTTGTGAGC	317
Db	26	LeuValGlnAspLeuSerIleSer---ThrCysArgIleMetGlyValAlaLeuValGly	44
QY	318	AAAAAGCGGAACACGACGCTGAATTCACAGAAGCTAAGGAGCCTGTAGGCTGTGGGA	377
Db	45	ArgAsnLysAsnProGlnMetAsnPheThrGluAlaAsnGluAlaCysLysMetLeuGly	64
QY	378	CTAAGTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGC	437
Db	65	LeuThrLeuAlaSerArgAspGlnValGluSerAlaGlnLysSerGlyPheGluThrCys	84
QY	438	AGCTATGGCTGGGTTGGAGATGGATTGCGTGTCTCTAGGATTAGCCCAACCCCAAG	497
Db	85	SerTyrGlyTrpValGlyGluGlnPheSerValIleProArgIlePheSerAsnProArg	104
QY	498	TGTGGAAAAAATGGGGTGGTGTCTGATTTTGGAAAGGTTCCAGTGAGCCGACAGTTTGA	557
Db	105	CysGlyLysAsnGlyLysGlyValLeuIleTrpAsnAlaProSerSerGlnLysPheLys	124
QY	558	GCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATTCAGAAAATTATCACC	617
Db	125	AlaTyrCysHisAsnSerSerAspThrTrpValAsnSerCysIleProGluIleValThr	144
QY	618	ACCAAAGATCCCATATTCAACACTCAAACTGCAACACAAACACAGAATTTATTGTCAGT	677
Db	145	ThrPheTyrProValLeuAspThrGln-----ThrProAlaThrGluPheSerValSer	162
QY	678	GACAGTACCTACTCGGTGGATCCCTTACTCTACTACAATACCTGCCCTTACTACTCCT	737
Db	163	SerSerAlaTyrLeuAlaSerSerProAspSerThrThrProValSerAlaThrThr---	181
QY	738	CCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAGTT	797
Db	182	ArgAlaProProLeuThrSerMetAlaArgLysThrLysLysIleCysIleThrGluVal	201
QY	798	TTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTTGTGTAATAAAGCAGCA	857
	:::	:::	:::

Db 202 TyrThrGluProIleThrMetAlaThrGluThrGluAlaPheValAlaSerGlyAlaAla 221
QY 858 TTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGCTCTGCTAGTGCTTGTCTC 917
Db 222 PheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeuLeuValLeuAlaLeu 241
QY 918 CTCTTCTTTTGGTGCAGCTGGTCTTGGATTTTGGCTATGTCAAAAGGTATGTGAAGCC 977
Db 242 LeuPhePheGlyAlaAlaAlaValLeuAlaValCysTyrValLysArgTyrValLysAla 261
QY 978 TTCCCTTTTACAAACAAGATCAGCAGAGGAAATGATCGAAACCAAGTAGTAAAGGAG 1037
Db 262 PheProPheThrThrLysAsnGlnGlnLysGluMetIleGluThrLysValValLysGlu 281
QY 1038 GAGAAGGCCAATGATAGCAACCTAATGAGGAATCAAAGAAAACTGATAAAACCCAGAA 1097
Db 282 GluLysAlaAspValAsnAlaAsnGluGluSerLysLysThrIleLysAsnProGlu 301
QY 1098 GAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCCTGGAAGCTGAAGTT 1148
Db 302 GluAlaLysSerProProLysThrThrValArgCysLeuGluAlaGluVal 318

RESULT 7
US-07-946-497-7
; Sequence 7, Application US/07946497
; Patent No. 5506119
; GENERAL INFORMATION:
; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut
; APPLICANT: GUENTHERT, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim
; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,497
; FILING DATE: 19921109
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 363 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: mCD44
US-07-946-497-7

Alignment Scores:
Pred. No.: 1.79e-16 Length: 363
Score: 231.50 Matches: 89
Percent Similarity: 40.90% Conservative: 57
Best Local Similarity: 24.93% Mismatches: 148

Query Match: 6.42% Indels: 63
DB: 1 Gaps: 14
US-10-079-111-2 (1-2029) x US-07-946-497-7 (1-363)
QY 225 TGGACCACGAGG-----CTCCTGGTCCAAGGCTCTTTGGCGTGCGAAGAGCCTTTCC 275
Db 6 TrpHisThrAlaTrpGlyLeuCysLeuLeuGlnLeuSerLeuAlaHisGlnGlnIleAsp 25
QY 276 ATCCAGGTGTCATGCAGAAATTATGGGATCACCCCTGTGAGCAAAAAGCGCAACGAGCAG 335
Db 26 LeuAsnValThrCysArgTyrAlaGlyValPheCysValGluLysAsnGlyArgTyrSer 45
QY 336 CTGAATTTACAGAAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGCGAAG 395
Db 46 IleSerArgThrGluAlaAlaAspLeuCysGlnAlaPheAsnSerThrLeuProThrMet 65
QY 396 GACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACTTGCAGCTATGGTGGTGGTGA 455
Db 66 AspGlnMetLysLeuAlaLeuSerLysGlyPheGluThrCysArgTyrGlyPheIle-- 84
QY 456 GATGGATTGCGTGCATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAAATGGGGTG 515
Db 85 GluGlyAsnValValIleProArgIleHisProAsnAlaIleCysAlaAlaAsnHisThr 104
QY 516 GGTGTCTCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCA 575
Db 105 GlyValTyrIleLeuValThrSerAsnThrSerHisTyrAspThrTyrCysPheAsnAla 124
QY 576 TCTGATACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAGATCCCATATTC 635
Db 125 SerAlaProProGluGluAspCys-----ThrSerValThrAspLeuPro 139
QY 636 AACACTCAAACCTGCAACACAAACAACAGAAATTTATGTGAGTGACAGTACC---TACTCG 692
Db 140 AsnSerPheAspGlyProValThrIleThrIleValAsnArgAspGlyThrArgTyrSer 159
QY 693 GTGGCATCCCTTACTCTACA-----ATACCTGCCCTACT----- 728
Db 160 LysLysGlyGluTyrArgThrHisGlnGluAspIleAspAlaSerAsnIleIleAspAsp 179
QY 729 -----ACTACTCTCTCTGCT---CCAGCTTCCACT 755
Db 180 AspValSerSerGlySerThrIleGluLysSerThrProGluGlyTyrIleLeuHisThr 199
QY 756 TCTATTCCACGGAGAAAAAATTGATTTGTGTGCACAGAAAGTTTATGGAAACTAGCACC 815
Db 200 TyrLeuProThrGluGlnProThrGlyAspGlnAspAspSerPhePheIleArgSerThr 219
QY 816 ATGCTCTACA---GAAACTGAACCATTTGTTGAAAAATAAGCAGCATTTCAAG----- 863
Db 220 LeuAlaThrArgAspArgAspSerSerLysAspSerArgGlySerSerArgThrValThr 239
QY 864 -----AATGAAGCTGCTGGGTTTGGAGGT----- 887
Db 240 HisGlySerGluLeuAlaGlyHisSerSerAlaAsnGlnAspSerGlyValThrThrThr 259
QY 888 -----GTCCCCACGGCTCTGCTAGTGTGCTGCTCTCTCTCTTC 923
Db 260 SerGlyProMetArgArgProGlnIleProGluTrpLeuIleIleLeuAlaSerLeu--- 278
QY 924 TTTGGTGTGCAGCTGGTCTTGGATTTTGTGATGTCAAAGGTATGTGAAGGCCTTCCCT 983
Db 279 LeuAlaLeuAlaLeuIleLeuAlaValCys-----IleAlaValAsnSer 293
QY 984 TTTACAAACAAGAATCAGCAGAGGAAATGATC-----GAAACCAAGTAGTAAAG 1034
Db 294 ArgArgArgCysGlyGlnLysLysLysLeuValIleAsnGlyGlyAsnGlyThrValGlu 313
QY 1035 GAGGAGAAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAAACTGATAAAACCCA 1094
Db 314 AspArgLysProSerGluLeuAsn---GlyGluAlaSerLysSerGlnGluMetValHis 332

; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,882
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,497
; FILING DATE: 19921109
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 363 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: mCD44
; US-08-478-882-7

Alignment Scores:
Pred. No.: 1.79e-16 Length: 363
Score: 231.50 Matches: 89
Percent Similarity: 40.90% Conservative: 57
Best Local Similarity: 24.93% Mismatches: 148
Query Match: 6.42% Indels: 63
DB: 2 Gaps: 14

US-10-079-111-2 (1-2029) x US-08-478-882-7 (1-363)

QY 225 TGGACCACGAGG-----CTCCTGGTCCAAGGCTCTTTGGCTGCAGAAAGAGCTTTCC 275
Db 6 TrpHisThrAlaTrpGlyLeuCysLeuLeuGlnLeuSerLeuAlaHisGlnGlnIleAsp 25
QY 276 ATCCAGGTGTCATGCAGAATTATGGGGATCACCCCTTGTGAGCAAAAAGCGGAACACGACAG 335
Db 26 LeuAsnValThrCysArgTyrAlaGlyValPheCysValGluLysAsnGlyArgTyrSer 45
QY 336 CTGAATTTACAGAAAGCTAAGGAGGCCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG 395
Db 46 IleSerArgThrGluAlaAlaAspLeuCysGlnAlaPheAsnSerThrLeuProThrMet 65
QY 396 GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGA 455
Db 66 AspGlnMetLysLeuAlaLeuSerLysGlyPheGluThrCysArgTyrGlyPheIle--- 84
QY 456 GATGGATTGCTGTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGGAAAAAATGGGGTG 515
Db 85 GluGlyAsnValValIleProArgIleHisProAsnAlaIleCysAlaAlaAsnHisThr 104
QY 516 GGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACACTCA 575
Db 105 GlyValTyrIleLeuValThrSerAsnThrSerHisTyrAspThrTyrCysPheAsnAla 124
QY 576 TCTGATACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAGATCCCATATTC 635

Db 125 SerAlaProProGluGluAspCys-----ThrSerValThrAspLeuPro 139
QY 636 AACACTCAAACCTGCAACACAAAACACAGAAATTTATTGTCAGTGACAGTACC---TACTCG 692
Db 140 AsnSerPheAspGlyProValThrIleThrIleValAsnArgAspGlyThrArgTyrSer 159
QY 693 GTGGCATCCCCCTTACTCTACA-----ATACCTGCCCTACT----- 728
Db 160 LysLysGlyGluTyrArgThrHisGlnGluAspIleAspAlaSerAsnIleIleAspAsp 179
QY 729 -----ACTACTCCTCCTGCT---CCAGCTTCCACT 755
Db 180 AspValSerSerGlySerThrIleGluLysSerThrProGluGlyTyrIleLeuHisThr 199
QY 756 TCTATTCCACGGAGAAAAAATTGATTGTGTGCACAGAAAGTTTTTATGGAAACTAGCACC 815
Db 200 TyrLeuProThrGluGlnProThrGlyAspGlnAspSerPhePheIleArgSerThr 219
QY 816 ATGTCTACA---GAAACTGAACCATTTGTTGAAATAAAAGCAGCATTCAAG----- 863
Db 220 LeuAlaThrArgAspArgAspSerSerLysAspSerArgGlySerSerArgThrValThr 239
QY 864 -----AATGAAGCTGCTGGGTTTGAGGT----- 887
Db 240 HisGlySerGluLeuAlaGlyHisSerSerAlaAsnGlnAspSerGlyValThrThrThr 259
QY 888 -----GTCCCCACGGCTCTGCTAGTGTGCTCTCTCTCTTC 923
Db 260 SerGlyProMetArgArgProGlnIleProGluTrpLeuIleIleLeuAlaSerLeu--- 278
QY 924 TTTGGTGTGCAGCTGCTTGGATTTTGTCTATGTCAAAGGTATGTGAAGGCTTCCCT 983
Db 279 LeuAlaLeuAlaLeuIleLeuAlaValCys-----IleAlaValAsnSer 293
QY 984 TTTACAAACAAGAATCAGCAGAAGGAAATGATC-----GAAACCAAGTAGTAAAG 1034
Db 294 ArgArgArgCysGlyGlnLysLysLeuValIleAsnGlyGlyAsnGlyThrValGlu 313
QY 1035 GAGGAGAAGGCCAATGATAGCAACCCCTAATAGGAATCAAGAAACATGATAAAACCCCA 1094
Db 314 AspArgLysProSerGluLeuAsn---GlyGluAlaSerLysSerGlnGluMetValHis 332
QY 1095 GAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCTGGAAGCTGAA 1145
Db 333 LeuValAsnLysGluProSerGluThrProAspGlnCysMetThrAlaAsp 349

RESULT 10

US-07-946-497-2
; Sequence 2, Application US/07946497
; Patent No. 5506119
; GENERAL INFORMATION:

; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut
; APPLICANT: GUENTHERT, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim
; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/946,497
; FILING DATE: 19921109
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 503 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-946-497-2

Alignment Scores:
Pred. No.: 4.64e-16 Length: 503
Score: 228.50 Matches: 126
Percent Similarity: 36.19% Conservative: 60
Best Local Similarity: 24.51% Mismatches: 242
Query Match: 6.34% Indels: 86
DB: 1 Gaps: 21

US-10-079-111-2 (1-2029) x US-07-946-497-2 (1-503)

QY 225 TGGACCAGCGCTCCTGGTCCAGGCTCTTTGCGTGCGAGAGAGCTTTCATCCAGGTG 284
Db 10 TrpGlyLeuLeuCysLeuLeuGlnLeuSerLeuAlaGlnGlnGlnIleAspLeuAsnIle 29
QY 285 TCATGCAGAAATTATGGGATCACCCCTTGTGAGCAAAAAGCGCAACCAGCAGCTGAATTTC 344
Db 30 ThrCysArgTyrAlaGlyValPheHisValGluLysAsnGlyArgTyrSerIleSerArg 49
QY 345 ACAGAAAGCTTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGCGCAAGGACCAAGTT 404
Db 50 ThrGluAlaAlaAspLeuCysGluAlaPheAsnThrThrLeuProThrMetAlaGlnMet 69
QY 405 GAAACAGCCTTGAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTC 464
Db 70 GluLeuAlaLeuArgLysGlyPheGluThrCysArgTyrGlyPheIle---GluGlyHis 88
QY 465 GTGGTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGTGCCTG 524
Db 89 ValValIleProArgIleHisProAsnAlaIleCysAlaAlaAsnAsnThrGlyValTyr 108
QY 525 ATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACATCATCTGATACT 584
Db 109 IleLeuLeuAlaSerAsnThrSerHisTyrAspThrTyrCysPheAsnAlaSerAlaPro 128
QY 585 TGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAA 644
Db 129 LeuGluGluAspCys-----ThrSerValThrAspLeuProAsnSerPhe 143
QY 645 ACTGCAACACAAACACAGAATTTATTGTCAGTGACAGTACC---TACTCGTGGCATCC 701
Db 144 AspGlyProValThrIleThrIleValAsnArgAspGlyThrArgTyrSerLysLysGly 163
QY 702 CCTTACTCTACA-----ATACCTGCCCTACT----- 728
Db 164 GluTyrArgThrHisGlnGluAspIleAspAlaSerAsnIleIleAspGluAspValSer 183
QY 729 -----ACTACTCTCCTGCT---CCAGCTTCCACTTCTATTCCA 764
Db 184 SerGlySerThrIleGluLysSerThrProGluGlyTyrIleLeuHisThrAspLeuPro 203
QY 765 CGGAGAAAAAATTGATTGTGTGCACAGAAGTTTTTATGGAAACTAGCACCATTGTCTACA 824
Db 204 ThrSerGlnProThrGlyAspArgAspAlaPhePheIleGlySerThrLeuAlaThr 223

QY 825 ---GAAACTGAACCATTTGTTGAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGTTT 881
Db 224 IleAlaThrThrProTrpValSerAlaHisThrLysGlnAsnGlnGluArgThrGlnTrp 243
QY 882 GGAGGTGTC-----CCCACGGCTCTGTAGTGTCTTGGCTCTCCTCTCTTTGGTGCT 932
Db 244 AsnProIleHisSerAsnProGluValLeuLeuGlnThrThrThrArgMetThrAspIle 263
QY 933 GCAGCTGCTCTTGGATTTTGTCTATGTCAAAAGGTATGTGAAG-----GCCTTCCCTTTT 986
Db 264 AspArgAsnSerThrSerAlaHisGlyGluAsnTrpThrGlnGluProGlnProPhe 283
QY 987 ACAACAAGAATCAGCAGAGGAA-----ATGATC 1016
Db 284 AsnAsnHisGluTyrGlnAspGluGluThrProHisAlaThrSerThrTrpAla 303
QY 1017 GAAACCAAGTAGTAAAGGAGGAGGAGGCCAATGATAGCAACCCTAATGAGGAATCAAAG 1076
Db 304 AspProAsnSerThrThrGluGluAlaAlaThrGlnLysGluLysTrpPheGluAsnGlu 323
QY 1077 AAAACTGATAAAAACCCA-----GAAGAGTCCAAGAGTCCAAGCAAAACTACC 1124
Db 324 TrpGlnGlyLysAsnProProThrProSerGluAspSerHisValThrGluGlyThrThr 343
QY 1125 GTCCGATGCCTGGAAGCTGAAGTTTAGATGAGA-----CAGAAATGAGGAGACACA 1175
Db 344 AlaSerAlaHisAsnAsnHisProSerGlnArgMetThrThrGlnSerGlnGluAspVal 363
QY 1176 CCTGAGGCTGGTTTCTTTTCATGTCCTTACCCTGCCCGCAGCTGGGAAATCAAAAGGCC 1235
Db 364 SerTrpThrAspPheAsp---ProIleSerHisProMetGlyGln-----Gly 379
QY 1236 AAAGAACCAAGAAAGAAAGTCCACCTTGGTTCTTAAGTGAATCAGCTCAGGACTGCCA 1295
Db 380 HisGlnThrGluSerLysGlyHis-----SerSerGly---Asn 391
QY 1296 TTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCT-----CCTTATTGAACCCCTGTC 1349
Db 392 GlnAspSerGlyValThrThrThrSerGlyProAlaArgArgProGlnIle---ProGlu 410
QY 1350 TGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCTTTCTAGCCTGGCTATGTCCTA 1409
Db 411 TrpLeu--IleIleLeuAlaSerLeuLeuAlaLeuAlaLeuIleLeuAlaValCys--- 428
QY 1410 ATAATATCCCACCTGGGAGAAAGGAGTTTGCAAAGTCCAAGGACCTAAACATCTCATCA 1469
Db 429 -----IleAlaValAsnSerArgArgCysGlyGlnLysLysLeuVal- 444
QY 1470 GTATCCAGTGGTAAA-----AAGGCC 1490
Db 445 IleAsnSerGlyAsnGlyThrValGluAspArgLysProSerGluLeuAsnGlyGluAla 464
QY 1491 TCCTGGCTGCTGAGGCTAGGTGGTTGAAAGCCAAGGAGTCACTGAGACC---AAGGCT 1547
Db 465 SerLysSerGlnGluMetValHisLeuValAsnLysGluProThrGluThrProAspGln 484
QY 1548 TTCTCTACTGATTCGCGAGCTCAGACCCCTTTCTTCA 1583
Db 485 PheMetThrAlaAspGluThrArgAsnLeuGlnSer 496

RESULT 11

US-08-483-322-2
; Sequence 2, Application US/08483322
; Patent No. 5760178
; GENERAL INFORMATION:
; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut
; APPLICANT: GUENTHERT, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim
; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY

Db 485 PheMetThrAlaAspGluThrArgAsnLeuGlnSer 496

RESULT 12

US-08-478-882-2

; Sequence 2, Application US/08478882

; Patent No. 5885575

; GENERAL INFORMATION:

; APPLICANT: HERRLICH, Peter

; APPLICANT: PONTA, Helmut

; APPLICANT: GUENTHERT, Ursula

; APPLICANT: MATZKU, Siegfried

; APPLICANT: WENZL, Achim

; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA

; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,

; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington, D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/478,882

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/946,497

; FILING DATE: 19921109

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 16915/145

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)672-5300

; TELEFAX: (202)672-5399

; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 503 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-478-882-2

Alignment Scores:

Pred. No.:	4.64e-16	Length:	503
Score:	228.50	Matches:	126
Percent Similarity:	36.19%	Conservative:	60
Best Local Similarity:	24.51%	Mismatches:	242
Query Match:	6.34%	Indels:	86
DB:	2	Gaps:	21

US-10-079-111-2 (1-2029) x US-08-478-882-2 (1-503)

QY 225 TGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTCAGAAAGAGCTTTCCATCCAGGTG 284

Db 10 TrpGlyLeuLeuCysLeuLeuGlnLeuSerLeuAlaGlnGlnIleAspLeuAsnIle 29

QY 285 TCATGCAGAATTATGGGGATCACCCCTTGTGAGCAAAAAGCGGAACCAGCAGCTGAATTTC 344

Db 30 ThrCysArgTyrAlaGlyValPheHisValGluLysAsnGlyArgTyrSerIleSerArg 49

QY 345 ACAGAAAGCTAAGGAGGCCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTT 404

Db 50 ThrGluAlaAlaAspLeuCysGluAlaPheAsnThrThrLeuProThrMetAlaGlnMet 69

QY 405 GAAACAGCCCTTGAAAGCTAGCTTTTGAACCTTGACAGCTATGGTGGTGGAGATGGATTTC 464

Db 70 GluLeuAlaLeuArgLysGlyPheGluThrCysArgTyrGlyPheIle---GluGlyHis 88

QY 465 GTGGTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGTGGTGTCTCTG 524

Db 89 ValValIleProArgIleHisProAsnAlaIleCysAlaAlaAsnAsnThrGlyValTyr 108

QY 525 ATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCCTATTGTTACAACCTCATCTGATACT 584

Db 109 IleLeuLeuAlaSerAsnThrSerHisTyrAspThrTyrCysPheAsnAlaSerAlaPro 128

QY 585 TGGACTAACTCGTGCATTCCAGAAATATCACCACCACCAAGATCCCATATTCAACACTCAA 644

Db 129 LeuGluGluAspCys-----ThrSerValThrAspLeuProAsnSerPhe 143

QY 645 ACTGCAACACAAAACACAGAATTATTGTTCAGTGACGTACC---TACTCGGTGGCATCC 701

Db 144 AspGlyProValThrIleThrIleValAsnArgAspGlyThrArgTyrSerLysLysGly 163

QY 702 CCTTACTCTACA-----ATACCTGCCCTACT----- 728

Db 164 GluTyrArgThrHisGlnGluAspIleAspAlaSerAsnIleAspGluAspValSer 183

QY 729 -----ACTACTCTCTCTGCT---CCAGCTTCCACTTCTATTCCA 764

Db 184 SerGlySerThrIleGluLysSerThrProGluGlyTyrIleLeuHisThrAspLeuPro 203

QY 765 CGGAGAAAAAATTTGATTGTGTACAGAAGTTTATTGGAACACTACACCATGTCTACA 824

Db 204 ThrSerGlnProThrGlyAspArgAspAlaPhePheIleGlySerThrLeuAlaThr 223

QY 825 ---GAAACTGAACCATTTGTTGAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTT 881

Db 224 IleAlaThrThrProTrpValSerAlaHisThrLysGlnAsnGlnGluArgThrGlnTrp 243

QY 882 GGAGGTGTC-----CCCACGGCTCTGCTAGTGTCTTGCTCTCTCTTCTTTGGTGCT 932

Db 244 AsnProIleHisSerAsnProGluValLeuLeuGlnThrThrThrArgMetThrAspIle 263

QY 933 GCAGCTGGTCTGGATTTTGCTATGTCAAAAAGGTATGTGAAG-----GCCTTCCCTTTT 986

Db 264 AspArgAsnSerThrSerAlaHisGlyGluAsnTrpThrGlnGluProGlnProPhe 283

QY 987 ACAAACAGAATCAGCAGAAAGAA-----ATGATC 1016

Db 284 AsnAsnHisGluTyrGlnAspGluGluThrProHisAlaThrSerThrThrTrpAla 303

QY 1017 GAAACCAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAAG 1076

Db 304 AspProAsnSerThrThrGluGluAlaAlaThrGlnLysGluLysTrpPheGluAsnGlu 323

QY 1077 AAAACTGATAAAACCCA-----GAAAGATCCAAGAGTCCCAAGCAAAAACCTACC 1124

Db 324 TrpGlnGlyLysAsnProProThrProSerGluAspSerHisValThrGluGlyThrThr 343

QY 1125 GTGCGATGCCCTGGAAGCTGAAGTTTATAGATGAGA-----CAGAAATGAGGAGACACA 1175

Db 344 AlaSerAlaHisAsnAsnHisProSerGlnArgMetThrThrGlnSerGlnGluAspVal 363

QY 1176 CCTGAGGCTGGTTTCTTTCATGCTCCTTACCTGCTCCAGTGGGGAATCAAAAGGGCC 1235

Db 364 SerTrpThrAspPheAsp---ProIleSerHisProMetGlyGln-----Gly 379

QY 1236 AAAGAACCAAGAGAAAGTCCACCCCTTGGTTCTTAAGTGAATCAGCTCAGGACTGCCA 1295

Db 380 HisGlnThrGluSerLysGlyHis-----SerSerGly---Asn 391

QY 1296 TTGGACTATGGAGTGCACCAAGAGAATGCCCTTCT-----CCTTATTGTAACCTGTC 1349

Db 392 GlnAspSerGlyValThrThrThrSerGlyProAlaArgProGlnIle---ProGlu 410

QY 1350 TGGATCCTATCTCTCTACCTCCAAAGCTTCCCACGGCCTTTCTAGCCTGGCTATGCTTA 1409

Db 411 TrpLeu--IleIleLeuAlaSerLeuAlaLeuAlaLeuIleLeuAlaValCys--- 428
QY 1410 ATAATATCCACTGGGAGAAAGGAGTTTTCGAAAGTGCAGGACCTAAACATCTCATCA 1469
Db 429 -----IleAlaValAsnSerArgArgCysGlyGlnLysLysLeuVal- 444
QY 1470 GTATCCAGTGGTAAA-----AAGGCC 1490
Db 445 IleAsnSerGlyAsnGlyThrValGluAspArgLysProSerGluLeuAsnGlyGluAla 464
QY 1491 TCCTGGCTGTCTGAGGCTAGGTGGTGGTTGAAAGCCAGGAGTCACTGAGACC---AAGGCT 1547
Db 465 SerLysSerGlnGluMetValHisLeuValAsnLysGluProThrGluThrProAspGln 484
QY 1548 TTCTCTACTGATTCGCGAGCTCAGACCCTTTCTTCA 1583
Db 485 PheMetThrAlaAspGluThrArgAsnLeuGlnSer 496

RESULT 13
US-08-892-880-3
; Sequence 3, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-892-880-3
Alignment Scores:
Pred. No.: 1.02e-15 Length: 339
Score: 224.50 Matches: 83
Percent Similarity: 41.39% Conservative: 54
Best Local Similarity: 25.08% Mismatches: 157
Query Match: 6.23% Indels: 37
DB: 2 Gaps: 11

US-10-079-111-2 (1-2029) x US-08-892-880-3 (1-339)

QY 225 TGGACCACGAGGCTCCTGGTCCAAAGGCTCTTTGGCTGGAGAAAGAGCTTTCCATCCAGGTG 284
Db 10 TrpGlyLeuLeuCysLeuLeuGlnLeuSerLeuAlaGlnGlnIleAspLeuAsnIle 29
QY 285 TCATGCAGAAATTATGGGATCACCCCTTGTGAGCAAAAAGCGCAACAGCAGCTGAATTTC 344
Db 30 ThrCysArgTyrAlaGlyValPheHisValGluLysAsnGlyArgTyrSerIleSerArg 49
QY 345 ACAGAAAGCTAAGGAGGCTGTAGGCTGTGGGACTAAGTTTGGCCGGCAAGGACCAAGTT 404
Db 50 ThrGluAlaAlaAspLeuCysGluAlaPheAsnThrThrLeuProThrMetAlaGlnMet 69
QY 405 GAAACAGCCCTTGAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTTC 464
Db 70 GluLeuAlaLeuArgLysGlyPheGluThrCysArgTyrGlyPheIle---GluGlyHis 88
QY 465 GTGGTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCCTG 524
Db 89 ValValIleProArgIleHisProAsnAlaIleCysAlaAlaAsnThrGlyValTyr 108
QY 525 ATTTGGAAGGTTCCAGTGAGCGGACAGATTTCAGCCCTATTGTTACAACTCATCTGATACT 584
Db 109 IleLeuLeuAlaSerAsnThrSerHisTyrAspThrTyrCysPheAsnAlaSerAlaPro 128
QY 585 TGGACTAACTCGTGCATTCCAGAAATTATCACCAACACCAAGATCCCATATTTCAACACTCAA 644
Db 129 LeuGluGluAspCys-----ThrSerValThrAspLeuProAsnSerPhe 143
QY 645 ACTGCAACACAAACAAACAGAAATTTATTGTCAGTGACAGTACC---TACTCGGTGGCATCC 701
Db 144 AspGlyProValThrIleThrIleValAsnArgAspGlyThrArgTyrSerLysLysGly 163
QY 702 CCTTACTCTACA-----ATACCTGCCCCCTACT----- 728
Db 164 GluTyrArgThrHisGlnGluAspIleAspAlaSerAsnIleIleAspGluAspValSer 183
QY 729 -----ACTACTCCTCCTGCT---CCAGCTTCCACTTCTATTCCA 764
Db 184 SerGlySerThrIleGluLysSerThrProGluGlyTyrIleLeuHisThrAspLeuPro 203
QY 765 CGGAGAAAAAAATTGATTTGTGTACAGAAAGTTTATGGAAGAACTAGCACCATTGTCTACA 824
Db 204 ThrSerGlnProThrGlyAspArgAspAlaPhePheIleGlySerThrLeuAlaThr 223
QY 825 ---GAAACTGAACCATTTGTTGAAAAATAAAGCAGCATTCAGAAGTGAAGCTGCTGGTTT 881
Db 224 GlyHisSerSerGlyAsnGlnAspSerGlyValThrThrThrSerGlyProAlaArgArg 243
QY 882 GGAGGTGTCCCCACGGCTCTGCTAGTGTCTGCTCTCTCTCTTCTTTGGTGTGCAGCTGGT 941
Db 244 ProGlnIleProGluTrpIleIleIleLeuAlaSerLeu---LeuAlaLeuAlaLeuIle 262
QY 942 CTTGGATTTTGTCTATGTCAAAAGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAAATCAG 1001
Db 263 LeuAlaValCys-----IleAlaValAsnSerArgArgCysGlyGln 277
QY 1002 CAGAAGGAAATGATCGAAACCAAA-----GTAGTAAAGGAGGAGAGGCAATGAT 1052
Db 278 LysLysLysLeuValIleAsnSerGlyAsnGlyThrValGluAspArgLysProSerGlu 297
QY 1053 AGCAACCCCTAATGAGGAATCAAAGAAAACTGATAAAAAACCCAGAGAGTCCAAAGATCCA 1112
Db 298 LeuAsn---GlyGluAlaSerLysSerGlnGluMetValHisLeuValAsnLysGluPro 316
QY 1113 AGCAAAACTACCGTGCATGCCTGGAAGCTGAA 1145
Db 317 ThrGluThrProAspGlnPheMetThrAlaAsp 327

RESULT 14
5504194-2

;Patent No. 5504194

; APPLICANT: ST.JOHN, THOMAS P.;GALLATIN, W. MICHAEL;IDZERDA,

REJEAN
; TITLE OF INVENTION: LYMPHOCYTE ADHESION RECEPTOR FOR HIGH
; ENDOTHELIAL, CD44
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION NUMBER: US/07/884,624
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 628,646
; FILING DATE: 12-DEC-1990
; APPLICATION NUMBER: 325,224
; FILING DATE: 17-MAR-1989
; SEQ ID NO:2:
; LENGTH: 362
5504194-2

Alignment Scores:
Pred. No.: 1.77e-15 Length: 362
Score: 222.50 Matches: 92
Percent Similarity: 37.40% Conservative: 43
Best Local Similarity: 25.48% Mismatches: 127
Query Match: 99 Indels: 99
DB: 16 Gaps: 16

US-10-079-111-2 (1-2029) x 5504194-2 (1-362)

QY 240 CTGGTCCAAGGCTCTTTGCGTGCAGAGAGCTTCCAGGTGTCAGCAAGATTATG 299
Db 14 LeuValGlnLeuSerLeu-----AlaGlnIleAspLeuAsnIleThrCysArgPheGlu 31
QY 300 GGGATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTTCACAGAGCTAAGGAG 359
Db 32 GlyIleTyrHisValGluLysAsnGlyArgTyrSerIleSerArgThrGluAlaAlaAsp 51
QY 360 GCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAGGACCAAGTTGAAACAGCCTTGAAA 419
Db 52 LeuCysLysAlaPheAsnSerThrLeuProThrMetAlaGlnMetGluLysAlaLeuSer 71
QY 420 GCTAGCTTTGAAACTTGACGCTATGGCTGGTGGAGATGGATTGCTGGTCACTCTAGG 479
Db 72 IleGlyPheGluThrCysArgTyrGlyPheIle---GluGlyHisValIleProArg 90
QY 480 ATTAGCCCAACCCCAAGTGTGGGAAAAATGGGTGGTGTCTGATTGGGAAGGTCCA 539
Db 91 IleHisProAsnSerIleCysAlaAlaAsnAsnThrGlyValTyrIleLeuThrSerAsn 110
QY 540 GTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATCTTGGACTAAGTCTGTC 599
Db 111 ThrSer--GlnTyrAspThrTyrCysPheAsnAlaSerAlaProProGlyGluAspCys 129
QY 600 ATCCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 659
Db 130 -----ThrSerValThrAspLeuProAsnAlaPheAspGlyProIleThr 144
QY 660 ACAGAAATTATTGTCAGTGACAGTACC---TACTCGGTGGCATCCCCTTACTCTACAATA 716
Db 145 IleThrIleValAsnArgAspGlyThrArgTyrValLysLysGlyGluTyrArgThrAsn 164
QY 717 CCT-----GCCCTACT----- 728
Db 165 ProGluAspIleAsnProSerSerProThrAspAspValSerSerGlySerSerSer 184
QY 729 -----ACTACTCCCTCT 740
Db 185 GluArgSerSerThrLeuGlyGlyTyrIlePheTyrAsnHisPheSerThrSerProPro 204
QY 741 GCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATTGATTGTGTACAGAAAGTTTTT 800
Db 205 IleProAspGluAspGly----- 210
QY 801 ATGGAAACTAGCACCATGTCTACAGAACTGAACCATTTGTTGAAATAAAGCAGCATTC 860
Db 211 ---ProTrpIleThrAspSerThrAspArgThrProAlaThrArgAspGlnGlyAlaPhe 229

QY 861 AAG-----AATGAAGCTGCTGGGTTT----- 881
Db 230 AspProSerGlyGlySerHisThrThrHisGlySerGluSerAlaGlyHisSerHisGly 249
QY 882 -----GGAGGT-----GTCCCCACG 896
Db 250 SerArgGluGlyGlyAlaAsnThrThrSerGlyProLeuArgThrProGlnIleProGlu 269
QY 897 GCTCTGCTAGTCTTGTCTCTCTCTCTCTTTGGTGTGCTGCAGCTGCTTGGATTTTGGCTAT 956
Db 270 TrpLeuIleIleLeuAlaSerLeu---LeuAlaLeuAlaLeuIleLeuAlaValCys--- 287
QY 957 GTCAAAAGGTATGTGAAGGCCCTTCCCTTTTACAAAACAAGAAATCAGCAGAAAGAAATGATC 1016
Db 288 -----IleAlaValAsnSerArgArgCysGlyGlnLysLysLysLeuVal 303
QY 1017 GAAACCAAA-----GTAGTAAAGGAGGAGGAGGCAATGATAGCAACCCCTAATGAG 1067
Db 304 IleAsnAsnGlyAsnGlyAlaValGluAspArgLysSerSerGlyLeuAsn---GlyGlu 322
QY 1068 GAATCAAGAAACTGATAAA-----AACCCAGAAAGAGTCCAAAGAGTCCCAAGC 1115
Db 323 AlaSerLysSerGlnGluMetValHisLeuValAsnLysGluSerSerGluThrProAsp 342
QY 1116 AAA 1118
Db 343 Gln 343
RESULT 15
US-07-946-497-6
; Sequence 6, Application US/07946497
; Patent No. 5506119
; GENERAL INFORMATION:
; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut
; APPLICANT: GUENTHERT, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim
; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,497
; FILING DATE: 19921109
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: hCD44

US-07-946-497-6									
Alignment Scores:									
Pred. No.:	9.1e-14	Length:	361						
Score:	207.00	Matches:	83						
Percent Similarity:	38.24%	Conservative:	47						
Best Local Similarity:	24.41%	Mismatches:	144						
Query Match:	5.74%	Indels:	66						
DB:	1	Gaps:	14						
US-10-079-111-2 (1-2029) x US-07-946-497-6 (1-361)									
QY	255	TTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGATCACCCTTTGTG	314						
Db	17	LeuSerLeuAlaGlnIleAspLeuAsnIleThrCysArgPheAlaGlyValPheHisVal	36						
QY	315	AGCAAAAGGCGAACACAGCAGCTGAATTTACAGAAAGCTAAGGAGGCCTGTAGGCTGCTG	374						
Db	37	GluLysAsnGlyArgTyrSerIleSerArgThrGluAlaAlaAspLeuCysLysAlaPhe	56						
QY	375	GGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACT	434						
Db	57	AsnSerThrLeuProThrMetAlaGlnMetGluLysAlaLeuSerIleGlyPheGluThr	76						
QY	435	TGCAGCTATGGCTGGGTGGAGATGGATTGCTGGTCATCTCTAGGATTAGCCCAACCCC	494						
Db	77	CysArgTyrGlyPheIle---GluGlyHisValValIleProArgIleHisProAsnSer	95						
QY	495	AAGTGTGGGAAAAAATGGGTGGGTGCTCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTT	554						
Db	96	IleCysAlaAlaAsnAsnThrGlyValTyrIleLeuThrTyrAsnThrSer---GlnTyr	114						
QY	555	GCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATTCAGAAATTATC	614						
Db	115	AspThrTyrCysPheAsnAlaSerAlaProProGluGluAspCys-----	129						
QY	615	ACCACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACAAGAAATTTATTGTC	674						
Db	130	ThrSerValThrAspLeuProAsnAlaPheAspGlyProIleThrIleThrIleValAsn	149						
QY	675	AGTGACAGTACC--TACTCGGTGGCATCCCTTACTCTACAATACCTGCC-----	722						
Db	150	ArgAspGlyThrArgTyrValGlnLysGlyGluTyrArgThrAsnProGluAspIleTyr	169						
QY	723	CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	782						
Db	170	ProSerAsnProThrAspAspValSerSerGlySerSerSerGluArgSerSerThr	189						
QY	783	TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATG-----	818						
Db	190	SerGlyGlyTyrIlePheTyrThrPheSerThrValHisProIleProAspGluAspSer	209						
QY	819	-----TCTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCATTC--	860						
Db	210	ProTrpIleThrAspSerThrAspArgIleProAlaThrArgAspGlnAspThrPheHis	229						
QY	861	-----AAGAATGAAGCTGCTGGGTTT-----	881						
Db	230	ProSerGlyGlySerHisThrThrHisGluSerGluSerAspGlyHisSerHisGlySer	249						
QY	882	-----GGAGGT-----	899						
Db	250	GlnGluGlyGlyAlaAsnThrThrSerGlyProIleArgThrProGlnIleProGluTrp	269						
QY	900	CTGCTAGTGTCTCTCCTCTCTTCTTTGGTGTGTCAGCTGGTCTTGGATTTTGCTATGTC	959						
Db	270	LeuIleIleLeuAlaSerLeu---LeuAlaLeuAlaLeuIleLeuAlaValCys-----	286						
QY	960	AAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAA	1019						
Db	287	-----IleAlaValAsnSerArgArgCysGlyGlnLysLysLeuValIle	303						
QY	1020	ACCAAA-----GTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAA	1070						

Db	304	AsnSerGlyAsnGlyAlaValGluAspArgLysProSerGlyLeuAsn---GlyGluAla	322
QY	1071	TCAAAGAAAACTGATAAA-----AACCAGAAAGAGTCCAAGAGTCCAAGCAAA	1118
Db	323	SerLysSerGlnGluMetValHisLeuValAsnLysGluSerSerGluThrProAspGln	342
Search completed: September 13, 2004, 10:33:31			
Job time : 53.5 secs			

B/gnk